



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 210734

TO: Manjunath N Rao
Location: REM-2A01/2C70
Art Unit: 1652
Wednesday, December 20, 2006
Case Serial Number: 10/616101

From: Usha Shrestha
Location: Biotech-Chem Library
REM-1A64
Phone: (571)272-3519

Usha.shrestha@uspto.gov

Search Notes

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Usha Shrestha
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-3519

*Please do not
change the order of pages
when scanning.
Thanks*

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12-759
STIC-Biotech/ChemLib

210734

From: Chan, Christina
Sent: 77025 Monday, December 18, 2006 8:56 AM
To: Rao, Manjunath N.; STIC-Biotech/ChemLib
Subject: RE: REquest for RUSH sequeunce search for case No. 10/616101

CRFE

~~Please Rush. Thanks. Chris~~

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Rao, Manjunath N.
Sent: Friday, December 15, 2006 2:23 PM
To: Chan, Christina
Subject: REquest for RUSH sequeunce search for case No. 10/616101

12/18
✓

Hello Christina,

Please authorize the search request below as RUSH. The reason being this is an amended case and applicants have now included SEQ ID NO for the claimed polypeptides.

Many Thanks
-Manjunath

Manjunath N. Rao, Ph.D.
Primary Examiner, Art Unit 1652
Room 2A01, Remsen Bldg.
United States Patent and Trademark Office
400, Dulany St.
Alexandria, VA 22314
Phone: 571-272-0939
Fax: 571-273-0939

2C70

1-3797na
2-3816na
3-1065aa
4-1240aa
LB

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 12-22-06
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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--
From: Manjunath N. Rao
Art Unit 1652, Room 2A01
Mail Box in Room 2C70
Phone: 272-0939

Date: 12-15-06

Please search the following as soon as possible for application with serial number 10/616101

1. SEQ ID NO: 1, 2 against all commercial nucleic acid sequence databases, issued patents/published applications nucleic acid sequence database and pending application nucleic acid sequence database. Please provide a print of results

2. SEQ ID NO: 3 and 4 against all commercial amino acid sequence databases, issued patents/published applications amino acid sequence database and pending application amino acid sequence database. Please provide a print of results.

If you have any questions please call me at the above phone number.

Thanks

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2006, 12:06:29 ; Search time 20529.6 Seconds
(without alignments)
11827.212 Million cell updates/sec

Title: US-10-616-101-1
Perfect score: 3797
Sequence: 1 ctttgaagacactggatttc.....cctttgctgaaaaa 3797

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb env.*
- 2: gb pat.*
- 3: gb ph.*
- 4: gb pl.*
- 5: gb pr.*
- 6: gb ro.*
- 7: gb sts.*
- 8: gb sv.*
- 9: gb un.*
- 10: gb vi.*
- 11: gb ov.*
- 12: gb htg.*
- 13: gb in.*
- 14: gb om.*
- 15: gb ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3797	100.0	3797	2	AR392872 Sequence
2	3797	100.0	3797	2	AR653623 Sequence
3	3393.4	89.4	3816	2	AR392873 Sequence
4	3393.4	89.4	3816	2	AR653624 Sequence
5	3388.8	89.2	4275	2	AR361486 Sequence
6	3388.8	89.2	6028	5	AF309033 Homo sapi
7	3388.8	89.2	6123	2	AX057579 Sequence
8	3387.2	89.2	3815	5	AF329696 Homo sapi
9	3387.2	89.2	4127	2	AX062241 Sequence
10	3387.2	89.2	4406	2	AX062247 Sequence
11	3387.2	89.2	4992	2	AX062275 Sequence
12	3387.2	89.2	5002	2	AX062273 Sequence
13	3387.2	89.2	5075	2	AR578380 Sequence
14	3387.2	89.2	5810	5	AF264912 Homo sapi
15	3387.2	89.2	6018	2	AR584137 Sequence
16	3387.2	89.2	6189	2	CQ896544 Sequence
17	3387.2	89.2	6189	2	CS019687 Sequence
18	3387.2	89.2	6189	2	CS023798 Sequence

19	3387.2	89.2	6189	5	AF438201	AF438201 Homo sapi
20	3386	89.2	3394	2	AR352002	AR352002 Sequence
21	3386	89.2	3394	2	AX133694	AX133694 Sequence
22	3382.8	89.1	4512	2	AR232161	AR232161 Sequence
23	3382.8	89.1	4512	2	AX076213	AX076213 Sequence
24	3338.4	87.9	4295	5	AF305081	AF305081 Homo sapi
25	3300.4	86.9	3501	5	AF342982	AF342982 Homo sapi
26	3297	86.8	3400	2	BD075726	BD075726 Potential
27	3297	86.8	3400	2	AX029397	AX029397 Sequence
28	3296.2	86.8	3508	2	AX062142	AX062142 Sequence
29	3291.8	86.7	3498	2	AR232162	AR232162 Sequence
30	3291.8	86.7	3498	2	AX076214	AX076214 Sequence
31	2969.6	78.2	4493	2	AR361484	AR361484 Sequence
32	2968.2	78.2	4297	2	AR361485	AR361485 Sequence
33	2774.6	73.1	5005	2	AX052530	AX052530 Sequence
34	2439.8	64.3	2971	2	AX062233	AX062233 Sequence
35	2439.8	64.3	3353	2	AX062229	AX062229 Sequence
36	2403.2	63.3	3930	11	AY142107	AY142107 Gallus ga
37	2357.8	62.1	3799	2	AX062231	AX062231 Sequence
38	1922.4	50.6	4130	5	HSM804989	AL833676 Homo sapi
39	1839.8	48.5	4054	6	BC057370	BC057370 Mus muscu
40	1813.4	47.8	3984	2	AX062144	AX062144 Sequence
41	1813.4	47.8	4134	2	BD235110	BD235110 Tankyrase
42	1813.4	47.8	4134	2	AR274521	AR274521 Sequence
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44	1813.4	47.8	4134	2	AX467061	AX467061 Sequence
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ALIGNMENTS

RESULT 1
AR392872
LOCUS AR392872 3797 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6617102.
ACCESSION AR392872
VERSION AR392872.1 GI:40118097
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3797)
AUTHORS Luo, Y., Chan, E., Xu, X., Huang, B. and Ososovskaya, V.
TITLE Tankyrase H, compositions involved in the cell cycle and methods of use
JOURNAL Patent: US 6617102-A 1 09-SEP-2003;
Rigel Pharmaceuticals, Inc.; South San Francisco, CA
FEATURES
source 1. 3797
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN	Query Match	Best Local Similarity	Score 3797;	DB 2;	Length 3797;
		100.0%;	100.0%;	0;	0;
		Matches 3797;	Conservative	0;	Mismatches
Qy	1	CTTTGAAGACACTGGATTTTCATCTTTTGCCTGGGGTTATCTCTGTGTCTCACTACAT	60		
Db	1	CTTTGAAGACACTGGATTTTCATCTTTTGCCTGGGGTTATCTCTGTGTCTCACTACAT	60		
Qy	61	AGACAAATATTAGCTGTGAGCAGATCTTTTGTGCTTCTGTAGTCCCTAGTTTGTAG	120		
Db	61	AGACAAATATTAGCTGTGAGCAGATCTTTTGTGCTTCTGTAGTCCCTAGTTTGTAG	120		
Qy	121	CAGAAACATCTGTGAGATAGATGTGGAAAGGAATCTAGCAAGAGTTTGTCTACTGTA	180		
Db	121	CAGAAACATCTGTGAGATAGATGTGGAAAGGAATCTAGCAAGAGTTTGTCTACTGTA	180		
Qy	181	TCATAAGGTTGTGATTTACATATTTAAGTTTATCTTTTGAACATCTGAAATGTATACA	240		
Db	181	TCATAAGGTTGTGATTTACATATTTAAGTTTATCTTTTGAACATCTGAAATGTATACA	240		

Qy	241	TACTAAATATGACAGAACTCTATTTGTAGAGTGAGAAACATTTTGAACTTTGAGCTTCAGTC	300
Ds	241	TACTAAATATGACAGAACTCTATTTGTAGAGTGAGAAACATTTTGAACTTTGAGCTTCAGTC	300
Qy	301	ACTTATTTTGTATTTCTTTCTTTGAGGTTAGCAGTAGTACCAACCAAGCAGCTGTAGGT	360
Ds	301	ACTTATTTTGTATTTCTTTCTTTGAGGTTAGCAGTAGTACCAACCAAGCAGCTGTAGGT	360
Qy	361	ACCACTGCTGTAGTGAGAGTCCCTCTGGCTTTATCATTTAAGGTTTTGGCGGAAAGA	420
Ds	361	ACCACTGCTGTAGTGAGAGTCCCTCTGGCTTTATCATTTAAGGTTTTGGCGGAAAGA	420
Qy	421	CGTAGTGAATATTTGCTTTCAAGATGTTGCAAGTGTCCAAGCAGTGAATGATGGGGCCT	480
Ds	421	CGTAGTGAATATTTGCTTTCAAGATGTTGCAAGTGTCCAAGCAGTGAATGATGGGGCCT	480
Qy	481	TATTCCTCTTCATTAATGATGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCCTTTTGGC	540
Ds	481	TATTCCTCTTCATTAATGATGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCCTTTTGGC	540
Qy	541	ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATCTCTCTCCATGAAGCTGC	600
Ds	541	ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATCTCTCTCCATGAAGCTGC	600
Qy	601	AATTAAGGAAGATTTGATTTTGCATTTGCTGTTACAGATGGAGCTGAGCCAAACAT	660
Ds	601	AATTAAGGAAGATTTGATTTTGCATTTGCTGTTACAGATGGAGCTGAGCCAAACAT	660
Qy	661	CGGAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCCATCTGCCAAGCAGTGCT	720
Ds	661	CGGAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCCATCTGCCAAGCAGTGCT	720
Qy	721	TACTGGTGAATATAAGAAAGATGAACCTTTAGAAAGTCCAGGAGTGCAATGAAGAAA	780
Ds	721	TACTGGTGAATATAAGAAAGATGAACCTTTAGAAAGTCCAGGAGTGCAATGAAGAAA	780
Qy	781	AATGATGCTCTACTCACACCATTAATAGTCAACTGCCACCGCAAGTGAATGCAAGAAATC	840
Ds	781	AATGATGCTCTACTCACACCATTAATAGTCAACTGCCACCGCAAGTGAATGCAAGAAATC	840
Qy	841	AACGCCATTAATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTTTACTGCA	900
Ds	841	AACGCCATTAATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTTTACTGCA	900
Qy	901	ACATGGAGCTGATGCTCAATGCTAAAGATAAAGGTGATCTGGTACCATTTACAAATGCTG	960
Ds	901	ACATGGAGCTGATGCTCAATGCTAAAGATAAAGGTGATCTGGTACCATTTACAAATGCTG	960
Qy	961	TTCTTATGGTCAATTAAGTAAGTAACTGAACTTTTGGTCAAGCATGGTGCCTGTGTAATGC	1020
Ds	961	TTCTTATGGTCAATTAAGTAAGTAACTGAACTTTTGGTCAAGCATGGTGCCTGTGTAATGC	1020
Qy	1021	AATGGACTTGGCAATTTCACTCTCTTCATGAGGCAGCTTCTAAGACAGGTTGAGT	1080
Ds	1021	AATGGACTTGGCAATTTCACTCTCTTCATGAGGCAGCTTCTAAGACAGGTTGAGT	1080
Qy	1081	ATGTTCTCTCTTTAAGTATGTTGTCAGACCCCAACACTGCTCAATTTGTCACAATAAAG	1140
Ds	1081	ATGTTCTCTCTTTAAGTATGTTGTCAGACCCCAACACTGCTCAATTTGTCACAATAAAG	1140
Qy	1141	TGCTATAGACTTGGCTCCCAACCAAGTAAAGAAAGATTTAGCATATGAATTTAAAG	1200
Ds	1141	TGCTATAGACTTGGCTCCCAACCAAGTAAAGAAAGATTTAGCATATGAATTTAAAG	1200
Qy	1201	CCACTCGTTCGCAAGCTGCACGAGAGCTGATCTTACTCGAATCAAAAACATCTCTC	1260
Ds	1201	CCACTCGTTCGCAAGCTGCACGAGAGCTGATCTTACTCGAATCAAAAACATCTCTC	1260
Qy	1261	TCTGGAATGGTGAATTTCAAGACATCTTCAACACATGAACAGCATTTGCTGCTGC	1320
Ds	1261	TCTGGAATGGTGAATTTCAAGACATCTTCAACACATGAACAGCATTTGCTGCTGC	1320

Qy	1321	TGCATCTCCATATCCCAAAAGAAAGCAAAATATGTGAACCTGTTGCTTAAGAAAGGAGCAAA	1380
Ds	1321	TGCATCTCCATATCCCAAAAGAAAGCAAAATATGTGAACCTGTTGCTTAAGAAAGGAGCAAA	1380
Qy	1381	CATCAATGAAAGAACTAAAGAAATTTCTTGAATCTCTCTGCACGTGGCATCTGAGAAAGCTCA	1440
Ds	1381	CATCAATGAAAGAACTAAAGAAATTTCTTGAATCTCTCTGCACGTGGCATCTGAGAAAGCTCA	1440
Qy	1441	TAATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAAAGGTTAATGCTCTGGATAATCT	1500
Ds	1441	TAATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAAAGGTTAATGCTCTGGATAATCT	1500
Qy	1501	TGCTCAGACTTCTCTACACAGAGCTGATATTGTTGGTCACTACAAAACCTGCCCTACT	1560
Ds	1501	TGCTCAGACTTCTCTACACAGAGCTGATATTGTTGGTCACTACAAAACCTGCCCTACT	1560
Qy	1561	CCTGAGCTATGGGTGTCATCTCTAACATTTATATCCCTTTCAGGGCTTTACTGCTTTACAGAT	1620
Ds	1561	CCTGAGCTATGGGTGTCATCTCTAACATTTATATCCCTTTCAGGGCTTTACTGCTTTACAGAT	1620
Qy	1621	GGGAAATGAAATGTACAGCAACTCTCCAAGAGGGTATCTCATTTAGGTAAATCAGAGGC	1680
Ds	1621	GGGAAATGAAATGTACAGCAACTCTCCAAGAGGGTATCTCATTTAGGTAAATCAGAGGC	1680
Qy	1681	AGACAGCAATTTGCTGAAAGCTGCAAAAGGCTGGAGATGTCGAACTCTGAAAAAATCTGTG	1740
Ds	1681	AGACAGCAATTTGCTGAAAGCTGCAAAAGGCTGGAGATGTCGAACTCTGAAAAAATCTGTG	1740
Qy	1741	TACTGTTTCAAGTGTCAACTGTCAGAGACATTTGAAGGGCTGAGTCTACACCACTTCATTT	1800
Ds	1741	TACTGTTTCAAGTGTCAACTGTCAGAGACATTTGAAGGGCTGAGTCTACACCACTTCATTT	1800
Qy	1801	TGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCTACAGCATGGAGCTGATGT	1860
Ds	1801	TGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCTACAGCATGGAGCTGATGT	1860
Qy	1861	GCATGCTTAAAGATAAAGAGGCTTTGACCTTTGCACAATGCAATGCTTTATGACCATTA	1920
Ds	1861	GCATGCTTAAAGATAAAGAGGCTTTGACCTTTGCACAATGCAATGCTTTATGACCATTA	1920
Qy	1921	TGAAGTTGCAAGACTCTTGTGTTAAACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAA	1980
Ds	1921	TGAAGTTGCAAGACTCTTGTGTTAAACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAA	1980
Qy	1981	ATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAAATATGAAATTTGCAAACTTCGCT	2040
Ds	1981	ATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAAATATGAAATTTGCAAACTTCGCT	2040
Qy	2041	CCAGCATGGTGCAGACCTTACCAAAAAAAGGAGATGGAATACTCCTTTGGATCTTGT	2100
Ds	2041	CCAGCATGGTGCAGACCTTACCAAAAAAAGGAGATGGAATACTCCTTTGGATCTTGT	2100
Qy	2101	TAAAGATGGAGATACAGATATTCAAGATCTGCTTGGGGAGATGAGCTTTGCTAGATGC	2160
Ds	2101	TAAAGATGGAGATACAGATATTCAAGATCTGCTTGGGGAGATGAGCTTTGCTAGATGC	2160
Qy	2161	TGCCAAGAGGGTTGTTTACGAGAGTGAAGAGTGTCTTCTCCTGATATGTAATTTG	2220
Ds	2161	TGCCAAGAGGGTTGTTTACGAGAGTGAAGAGTGTCTTCTCCTGATATGTAATTTG	2220
Qy	2221	CCGCGATACCCNAGGACAGATTTCAACACCTTTACATTTAGCAGCTGGTTATATATTT	2280
Ds	2221	CCGCGATACCCNAGGACAGATTTCAACACCTTTACATTTAGCAGCTGGTTATATATTT	2280
Qy	2281	AGAAAGTTGCAAGATTTGTTTACAAACCGAGCTGATGTGAATGCCAAGAACAGGAGG	2340
Ds	2281	AGAAAGTTGCAAGATTTGTTTACAAACCGAGCTGATGTGAATGCCAAGAACAGGAGG	2340
Qy	2341	ACTTATTTCTTTTACATTAATGACAGCATCTTACGGGCGATGTAGATGTAGCAGCTCTACTAAT	2400
Ds	2341	ACTTATTTCTTTTACATTAATGACAGCATCTTACGGGCGATGTAGATGTAGCAGCTCTACTAAT	2400
Qy	2401	AAAGTATAATGCAATGTCATGCAATGCGGACCAATGGGCTTTTCACACCTTTGACGAGG	2460

QY 361 ACCACTGCTTGTAGTGGAGAGTCCCTCTGGCTTTATCATTTAAGGTTTGGCGGGAAGA 420
DB 361 ACCACTGCTTGTAGTGGAGAGTCCCTCTGGCTTTATCATTTAAGGTTTGGCGGGAAGA 420
QY 421 CGTAGTTGAAATATTTGCTTTCAGATGGTGAAGTGTCCAAGCAGTGAATGATGGGGCCT 480
DB 421 CGTAGTTGAAATATTTGCTTTCAGATGGTGAAGTGTCCAAGCAGTGAATGATGGGGCCT 480
QY 481 TATTCCTCTTCATTAATGATGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCCTTTTGG 540
DB 481 TATTCCTCTTCATTAATGATGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCCTTTTGG 540
QY 541 ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATATCTCCTCTCCATGAAGCTGC 600
DB 541 ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATATCTCCTCTCCATGAAGCTGC 600
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DB 601 AATTTAAAGGAAGATGTGATGTTTGCATTTGCTGTGTACAGATGGAGCTGAGCCAAACAT 660
QY 661 CCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATCCATCTGCGCAAGCAGTGCT 720
DB 661 CCGAAATACAGATGGAAGGACAGCATTGGATTTAGCAGATCCATCTGCGCAAGCAGTGCT 720
QY 721 TACTGGTGNATATGAAGAGTGAACCTTTAGAAAGTCCAGGAGTGGCAATGAAGAAA 780
DB 721 TACTGGTGNATATGAAGAGTGAACCTTTAGAAAGTCCAGGAGTGGCAATGAAGAAA 780
QY 781 AATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACCAAGTGAATGGCAAGATC 840
DB 781 AATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACCAAGTGAATGGCAAGATC 840
QY 841 AACTCCATTAATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTTTACTGCA 900
DB 841 AACTCCATTAATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTTTACTGCA 900
QY 901 ACATGGAGCTGATGTCATGCTAAAGATAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 960
DB 901 ACATGGAGCTGATGTCATGCTAAAGATAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 960
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DB 961 TTCTTATGGTCATTTAAGTAACTGTAACCTTTTGGTCAAGCATGGTCTGTGTAATGTC 1020
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DB 1021 AATGGACTTGTGGCAATTCACCTCTCTTCATGAGGAGCTTCTAAGAACAGGGTTGAAGT 1080
QY 1081 ATGTTCTCTCTTAAAGTAACTGTAACCTTTTGGTCAAGCATGGTCTGTGTAATGTC 1140
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DB 2221 CCGCATACCAAGGAGACATTCACACCTTTACATTTAGCAGCTGGTTATATAATTT 2280
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AR392873
LOCUS AR392873 3816 bp DNA linear PAT 18-DEC-2003
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3816)
AUTHORS Luo, Y., Chan, E., Xu, X., Huang, B. and Ossofskaya, V.
TITLE Tankyrase H, compositions involved in the cell cycle and methods of use
JOURNAL Patent: US 6617102-A 2 09-SEP-2003;
Rigel Pharmaceuticals, Inc.; South San Francisco, CA
FEATURES
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/organism="unknown"
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ORIGIN
Query Match 89.4%; Score 3393.4; DB 2; Length 3816;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 422 AGTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGTCGAAAGTGTCAAGC 481
Qy 463 ACGTGATGATGGGGCCCTTATTCCTCTTCAATATGTCATGCTCTTTTGTGTCATGCTGAAGT 522
Db 482 ACGTGATGATGGGGCCCTTATTCCTCTTCAATATGTCATGCTCTTTTGTGTCATGCTGAAGT 541
Qy 523 AGTCAATCTCTTTTGGACATGTCGACAGCCCAATGCTCGAGATAATTGGAATTATAC 582
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Qy 583 TCCTCTCATGAGCTGCAATTAAGGAAAGATTGATGTTTGCATGTTGCTGTTCAGCA 642
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Qy 643 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTAGCAGATCC 702
Db 662 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTAGCAGATCC 721
Qy 703 ATCTGCCAAAGCAGTGTCTTACTGTTGAATATAAGAAAGATGAACCTTTAGAAAGTCCAG 762
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Qy 763 GAGTGGCAATGAAGAAAAATGATGGCTCTACTACACCATTAATGTCACTGCCAGC 822
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Qy 823 AAGTGTGGCAGAAAGTCACTCCATTACATTTTGCAGCAGATATACAGAGTAAAGAT 882
Db 842 AAGTGTGGCAGAAAGTCACTCCATTACATTTTGCAGCAGATATACAGAGTAAAGAT 901
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[illegible]

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2023	AATTTGCAAACTTCTGCTCCAGCATGGTCAGACCTTACCAAAAAAACAAGGATGGAAA	2082	TTTAAAGGAGTTCGAGAGACTTATCTCCGACAAACAAAGGTCCTTAAACCCATATTTAAACCTTT
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1963	Qy	TGTAGCTGATTTATGGAAATTTTACACTTTTACATGAAGAGCAGCAGAAAAGGAAAATATGA	2022
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2023	Qy	AAATTCGAACTTCTGCTCCAGCATGGTCAGACCTTACCACAAAANAACAGGGAGTGGAAA	2082
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2083	Qy	TACTCTCTTTGGATCTTGTTTAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA	2142
2102	Db	TACTCTCTTTGGATCTTGTTTAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA	2161
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2162	Db	TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTTTAGCCAGAGTGGAAGTTGCTTC	2221
2203	Qy	TCTCTGATATGTAAATTTGCCCGCATACCCAAAGGCAGACATTTCAACACTTTTACATTTAGC	2262
2222	Db	TCTCTGATATGTAAATTTGCCCGCATACCCAAAGGCAGACATTTCAACACTTTTACATTTAGC	2281
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Db	2702	TTCAGGTCCATCTAGGCCATCAAGCCCTTTCTGAGAGCCAGCAGTCTTGACAACTTATCTGG	2761
Qy	2743	GAGTTTTTCAGAACTGTCTTTCAGTAGTTAGTTCAAAGTGGAAACAGAGGGTCTTCCAGTTT	2802
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Qy	2863	ACTTGAGCACTTAATGGATATATTTGAGAGAGAAACAGATCACTTTGGATGTATTAGTTGA	2922
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Qy	2923	GATGGGCAACAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGAACATAGGCACAAACT	2982
Db	2942	GATGGGCAACAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGAACATAGGCACAAACT	3001
Qy	2983	AATTTAAGGAGTCGAGAGACTTATCTCCGAGAACAAAGGCTTTAAACCATATTTAACTTT	3042
Db	3002	AATTTAAGGAGTCGAGAGACTTATCTCCGAGAACAAAGGCTTTAAACCATATTTAACTTT	3061
Qy	3043	GAACACCTCTGGTAGTGGAACTTCTTATAGATCTGTCTCCTGATGATAAAGAGTTTCA	3102
Db	3062	GAACACCTCTGGTAGTGGAACTTCTTATAGATCTGTCTCCTGATGATAAAGAGTTTCA	3121
Qy	3103	GTCTGTGGAGAAAGAGATGCAAAAGTACAGTTTCAGAGACACAGAGATGGAGGTCATGCAGG	3162
Db	3122	GTCTGTGGAGAAAGAGATGCAAAAGTACAGTTTCAGAGACACAGAGATGGAGGTCATGCAGG	3181
Qy	3163	TGGAATCTTCAACAGATACAAATATCTCAAGATTCAGAAGTTTGTAAACAAGAAACTATG	3222
Db	3182	TGGAATCTTCAACAGATACAAATATCTCAAGATTCAGAAGTTTGTAAACAAGAAACTATG	3241
Qy	3223	GGAAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACAATGCCAAATGA	3282
Db	3242	GGAAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACAATGCCAAATGA	3301
Qy	3283	ACGAATGCTATTTTCATGGGTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATGA	3342
Db	3302	ACGAATGCTATTTTCATGGGTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATGA	3361
Qy	3343	AAGGCATGCGTACATAGGTGGTATGTTTGAGCTGGCATTTATTTTCTGAAACTCTTTC	3402
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LOCUS	AR361486	4275 bp	DNA	linear PAT 17-AUG-2003
DEFINITION	Sequence 5 from patent US 6599728.			
ACCESSION	AR361486			
VERSION	AR361486.1 GI:33769334			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified			
REFERENCE	1 (bases 1 to 4275)			
AUTHORS	Morin,G.B., Funk,W.D. and Piatyszek,M.A.			
TITLE	Second mammalian tankyrase			
JOURNAL	Patent: US 6599728-A 5 29-JUL-2003;			
	Geron Corporation; Menlo Park, CA			
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Best Local Similarity	99.9%; Pred. No. 0;			
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RESULT 6

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DEFINITION Homo sapiens tankyrase-2 (TNKS-2) mRNA, complete cds.

AF309033 ACCESSION

AF309033.1 GI:15042551

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

Chi, N.-W. and Lodish, H.F.

A novel homolog of Tankyrase

Unpublished

REFERENCE 2 (bases 1 to 6028)

Chi, N.-W. and Lodish, H.F.

Direct Submission

Submitted (27-SEP-2000) Whitehead Institute for Biomedical

Research, 9 Cambridge Center, Cambridge, MA 02142, USA

Location/Qualifiers

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DEFINITION Sequence 2 from Patent WO0077225.
ACCESSION AX057579
VERSION AX057579.1 GI:12310301
KEYWORDS Homo sapiens (human)
SOURCE ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Chi, N. W. and Lodish, H. F.
TITLE A novel insulin signaling molecule
JOURNAL Patent: WO 0077225-A 2 21-DEC-2000;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; THE GENERAL
HOSPITAL CORPORATION (US)
FEATURES Location/Qualifiers
source 1. .6123

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ORIGIN

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Matches 3390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db |||||
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Db |||||
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Db |||||
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AF329696
LOCUS
DEFINITION Homo sapiens tankyrase 2 mRNA, complete cds.
ACCESSION AF329696
VERSION AF329696.1 GI:13161041
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
REFERENCE
1 (bases 1 to 3815)
Lyons,R.J., Deane,R., Lynch,D.K., Ye,Z.S., Sanderson,G.M.,
Eyre,H.J., Sutherland,G.R. and Daly,R.J.
Identification of a novel human tankyrase through its interaction
with the adaptor protein Grb14
J. Biol. Chem. 276 (20), 17172-17180 (2001)
11278563
REFERENCE
2 (bases 1 to 3815)
Lyons,R.J., Deane,R., Lynch,D.K., Ye,Z.-S.J., Sanderson,G.M.,
Eyre,H.J., Sutherland,G.R. and Daly,R.J.
Direct Submission
Submitted (17-DEC-2000) Cancer Research, Garvan Institute of
Medical Research, 384 Victoria St., Sydney, NSW 2010, Australia
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ORIGIN

Query Match		89.2%	Score 3387.2;	DB 5;	Length 3815;		
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Qy	763	GAGTGGCAATGAAGAAATAATGATGGCTCTACTACACCAATTAATGTCACATGCCACGC	822				
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Qy	1423	GGCATCTGAGAAAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAAAGT	1482				
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Db	1417	TAATGCTCTGATATCTTGGTTCAGACTTCTCTACACAGAGCTGCATATTTGGTTCATCT	1476				
Qy	1543	ACAAACCTGCCGCCTACTCTCTGAGCTATGGGTGATCCTTAACATATATATCCCTTCAGGG	1602				
Db	1477	ACAAACCTGCCGCCTACTCTCTGAGCTATGGGTGATCCTTAACATATATATCCCTTCAGGG	1536				
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Db	1537	CTTTACTGCTTTTACAGATGGGAAATGAAATGTAACAGCACTCTCTCAAGAGGGTATCTC	1596				
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Db	1597	ATTAGTAAATTCAGAGCAGACAGCAATTCCTCGNAGCTCGAAAGGCTGGAGATGTGGA	1656				
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Qy	1903	ATGTTCTTATGGAACATTTATGAAGTTGCAAGACTTCTGTTAAACATGAGCAGTAGTTAA	1962				
Db	1837	ATGTTCTTATGGAACATTTATGAAGTTGCAAGACTTCTGTTAAACATGAGCAGTAGTTAA	1896				
Qy	1963	TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2022				
Db	1897	TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA	1956				
Qy	2023	AAATTTGCAAACTTCTGCTCCAGATGTCAGACCCCTACCAAAAACACAGGATGGAA	2082				
Db	1957	AAATTTGCAAACTTCTGCTCCAGATGTCAGACCCCTACCAAAAACACAGGATGGAA	2016				
Qy	2083	TACTCTCTTTGGATCTGTTTAAAGATGGAGATACAGATATTTCAAGATCTGTTAGGGGAGA	2142				
Db	2017	TACTCTCTTTGGATCTGTTTAAAGATGGAGATACAGATATTTCAAGATCTGTTAGGGGAGA	2076				
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DEFINITION Sequence 100 from Patent WO0100849.
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KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Christenson, E., Demaggio, A.J., Goldman, P.S. and Mcelligott, D.L.
TITLE Tankyrase2 materials and methods
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ICOS CORPORATION (US)
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ACCESSION AX062275
VERSION AX062275.1 GI:12540176
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
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LOCUS AR578380 AR578380 5075 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 556 from patent US 6783969.
ACCESSION AR578380
VERSION AR578380.1 GI:56581176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 5075)
Tang,Y.T., Goodrich,R.W., Asundi,V. and Drmanac,R.T.
TITLE Cathespin V-like polypeptides
JOURNAL Patent: US 6783969-A 556 31-AUG-2004;
Nuvelo, Inc.; Sunnyvale, CA
FEATURES
source Location/Qualifiers
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Kulmov, A.N., Kuprash, D.V., Petrov, V.N., Vdovichenko, K.K.,
Scanlan, M.J., Jongeneel, C.V., Lagarkova, M.A. and Nedospasov, S.A.
Cloning and characterization of TNKL, a member of tankyrase gene
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Genes Immun. 2 (1), 52-55 (2001)
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PUBMED
2 (bases 1 to 5810)
Kulmov, A.N., Kuprash, D.V., Petrov, V.N., Vdovichenko, K.K.,
Kashkarova, U.A., Bolichenko, V.E., Nedospasov, S.A. and
Lagarkova, M.A.
Direct Submission
Submitted (08-MAY-2000) Laboratory of Molecular Immunology, A.N.
Belozersky Institute of Physico-Chemical Biology, Moscow State
University, Moscow 119899, Russia
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Ludwig Institute for Cancer Research and Cornell Research
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Qy 883 TGTACAGCTGTACTGCAACATGGAGCTGATGTCATGCTTAAAGATAAAGGTGATCTGGT 942
Db 898 TGTACAGCTGTACTGCAACATGGAGCTGATGTCATGCTTAAAGATAAAGGTGATCTGGT 957
Qy 943 ACCATTACACAATGCCCTGTTCTTATGCTCAATTAAGAGTAACTGAACTTTTGGTCAAGCA 1002
Db 958 ACCATTACACAATGCCCTGTTCTTATGCTCAATTAAGAGTAACTGAACTTTTGGTCAAGCA 1017
Qy 1003 TGGTGCTGTGTAATGCAATGGCAATTTGTCGCAATTCACCTCTTCTCATGAGGCGCTTC 1062
Db 1018 TGGTGCTGTGTAATGCAATGGCAATTTGTCGCAATTCACCTCTTCTCATGAGGCGCTTC 1077
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Qy 1183 AGCATATGAATTTAAAGGCCACTCGTTGTCGAGCTGCCAGAGCTGATGTTACTCG 1242
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Job time : 20536.6 secs
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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2006, 11:40:30 ; Search time 2052.86 Seconds
(without alignments)
12895.949 Million cell updates/sec

Title: US-10-616-101-1

Perfect score: 3797

Sequence: 1 ctttgaagacactgatttc.....cctttgctgaaaaaaaaa 3797

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
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- 11: geneseqn2003ds:*
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- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3797	100.0	3797	4	Aa91487 Tankyrase
2	3797	100.0	3797	8	Abq77066 Tankyrase
3	3797	100.0	3797	10	Adh69414 Human tan
4	3797	100.0	3797	14	Ady97759 Human tan
5	3393.4	89.4	3816	4	Aa91488 Tankyrase
6	3393.4	89.4	3816	8	Abq77067 Tankyrase
7	3393.4	89.4	3816	10	Adh69415 Human tan
8	3393.4	89.4	3816	14	Ady97760 Human tan
9	3388.8	89.2	4275	3	Aac66825 Human tan
10	3388.8	89.2	6019	4	Aac85294 Human SPA
11	3387.2	89.2	4127	5	Aaf63926 Human tan
12	3387.2	89.2	4406	5	Aaf63930 Human tan
13	3387.2	89.2	4992	5	Aaf63953 Human tan
14	3387.2	89.2	5002	5	Aaf63952 Human tan
15	3387.2	89.2	5075	6	Abz11674 Human pol
16	3387.2	89.2	5075	12	Adm44192 Novel hum
17	3387.2	89.2	6018	10	Aad54031 Human col
18	3387.2	89.2	6189	13	Adr14766 Nucleotid

ALIGNMENTS

RESULT 1

AAA91487

ID AAA91487 standard; DNA; 3797 BP.

AC AAA91487;

XX AC AAA91487;

DT 06-AUG-2001 (first entry)

XX Tankyrase homologue isotype 1 coding sequence.

DE Tankyrase homologue isotype 1; TaHo-1; TaHo-2; cell proliferation;

XX cell cycle protein; cell cycle associated disorder; cancer; gene mapping;

KW chromosome mapping; gene therapy; vaccine; ds.

XX Unidentified.

OS Unidentified.

XX Key Location/Qualifiers

FT CDS 404..3706

FT /tag= a

FT /partial

FT /product= "TaHo1"

FT /note= "Tankyrase homologue isotype 1; No start codon given"

XX WO200130987-A2.

PN 03-MAY-2001.

PD 25-OCT-2000; 2000WO-US041528.

XX 25-OCT-1999; 99US-00427154.

XX (RIGE-) RIGEL PHARM INC.

PI Luo Y, Chan E, Xu X, Huang B;

XX WPI; 2001-300503/31.

XX P-PSDB; AAY97748.

Adr66604 Human pro
Adr66262 Human pro
Adw86202 Human Tan
Adw92026 DNA seque
Aac02578 Human tan
Aax25366 Human Grb
Aaf63837 Human tan
Aac66823 Human tan
Aac66824 Human tan
Aac89706 Human adu
Aaf63919 Human tan
Aaf63917 Human tan
Aaf63918 Human tan
Aaf63938 Human tan
Aaz29627 Human tan
Aac66826 Human tan
ABK48629 Human tan
Adr14765 Nucleotid
Aac85295 Mouse SPA
Adn03876 Antipeori
Ade53995 Human pro
Aaz29632 Human tru
ABK48634 Truncated
Adw86201 Human Tan
Adw92025 Human gen
Aaf63925 Human tan
Aaz29633 Human tru

or preventing cell cycle associated disorders such as cancer.

Claim 13; Fig 1; 63pp; English.

This sequence encodes the Tankyrase homologue isotype 1 (TaHo-1) protein of the invention. The invention also relates to the TaHo-2 protein. The TaHo proteins are useful for inducing or preventing cell proliferation in cells, and in the study or treatment of conditions mediated by the cell cycle proteins, such as to diagnose, treat or prevent cell cycle associated disorders, preferably cancer. The TaHo coding sequences are useful as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense DNA and RNA. The coding sequences are also useful for the preparation of TaHo, for generating either transgenic animals or knock out animals which, in turn, are useful in a development and screening of therapeutically useful agents, in gene therapy, as vaccine, and for construction of hybridisation probes for mapping the gene which encodes TaHo and for the genetic analysis of individuals with genetic disorders. The TaHo proteins, and their coding sequences are useful in screening assays

Sequence 3797 BP; 1153 A; 732 C; 850 G; 1062 T; 0 U; 0 Other;

Query Match 100.0%; Score 3797; DB 4; Length 3797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 AGACAAATATTAGCTGTGAGCAGATCTTTTGGTGGTCTTGTAGTCCCGAGTTTAG 120
121 CAGAAACATCTGTGAGATAGATGTGGAAGGAATTTCTAGCAAGAGTTTGTCACTGTA 180
121 CAGAAACATCTGTGAGATAGATGTGGAAGGAATTTCTAGCAAGAGTTTGTCACTGTA 180
181 TCATAAGGTTGTGATTACATATTTAAAGTTTATCTTTGAAACATCTGAAATGTATACA 240
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301 ACTTATTTTGTATTCTTTCTTTGAGGTTAGCAGTAGTACACCCAGGCAGCTGTAGGT 360
301 ACTTATTTTGTATTCTTTCTTTGAGGTTAGCAGTAGTACACCCAGGCAGCTGTAGGT 360
361 ACCACTGCTGTAGTGGAGAGTCCCTCTGGCTTTATCATTTAAGGTTTGGCGGGAAGA 420
361 ACCACTGCTGTAGTGGAGAGTCCCTCTGGCTTTATCATTTAAGGTTTGGCGGGAAGA 420
421 CGTAGTTGAAATATTTGCTTCAGATGTGCAAGTGTCCNAGCAGCTGATGATGGGGCCT 480
421 CGTAGTTGAAATATTTGCTTCAGATGTGCAAGTGTCCNAGCAGCTGATGATGGGGCCT 480
481 TATTCTCTTTCATATGATGCTCTTTTGGTTCATGCTGAGTAGTCAATCTCTTTTGGC 540
481 TATTCTCTTTCATATGATGCTCTTTTGGTTCATGCTGAGTAGTCAATCTCTTTTGGC 540
541 ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATCTCTCTCCATGAAGCTGC 600
541 ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATCTCTCTCCATGAAGCTGC 600
601 AATTAAAGGAAGATTGATTTGCTGATGCTGTTACAGCATGAGCTGAGCCAAACAT 660
601 AATTAAAGGAAGATTGATTTGCTGATGCTGTTACAGCATGAGCTGAGCCAAACAT 660
661 CCGAAATACAGATGGAAGGACGATTTGGATTTAGCAGATCCATCTGCGAAAGCAGTGCT 720
661 CCGAAATACAGATGGAAGGACGATTTGGATTTAGCAGATCCATCTGCGAAAGCAGTGCT 720

721 TACTGTGAATATATAAGAAAGATGAATCTTTAGAAAGTGCACGAGTGGCAATGAAGAAA 780
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901 ACATGAGCTGTATGCTCAATGCTTAAAGTAAAGTGTATGCTGATGCTTACCAATGCTG 960
901 ACATGAGCTGTATGCTCAATGCTTAAAGTAAAGTGTATGCTGATGCTTACCAATGCTG 960
961 TTCTTATGCTCATTTATGAAGTAACTGAACCTTTTGGTCAAGCATGCTGCTGTGTAATGC 1020
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1021 AATGGACTTGTGGCAATTCACCTCTTTCATGAGGCAAGCTTCTTAAGAACAGGGTTGAAGT 1080
1081 ATGTTCTCTCTCTTAAAGTTATGCTGAGAGCCCAACACTGCTCAATTTGTCAATAAAG 1140
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1141 TGCTATAGATCTGGCTCCACACACAGATTTAAAGAAAGATTAGCATATGAATTTAAAG 1200
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DB 2041 CCAGCATGGTGAGACCTTACCAAAAAAACAAGGATGGAATATCTCTTTGGATCTTTGT 2100
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QY 3781 TTGCTGAAAAAATAA 3797
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RESULT 2

ABQ77066

ID ABQ77066 standard; DNA; 3797 BP.

XX ABQ77066;

AC ABQ77066;

XX 08-APR-2003 (first entry)

XX Tankyrase H isotype 1 TaHo-1 DNA from clone TH-1.

DE

XX Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-1;
 KW TaHo; cytostatic; immunostimulant; Gene therapy; vaccine; cancer; tumour;
 KW cell cycle related disorder; poly ADP-ribose polymerase; PARP; ds.
 XX Unidentified.
 XX
 XX Key Location/Qualifiers
 FT CDS 404..3706
 FT /*tag= a
 FT /product= "TaHo-1"
 FT /partial
 FT /note= "No start codon given"
 XX
 XX WO200286170-A1.
 XX
 XX 31-OCT-2002.
 XX
 XX 25-APR-2002; 2002WO-US013185.
 XX
 XX 25-APR-2001; 2001US-00843159.
 XX (RIGE-) RIGEL PHARM INC.
 XX
 XX Luo Y, Chan E, Xu X, Huang B, Ososovskaya V;
 XX
 XX WPI; 2003-093158/08.
 XX DR P-PSDB; ABG73730.
 XX
 XX New recombinant nucleic acid encoding a cell cycle protein, useful for
 PT diagnosing and treating a cell cycle related disorder, e.g. cancer.
 XX
 XX Claim 13; Fig 1A-B; 90pp; English.
 XX
 XX This invention describes a novel recombinant nucleic acid encoding the
 CC cell cycle protein TaHo, a tankyrase H isoform. The products of the
 CC invention have cytostatic and immunostimulant activity and can be used
 CC for gene therapy and in vaccines. The cell cycle protein TaHo and the
 CC nucleic acid encoding the protein are useful for diagnosing and treating
 CC a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a
 CC tumour cell. The methods are useful for screening for a bioactive agent
 CC capable of binding to a cell cycle protein tankyrase H, or a bioactive
 CC agent capable of modulating a cell cycle protein tankyrase H or PARP
 CC (poly ADP-ribose polymerase) activity. The antibodies are useful for
 CC inducing an immune response against the cell cycle proteins. This
 CC sequence encodes the tankyrase H isoform 1, TaHo-1, isolated from clone
 CC TH-1 which is described in the disclosure of the invention
 XX
 XX Sequence 3797 BP; 1153 A; 732 C; 850 G; 1062 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 3797; DB 8; Length 3797;
 XX Best Local Similarity 100.0%; Pred. No. 0;
 XX Matches 3797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 XX 1 CTTTGAGACACTGGATTTCATCTTTTGGCTGGGGTAACTCTCTGTGCTCACTACAT 60
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 XX 1 CTTTGAAGACACTGGATTTCATCTTTTGGCTGGGGTAACTCTCTGTGCTCACTACAT 60
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Db	1381	CATCAATGAAAGAAGACTAAAGAAATCTTTGACCTCTGCACTGGCATCTGAGAAAGCTCA	1440
Qy	1441	TAATGATGTTGTTGCAAGTGTAGTGGTGAACAACATGAAGCAAAAGTTAACTGCTCTGGATATCT	1500
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Qy	1501	TGGTCAGACTTCTCTACACAGAGCTGCATATTTGTGGTCATCTACAAACCTGCCGCCTACT	1560
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Qy	1561	CCTGAGCTATGGGTGTGATCCTTAACATATATATCCCTTCAGGGCTTTACTGCTTTACAGAT	1620
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Qy	1621	GGGAAATGAAATCTGTACAGCAACTCCTCCAAGAGGGTATCTCAATAGTAAATTCAGAGGC	1680
Db	1621	GGGAAATGAAATCTGTACAGCAACTCCTCCAAGAGGGTATCTCAATAGTAAATTCAGAGGC	1680
Qy	1681	AGACAGACAATTTGCTGGAAGCTGCAGAAAGCGCTGGAGATGTCGAAACCTGTAAGAAACCTGTG	1740
Db	1681	AGACAGACAATTTGCTGGAAGCTGCAGAAAGCGCTGGAGATGTCGAAACCTGTAAGAAACCTGTG	1740
Qy	1741	TACTGTTTTCAGAGTGTCTAACTGTGAGAGACATTTGAAGGGCGTCAGTCTACACCACTTCATTT	1800
Db	1741	TACTGTTTTCAGAGTGTCTAACTGTGAGAGACATTTGAAGGGCGTCAGTCTACACCACTTCATTT	1800
Qy	1801	TGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCTACAGCATGGAGCTGATGT	1860
Db	1801	TGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCTACAGCATGGAGCTGATGT	1860
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Db	1921	TGAAGTTGCGAGAACTTCTTGTATAACATGGAGCAGTAGTTAAATGTAGCTGAATTTATGGAA	1980
Qy	1981	ATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGAAATTTGCAAACTTCGTCT	2040
Db	1981	ATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGAAATTTGCAAACTTCGTCT	2040
Qy	2041	CCAGCATGTTGCAGACCCCTTCCAAAAAACAAGGGATGGAATACTCCTTTGGATCTTGT	2100
Db	2041	CCAGCATGTTGCAGACCCCTTCCAAAAAACAAGGGATGGAATACTCCTTTGGATCTTGT	2100
Qy	2101	TAAAGATGGAGATACAGATATTCAGATCTCTTTAGGGGAGATGCACTTTTGTAGATGC	2160
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Db	2161	TGCCAAGAAGGGTTGTTTGGCAGAGTGAAGAGTTGTCCTTCTGATTAATGTAAATTG	2220
Qy	2221	CCGCGATACCCAAGCGCAGACATTCACACCTTTTACATTTAGCAGCTGGTTATATAATTT	2280
Db	2221	CCGCGATACCCAAGCGCAGACATTCACACCTTTTACATTTAGCAGCTGGTTATATAATTT	2280
Qy	2281	AGAAAGTTGCGAGATATTTGTTTACACACGAGAGCTGATGTGAATGCCCAAGCAAAAGGAGG	2340
Db	2281	AGAAAGTTGCGAGATATTTGTTTACACACGAGAGCTGATGTGAATGCCCAAGCAAAAGGAGG	2340
Qy	2341	ACTTATTTCTTTTACATTAATGCGACATCTTACGGGCGATGTAGATGTAGCAGCTCTACTAAT	2400
Db	2341	ACTTATTTCTTTTACATTAATGCGACATCTTACGGGCGATGTAGATGTAGCAGCTCTACTAAT	2400
Qy	2401	AAAGTATAATGTCATGTCTAATGCCCGGCAAAATGGCTTTTACACCTTTTGACCAAGGAGC	2460
Db	2401	AAAGTATAATGTCATGTCTAATGCCCGGCAAAATGGCTTTTACACCTTTTGACCAAGGAGC	2460
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[illegible]

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 Db 3781 TTGCTGAAAAA 3797
 RESULT 3
 ADH69414
 ID ADH69414 standard; DNA; 3797 BP.
 XX AC ADH69414;
 XX 25-MAR-2004 (first entry)
 DE Human tankyrase homologue isotype 1 (TaHo-1) DNA.
 KW Tankyrase H cell cycle protein; p21; gene therapy;
 KW bioactive agent screening; cancer; cytostatic; gene; human; ds.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS 404..3706
 XX /*tag= a
 XX /product= "Human tankyrase homologue isotype 1"
 XX /partial
 XX /note= "no start codon given"
 XX
 XX US6617102-B1.
 XX
 XX 09-SEP-2003.
 XX
 XX 25-OCT-2000; 2000US-00696668.
 XX
 XX 25-OCT-1999; 99US-00427154.
 XX
 XX (RIGE-) RIGEL PHARM INC.
 XX
 XX Luo Y, Chan E, Xu X, Huang B, Ossoveskaya V;
 XX
 XX WPI: 2003-895391/82.
 XX P-PSDB; ADH69405.
 XX
 XX Screening for a bioactive agent capable of interfering with the binding
 XX of a tankyrase H cell cycle protein and p21 for diagnosing or treating
 XX cancer by combining a tankyrase H cell cycle protein, a candidate
 XX bioactive agent and p21.
 XX
 XX Disclosure; SEQ ID NO 1; 39pp; English.
 XX
 XX The invention relates to a method for screening a bioactive agent capable
 XX of interfering with the binding of a tankyrase H cell cycle protein and
 XX p21. The invention is useful in gene therapy. The method is useful for
 XX screening for a bioactive agent capable of interfering with the binding
 XX of a tankyrase H cell cycle protein and p21 for preparing a composition
 XX for diagnosing or treating cancer. The present sequence is human
 XX tankyrase homologue isotype 1 (TaHo-1) DNA.
 XX
 XX Sequence 3797 BP; 1153 A; 732 C; 850 G; 1062 T; 0 U; 0 Other;

Query Match 100.0%; Score 3797; DB 10; Length 3797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CTTTGAAGACACATGGATTTCATATCTTTTGGCTGGGGTTATCTCTCTGTCTCTCACTACAT 60
 Db 1 CTTTGAAGACACATGGATTTCATATCTTTTGGCTGGGGTTATCTCTCTGTCTCTCACTACAT 60
 Qy 61 AGACAAATATTAGCTGTGACAGATCTTTTGTGTTGTTCTTGTAGTCCCCAGTTTGTAG 120
 Db 61 AGACAAATATTAGCTGTGACAGATCTTTTGTGTTGTTCTTGTAGTCCCCAGTTTGTAG 120
 Qy 121 CAGAAACATTTCTGTAGATAGATGTGGAAAGGAATTTCTAGCAAGAGTTTGTCACTGTA 180
 Db 121 CAGAAACATTTCTGTAGATAGATGTGGAAAGGAATTTCTAGCAAGAGTTTGTCACTGTA 180
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 Db 241 TACTAAATATGCAGAACTCTATTGTAGAGTGAGAGAAACATTTGAACTTTGAGCTTTCAGTC 300
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 Db 661 CCGAAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCCCATCTGCCAAGCAGTGCT 720
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 Db 721 TACTGTTGAATATAAGAAAGATGAACCTCTTAGAAGTCCAGGAGTGGCAATGAAGAAA 780
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QY 421 CGTAGTTGAATATTTTGGCTTTCAGAAATGGTGCAGAGTGTCCAAAGCACGATGATGATGGGGCT 480
DB 421 CGTAGTTGAATATTTTGGCTTTCAGAAATGGTGCAGAGTGTCCAAAGCACGATGATGATGGGGCT 480
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3361 TGGTATGTTTGGAGCTGGCATTTATTTTGTGTAAGAACTCTTCCAAAGCAATCAATATGT 3420
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Db
3421 ATATGGAATTGGAGGAGTACTGGGTGTCAGTTTCAAAAGACAGATCTTGTACATTGG 3480
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3481 CCACAGGAGCTGCTCTTTTGGCGGGTAACTTCTGGGAAAGTCTTCTGCAAGTTTCAGTGC 3540
Db
3481 CCACAGGAGCTGCTCTTTTGGCGGGTAACTTCTGGGAAAGTCTTCTGCAAGTTTCAGTGC 3540
Qy
3541 AATGAAATGGCAATTTCTCTCCAGGTCATCACTCAGTCACTGGTAGGCCCGAGTGA 3600
Db
3541 AATGAAATGGCAATTTCTCTCCAGGTCATCACTCAGTCACTGGTAGGCCCGAGTGA 3600
Qy
3601 TGGCCTAGCATTAAGTAAATGTTTACAGAGGAGAACAGGCTTATCTGAGTATTT 3660
Db
3601 TGGCCTAGCATTAAGTAAATGTTTACAGAGGAGAACAGGCTTATCTGAGTATTT 3660
Qy
3661 AATTACTTACCAGATTATGAGGCTGAGGTTATCGTGCATGATAAATAGTATTTTAAAG 3720
|||||

Db 3661 AATTACTTACCAGATTATGAGGCTGAGGTCATGATGGTAAATAGTATTTTAAAG 3720
Qy
3721 AACTAATTCACCTGAACTTAAATCATCAAGCAGAGTGGCTCTACGTTTACTCCT 3780
Db
3721 AACTAATTCACCTGAACTTAAATCATCAAGCAGAGTGGCTCTACGTTTACTCCT 3780
Qy
3781 TTGCTGAAAAAANA 3797
Db
3781 TTGCTGAAAAAANA 3797
RESULT 5
AA91488
ID AAA91488 standard; DNA; 3816 BP.
XX
AC AAA91488;
XX
DT 06-AUG-2001 (first entry)
XX
DE Tankyrase homologue isotype 2 coding sequence.
XX
KW Tankyrase homologue isotype 2; TaHo-1; TaHo-2; cell proliferation;
KW cell cycle protein; cell cycle associated disorder; cancer; gene mapping;
KW chromosome mapping; gene therapy; vaccine; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
CDS 2..3726
FT /*tag= a
FT /partial
FT /product= "TaHo2"
FT /note= "Tankyrase homologue isotype 2; No start codon given"
XX
PN WO200130987-A2.
XX
PD 03-MAY-2001.
XX
PF 25-OCT-2000; 2000WO-US041528.
XX
PR 25-OCT-1999; 99US-00427154.
XX
PA (RIGE-) RIGEL PHARM INC.
XX
PI Luo Y, Chan E, Xu X, Huang B;
XX
PS WPI: 2001-300503/31.
P-PSDB: AAY97749.
XX
PT Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing or preventing cell proliferation in cells, and for diagnosing, treating or preventing cell cycle associated disorders such as cancer.
XX
PS Claim 13; Fig 2; 63pp; English.
XX
CC This sequence encodes the Tankyrase homologue isotype 2 (TaHo-2) protein of the invention. The invention also relates to the TaHo-1 protein. The TaHo proteins are useful for inducing or preventing cell proliferation in cells, and in the study or treatment of conditions mediated by the cell cycle proteins, such as to diagnose, treat or prevent cell cycle associated disorders, preferably cancer. The TaHo coding sequences are useful as hybridisation probes, in chromosome and gene mapping and in the generation of anti-sense DNA and RNA. The coding sequences are also useful for the preparation of TaHo, for generating either transgenic animals or knock out animals which, in turn, are useful in a development and screening of therapeutically useful agents, in gene therapy, as vaccine, and for construction of hybridisation probes for mapping the gene which encodes TaHo and for the genetic analysis of individuals with genetic disorders. The TaHo proteins, and their coding sequences are useful in screening assays
XX
SQ Sequence 3816 BP; 1097 A; 806 C; 949 G; 964 T; 0 U; 0 Other;

Query Match		89.4%	Score 3393.4;	DB 4;	Length 3816;	
Best Local Similarity		99.9%	Pred No. 0;			
Matches 3394;		Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
Qy	403	AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAGTGTCCAAAGC	462			
Db	422	AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAGTGTCCAAAGC	481			
Qy	463	ACGTGATGATGGGGCCCTTATCTCTTCATATGCGATGCTCTTTGGTGCATGCTGAAGT	522			
Db	482	ACGTGATGATGGGGCCCTTATCTCTTCATATGCGATGCTCTTTGGTGCATGCTGAAGT	541			
Qy	523	AGTCAATCTCTTTTGGCACATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTTATAC	582			
Db	542	AGTCAATCTCTTTTGGCACATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTTATAC	601			
Qy	583	TCCTCTCATGAAGTGCATTAATAAGGAAAGATTGATTTTGCATTTGCTGTGTTACAGCA	642			
Db	602	TCCTCTCATGAAGTGCATTAATAAGGAAAGATTGATTTTGCATTTGCTGTGTTACAGCA	661			
Qy	643	TGGAGCTGAGCCACCATCCGAAATACAGATGGAGGACAGCATTTGGATTAGCAGATCC	702			
Db	662	TGGAGCTGAGCCACCATCCGAAATACAGATGGAGGACAGCATTTGGATTAGCAGATCC	721			
Qy	703	ATCTGCCAAAGCAGTGTCTTACTGTGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG	762			
Db	722	ATCTGCCAAAGCAGTGTCTTACTGTGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG	781			
Qy	763	GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCAACCATTTAAATGTCAACTGCCACGC	822			
Db	782	GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCAACCATTTAAATGTCAACTGCCACGC	841			
Qy	823	AAGTGATGGCAGAAAGTCACTCCATTTACATTTGGCAGCAGGATATAACAGATAAAGAT	882			
Db	842	AAGTGATGGCAGAAAGTCACTCCATTTACATTTGGCAGCAGGATATAACAGATAAAGAT	901			
Qy	883	TGTAAGCTGTTTACTGCAACATGGAGCTGTGCTCCATGCTTAAAGATAAAGTGATCTGGT	942			
Db	902	TGTAAGCTGTTTACTGCAACATGGAGCTGTGCTCCATGCTTAAAGATAAAGTGATCTGGT	961			
Qy	943	ACCATTAACAATGCTGCTTCTTATGGTCAATTAAGATAAAGTAACTGAACTTTTGGTCAAGCA	1002			
Db	962	ACCATTAACAATGCTGCTTCTTATGGTCAATTAAGATAAAGTAACTGAACTTTTGGTCAAGCA	1021			
Qy	1003	TGGTGCCTGTGTAATGCAATGGACTTTGGCAATTTCACTCTCTTCATGAGGAGCTTC	1062			
Db	1022	TGGTGCCTGTGTAATGCAATGGACTTTGGCAATTTCACTCTCTTCATGAGGAGCTTC	1081			
Qy	1063	TAAGAAACAGGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGAGACCCCAACACTGCT	1122			
Db	1082	TAAGAAACAGGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGAGACCCCAACACTGCT	1141			
Qy	1123	CAATTTGTCACATAAAGTGTCTATAGACTTTGGCTCCCAACACACAGTTTAAAGAAAGATT	1182			
Db	1142	CAATTTGTCACATAAAGTGTCTATAGACTTTGGCTCCCAACACACAGTTTAAAGAAAGATT	1201			
Qy	1183	AGCATATGAATTTAAAGGCGACTGTTGCTGCAAGCTGCAAGAGCTGATGTTACTCG	1242			
Db	1202	AGCATATGAATTTAAAGGCGACTGTTGCTGCAAGCTGCAAGAGCTGATGTTACTCG	1261			
Qy	1243	AATCAAAAACATCTCTCTCTGGAATGCTGAATTTCAAGCATCTCAACACACATGAAC	1302			
Db	1262	AATCAAAAACATCTCTCTCTGGAATGCTGAATTTCAAGCATCTCAACACACATGAAC	1321			
Qy	1303	AGCATTTGATTTGCTGCTGATCTCCATATCCCAAAAAGAAAGCAATATGTGAACCTGTT	1362			
Db	1322	AGCATTTGATTTGCTGCTGATCTCCATATCCCAAAAAGAAAGCAATATGTGAACCTGTT	1381			
Qy	1363	GCTAAGAAAAGAGCAAAATCAATGAATAAGAAAGCTTAAAGAAATTTCTTCTGACGT	1422			
Db	1382	GCTAAGAAAAGAGCAAAATCAATGAATAAGAAAGCTTAAAGAAATTTCTTCTGACGT	1441			

Qy	1423	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT	1482			
Db	1442	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT	1501			
Qy	1483	TAATGCTCTGATTAATCTTTGGTCAAGCTTCTCTACACAGAGCTGCATATTGTTGTCATCT	1542			
Db	1502	TAATGCTCTGATTAATCTTTGGTCAAGCTTCTCTACACAGAGCTGCATATTGTTGTCATCT	1561			
Qy	1543	ACAAACCTGCCGCTTACTCTGAGCTATGGTGTGATCCTTAACATTTATATCCCTTCAGGG	1602			
Db	1562	ACAAACCTGCCGCTTACTCTGAGCTATGGTGTGATCCTTAACATTTATATCCCTTCAGGG	1621			
Qy	1603	CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCCAAAGGGGTATCTC	1662			
Db	1622	CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCCAAAGGGGTATCTC	1681			
Qy	1663	ATTAGGTAAATTCAGAGCAGACAGACAAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGCGA	1722			
Db	1682	ATTAGGTAAATTCAGAGCAGACAGACAAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGCGA	1741			
Qy	1723	AACGTGTAATAAACTGTGTACTGTTACAGAGTGTCAACTGACAGACACATTTGAAGGGCGTCA	1782			
Db	1742	AACGTGTAATAAACTGTGTACTGTTACAGAGTGTCAACTGACAGACACATTTGAAGGGCGTCA	1801			
Qy	1783	GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT	1842			
Db	1802	GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT	1861			
Qy	1843	ACAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGAGGGCTTGTACTCTTTGCACAATGC	1902			
Db	1862	ACAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGAGGGCTTGTACTCTTTGCACAATGC	1921			
Qy	1903	ATGTTCTTATGGACATTTAAGTTGACAGACTTCTTGTGTTAAACATGAGCAGTAGTTAA	1962			
Db	1922	ATGTTCTTATGGACATTTAAGTTGACAGACTTCTTGTGTTAAACATGAGCAGTAGTTAA	1981			
Qy	1963	TGTAAGCTGATTTATGGAAATTTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2022			
Db	1982	TGTAAGCTGATTTATGGAAATTTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2041			
Qy	2023	AATTTGCAAACTTCTGCTCCAGCATGTTGTCAGACCCCTTACCAAAAAACACGGGATGGAAA	2082			
Db	2042	AATTTGCAAACTTCTGCTCCAGCATGTTGTCAGACCCCTTACCAAAAAACACGGGATGGAAA	2101			
Qy	2083	TACTCTCTTGATCTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGAGA	2142			
Db	2102	TACTCTCTTGATCTGTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGAGA	2161			
Qy	2143	TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGAAAGTTGCTTTC	2202			
Db	2162	TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGAAAGTTGCTTTC	2221			
Qy	2203	TCCTGATAATGTAATTTGCCGCGATACCCAGGCGAGACATTTCAACACCTTTACATTTAGC	2262			
Db	2222	TCCTGATAATGTAATTTGCCGCGATACCCAGGCGAGACATTTCAACACCTTTACATTTAGC	2281			
Qy	2263	AGCTGGTTATAATTAATTTAGAAAGTTGACAGATATTGTTTACCAACACGAGCTGATGTGAA	2322			
Db	2282	AGCTGGTTATAATTAATTTAGAAAGTTGACAGATATTGTTTACCAACACGAGCTGATGTGAA	2341			
Qy	2323	TGCCCAAGACAAAGGAGGACTTATTTCTTTTACATAATGACAGCATCTTACGGGCGATGAGA	2382			
Db	2342	TGCCCAAGACAAAGGAGGACTTATTTCTTTTACATAATGACAGCATCTTACGGGCGATGAGA	2401			
Qy	2383	TGTAGCAGCTCTACTAATAAAGTATAATGATGTGTCATATGCCACCGCAAAATGGGCTTTT	2442			
Db	2402	TGTAGCAGCTCTACTAATAAAGTATAATGATGTGTCATATGCCACCGCAAAATGGGCTTTT	2461			
Qy	2443	CACACCTTTGCAACAGCAGCCCAAAAGGAGCAACACAGCTTTGCTTTGTTGCTAGC	2502			
Db	2462	CACACCTTTGCAACAGCAGCCCAAAAGGAGCAACACAGCTTTGCTTTGTTGCTAGC	2521			
Qy	2503	CCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGACAAACACCTTTTAGATTGTTTC	2562			

Db 2522 CCATGGAGCTGACCCGACTCTTAAATAATCAGGAAGGACAAACACCTTTAGATTAGTTTC 2581
Qy 2563 AGCGGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCCCCATCTGCTCTGCCCTCTTG 2622
Db 2582 AGCGGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCCCCATCTGCTCTGCCCTCTTG 2641
Qy 2623 TTACAGGCTCAAGTGTCTCAATGTGTGAGAGGCCAGGCCACTGCGAGATGCTCTCTC 2682
Db 2642 TTACAGGCTCAAGTGTCTCAATGTGTGAGAGGCCAGGCCACTGCGAGATGCTCTCTC 2701
Qy 2683 TTACAGGCTCAATGTGTGAGAGGCCAGGCCACTGCGAGATGCTCTCTC 2742
Db 2702 TTACAGGCTCAATGTGTGAGAGGCCAGGCCACTGCGAGATGCTCTCTC 2761
Qy 2743 GAGTTTTTTCAGAACTGTCTTCCAGTAGTTAGTTTCAAGTGGAAACAGAGGGTGTCTCCAGTTT 2802
Db 2762 GAGTTTTTTCAGAACTGTCTTCCAGTAGTTAGTTTCAAGTGGAAACAGAGGGTGTCTCCAGTTT 2821
Qy 2803 GGAGAAAAGAGAGGTTCCAGGAGTAGATTTTAGCATTAATCTCAATTCGTAAAGGAATCTTGG 2862
Db 2822 GGAGAAAAGAGAGGTTCCAGGAGTAGATTTTAGCATTAATCTCAATTCGTAAAGGAATCTTGG 2881
Qy 2863 ACTTGAGCACCTAATGGATATATTTTGAGAGAGAACAGATCACTTTTGGATGTATTAGTTGA 2922
Db 2882 ACTTGAGCACCTAATGGATATATTTTGAGAGAGAACAGATCACTTTTGGATGTATTAGTTGA 2941
Qy 2923 GATGGGACAAAGAGCTGAAAGAGATTTGGAATCAATGCTTTATGGACATAGGCACAACT 2982
Db 2942 GATGGGACAAAGAGCTGAAAGAGATTTGGAATCAATGCTTTATGGACATAGGCACAACT 3001
Qy 2983 AATTAAAGGAGTCAGAGACTTTATCTCGGACAAAGGCTTTAAACCATATTAACTTTT 3042
Db 3002 AATTAAAGGAGTCAGAGACTTTATCTCGGACAAAGGCTTTAAACCATATTAACTTTT 3061
Qy 3043 GAACACCTCTGGTAGTGGAACTTTCTATAGATCTGTCTCTCATGATATAAGAGTTTCA 3102
Db 3062 GAACACCTCTGGTAGTGGAACTTTCTATAGATCTGTCTCTCATGATATAAGAGTTTCA 3121
Qy 3103 GTCTGTGGAGGAGAGATGCAAGTACAGTTTCGAGAGCAGACAGATGGAGTCAATGAGG 3162
Db 3122 GTCTGTGGAGGAGAGATGCAAGTACAGTTTCGAGAGCAGACAGATGGAGTCAATGAGG 3181
Qy 3163 TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTATG 3222
Db 3182 TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTATG 3241
Qy 3223 GGAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCAATGCCAATGA 3282
Db 3242 GGAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCAATGCCAATGA 3301
Qy 3283 ACGAATGCTATTTTCAATGGGTCTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATGA 3342
Db 3302 ACGAATGCTATTTTCAATGGGTCTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATGA 3361
Qy 3343 AAGGATCGGTACATAGTGTGTATTTTGGAGCTGGCAATTTATTTTGTGTAAGAACTCTTC 3402
Db 3362 AAGGATCGGTACATAGTGTGTATTTTGGAGCTGGCAATTTATTTTGTGTAAGAACTCTTC 3421
Qy 3403 CAAAGCAATCAATATGATATGTAATTTGAGAGGAGTACTGGGTGTCAGTTTCAACAAGA 3462
Db 3422 CAAAGCAATCAATATGATATGTAATTTGAGAGGAGTACTGGGTGTCAGTTTCAACAAGA 3481
Qy 3463 CAGATCTTTGTATATTTGCCACAGGAGCTGCTCTTTTCCGGGTAACTTTGGGAAAGTC 3522
Db 3482 CAGATCTTTGTATATTTGCCACAGGAGCTGCTCTTTTCCGGGTAACTTTGGGAAAGTC 3541
Qy 3523 TTTCTGAGTTCAGTGCATGAAATGGGACATTTCTCTCCAGGTCTATCTCAGTCAC 3582
Db 3542 TTTCTGAGTTCAGTGCATGAAATGGGACATTTCTCTCCAGGTCTATCTCAGTCAC 3601
Qy 3583 TGGTAGGCCAGTGTAAATGGCCCTAGCATTTAGCTGAATATGTTTATACAGAGAGAAC 3642

Db 3602 TGGTAGGCCAGTGTAAATGGCCCTAGCATTTAGCTGAATATGTTTATACAGAGAGAAC 3661
Qy 3643 GGCTTATCTCTGAGTATTTTAATTTACTTTACAGATTTATAGGCTTGAAGGTATGTCGATGG 3702
Db 3662 GGCTTATCTCTGAGTATTTTAATTTACTTTACAGATTTATAGGCTTGAAGGTATGTCGATGG 3721
Qy 3703 ATAAATAGTATTTTAAAGAACTAAATTTCCACTGAACCTAAATCATCAAGCAGCAGTGG 3762
Db 3722 ATAAATAGTATTTTAAAGAACTAAATTTCCACTGAACCTAAATCATCAAGCAGCAGTGG 3781
Qy 3763 CCTCTAGCTTTTACTCTCTTTGCTGAAAAA 3797
Db 3782 CCTCTAGCTTTTACTCTCTTTGCTGAAAAA 3816
RESULT 6
ABQ77067
ID ABQ77067 standard; DNA; 3816 BP.
XX
AC ABQ77067;
XX
DT 08-APR-2003 (first entry)
XX
DE Tankyrase H isotype 2 TaHo-2 DNA from clone K23.
XX
KW Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-2;
KW TaHo; cytosolic; immunostimulant; gene therapy; vaccine; cancer; tumour;
KW cell cycle related disorder; poly ADP-ribose polymerase; PARP; ds.
XX
OS Unidentified.
XX
PH Key Location/Qualifiers
FT CDS 3..3725
FT /*tag= a
FT /product= "TaHo-2"
FT /partial
FT /note= "no start codon"
XX
PN WO200286170-A1.
XX
PD 31-OCT-2002.
XX
PF 25-APR-2002; 2002WO-US013185.
XX
PR 25-APR-2001; 2001US-00843159.
XX
PA (RIGE-) RIGEL PHARM INC.
XX
PI Luo Y, Chan E, Xu X, Huang B, Ossovskaya V;
XX
DR WPI; 2003-093158/08.
XX
DR P-PSDB; ABG73731.
XX
PT New recombinant nucleic acid encoding a cell cycle protein, useful for
PT diagnosing and treating a cell cycle related disorder, e.g. cancer.
XX
PS Claim 13; Fig 2A-B; 90pp; English.
XX
CC This invention describes a novel recombinant nucleic acid encoding the
CC cell cycle protein TaHo, a tankyrase H isoform. The products of the
CC invention have cytostatic and immunostimulant activity and can be used
CC for gene therapy and in vaccines. The cell cycle protein TaHo and the
CC nucleic acid encoding the protein are useful for diagnosing and treating
CC a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a
CC tumour cell. The methods are useful for screening for a bioactive agent
CC capable of binding to a cell cycle protein tankyrase H, or a bioactive
CC agent capable of modulating a cell cycle protein tankyrase H or PARP
CC (poly ADP-ribose polymerase) activity. The antibodies are useful for
CC inducing an immune response against the cell cycle proteins. This
CC sequence encodes the tankyrase H isoform 2, TaHo-2, isolated from clone
XX K23 which is described in the disclosure of the invention
SQ Sequence 3816 BP; 1097 A; 806 C; 949 G; 964 T; 0 U; 0 Other;

Query Match		89.4%; Score 3393.4; DB 8; Length 3816;	
Best Local Similarity		99.9%; Pred. No. 0;	
Matches 3394; Conservative		0; Mismatches 1; Indels 0; Gaps 0;	
Qy	403	AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAGTGTCCAAGC	462
Db	422	AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAAATGTCNAGC	481
Qy	463	ACGTGATGATGGGGCCCTTATTCCTCTTCATAATGTCATGCTCTTTTGGTCATGCTGAAGT	522
Db	482	ACGTGATGATGGGGCCCTTATTCCTCTTCATAATGTCATGCTCTTTTGGTCATGCTGAAGT	541
Qy	523	AGTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATAC	582
Db	542	AGTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATAC	601
Qy	583	TCCTCTCCATGAAGTCGCAATTTAAAGAAAGATTTGATGTTTGCATTTGCTGTTTACAGCA	642
Db	602	TCCTCTCCATGAAGTCGCAATTTAAAGAAAGATTTGATGTTTGCATTTGCTGTTTACAGCA	661
Qy	643	TGGAGCTGAGCCAAACCATCCGAAATAACAGATGGAAGGACAGCATTTGATTTAGCAGATCC	702
Db	662	TGGAGCTGAGCCAAACCATCCGAAATAACAGATGGAAGGACAGCATTTGATTTAGCAGATCC	721
Qy	703	ATCTGCCAAAGCAGTGTCTTACTGTTGGAATATTAAGAAAGATGAATCTTTAGAAAGTGCCAG	762
Db	722	ATCTGCCAAAGCAGTGTCTTACTGTTGGAATATTAAGAAAGATGAATCTTTAGAAAGTGCCAG	781
Qy	763	GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACCATTAATGTCATGTCACACGC	822
Db	782	GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACCATTAATGTCATGTCACACGC	841
Qy	823	AAGTGATGGCAGAAAGTCAACTCCATTTACATTTTGGCAGCAGGATATAACAGAGTAAGAAT	882
Db	842	AAGTGATGGCAGAAAGTCAACTCCATTTACATTTTGGCAGCAGGATATAACAGAGTAAGAAT	901
Qy	883	TGTACAGCTGTTTACTGCAACATGGAGCTGATGCTCATGCTTAAAGATAAAGGTGATCTGGT	942
Db	902	TGTACAGCTGTTTACTGCAACATGGAGCTGATGCTCATGCTTAAAGATAAAGGTGATCTGGT	961
Qy	943	ACCATTAACAATGCTGCTGTTCTTATGCTCATTTAAGTAAGTAACTGAACTTTTGGTCAAGCA	1002
Db	962	ACCATTAACAATGCTGCTGTTCTTATGCTCATTTAAGTAAGTAACTGAACTTTTGGTCAAGCA	1021
Qy	1003	TGGTGCCTGTGTAATGCAATGGACTTGTGGCAATTCACCTCCTCTTCATGAGGCGAGCTTC	1062
Db	1022	TGGTGCCTGTGTAATGCAATGGACTTGTGGCAATTCACCTCCTCTTCATGAGGCGAGCTTC	1081
Qy	1063	TAAGAACAGGGTTGAAGTATGTTCTCTTCTTTAAAGTTATGGTGAGACCCCAACACTGCT	1122
Db	1082	TAAGAACAGGGTTGAAGTATGTTCTCTTCTTTAAAGTTATGGTGAGACCCCAACACTGCT	1141
Qy	1123	CAATTTGTCAATAAAGTGTATAGACTTTGGCTTCCACACACAGTTTAAAGAAAGATT	1182
Db	1142	CAATTTGTCAATAAAGTGTATAGACTTTGGCTTCCACACACAGTTTAAAGAAAGATT	1201
Qy	1183	AGCATATGAATTTAAAGGCCACCTGTTGCTGCAAGCTGCAAGAGAGCTGATGTTACTCG	1242
Db	1202	AGCATATGAATTTAAAGGCCACCTGTTGCTGCAAGCTGCAAGAGAGCTGATGTTACTCG	1261
Qy	1243	AATCAAAAAACATCTCTCTCTGGAATGTTGAATTTTCAAGCATCCTCAAAACACATGAAC	1302
Db	1262	AATCAAAAAACATCTCTCTCTGGAATGTTGAATTTTCAAGCATCCTCAAAACACATGAAC	1321
Qy	1303	AGCATTGCAATTTGCTGCTGCACTCCATATCCCAAAAGAAAGCAATATGTTGAATCTGTT	1362
Db	1322	AGCATTGCAATTTGCTGCTGCACTCCATATCCCAAAAGAAAGCAATATGTTGAATCTGTT	1381
Qy	1363	GCTAAGAAAAAGGAGCAACATCAATGAAAGACTTAAGAAATTTCTGACTCTCTGCAAGT	1422
Db	1382	GCTAAGAAAAAGGAGCAACATCAATGAAAGACTTAAGAAATTTCTGACTCTCTGCAAGT	1441

Qy	1423	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT	1482
Db	1442	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT	1501
Qy	1483	TAATGCTCTGATTAATCTTGGTTCAGACTTCTCTTACACAGAGCTGCATATTTGTTGTCATCT	1542
Db	1502	TAATGCTCTGATTAATCTTGGTTCAGACTTCTCTTACACAGAGCTGCATATTTGTTGTCATCT	1561
Qy	1543	ACAAACCTGCGCGCTACTCTCTGAGCTATGGGTGTGATCCTAACATTAATATCCCTTCAGGG	1602
Db	1562	ACAAACCTGCGCGCTACTCTCTGAGCTATGGGTGTGATCCTAACATTAATATCCCTTCAGGG	1621
Qy	1603	CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCCAGAGGGTATCTC	1662
Db	1622	CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCCAGAGGGTATCTC	1681
Qy	1663	ATTAGGTAATTCAGAGGAGACAGACAAATTTGCTGGAAGCTGCAAAAGGCTGAGATGTGGA	1722
Db	1682	ATTAGGTAATTCAGAGGAGACAGACAAATTTGCTGGAAGCTGCAAAAGGCTGAGATGTGGA	1741
Qy	1723	AACGTGTAATAAACTGTGTACTGTTTCAGAGTGTCAACTGTCAGAGACATTTGAAGGCGTCA	1782
Db	1742	AACGTGTAATAAACTGTGTACTGTTTCAGAGTGTCAACTGTCAGAGACATTTGAAGGCGTCA	1801
Qy	1783	GTCTACACCACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT	1842
Db	1802	GTCTACACCACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT	1861
Qy	1843	ACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGAGGAGCCCTGTACCTTTGCACAATGC	1902
Db	1862	ACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGAGGAGCCCTGTACCTTTGCACAATGC	1921
Qy	1903	ATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTGTAAACATGAGCAGTAGTTAA	1962
Db	1922	ATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTGTAAACATGAGCAGTAGTTAA	1981
Qy	1963	TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2022
Db	1982	TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2041
Qy	2023	AATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACCAAAAAAACAAGGATGGAAA	2082
Db	2042	AATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACCAAAAAAACAAGGATGGAAA	2101
Qy	2083	TACTCTTTGGATCTGTTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTTAGGGGAGA	2142
Db	2102	TACTCTTTGGATCTGTTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTTAGGGGAGA	2161
Qy	2143	TGCAGCTTTGCTAGATGCTGCAAGAAAGGGTGTGTTAGCCAGAGTGAAGAAAGTTGCTTTC	2202
Db	2162	TGCAGCTTTGCTAGATGCTGCAAGAAAGGGTGTGTTAGCCAGAGTGAAGAAAGTTGCTTTC	2221
Qy	2203	TCCTGATAATGTAATTTGCGCGATACCCAAAGGAGACATTTCAACACTTTTACATTTAGC	2262
Db	2222	TCCTGATAATGTAATTTGCGCGATACCCAAAGGAGACATTTCAACACTTTTACATTTAGC	2281
Qy	2263	AGCTGGTTTAAATTAATTTAGAAAGTTGAGAGTATTTGTTTAAACACGAGCTGATGTA	2322
Db	2282	AGCTGGTTTAAATTAATTTAGAAAGTTGAGAGTATTTGTTTAAACACGAGCTGATGTA	2341
Qy	2323	TGCCCAAGACAAAGGAGGACTTATTTCTTTTACATAATGTCAGCATCTTACGGGCGATGAGA	2382
Db	2342	TGCCCAAGACAAAGGAGGACTTATTTCTTTTACATAATGTCAGCATCTTACGGGCGATGAGA	2401
Qy	2383	TGTAGAGCTCTACTAATAAAGTATAATGATGTGTCATGTCGCAAGGCAATATGGGCTTT	2442
Db	2402	TGTAGAGCTCTACTAATAAAGTATAATGATGTGTCATGTCGCAAGGCAATATGGGCTTT	2461
Qy	2443	CACACCTTTGACCAAGCAGCCCAAAAGGAGCAACACAGCTTTGTGCTTTGTTGCTAGC	2502
Db	2462	CACACCTTTGACCAAGCAGCCCAAAAGGAGCAACACAGCTTTGTGCTTTGTTGCTAGC	2521
Qy	2503	CCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGACAAACACTTTTAGATTTTCTTC	2562

QY 403 AGGTTTTGGGGGAAAGAGCTAGTTGAATATTTGGCTTCAGAAATGGTGCAGAGTGTCCAAAGC 462
DB 422 AGGTTTTGGGGGAAAGAGCTAGTTGAATATTTGGCTTCAGAAATGGTGCAGAGTGTCCAAAGC 481
QY 463 ACGTGATGATGGGGCCCTTATTCCTCTTCAATAATGCATGCTCTTTTGGTGCATGCTGAAAGT 522
DB 482 ACGTGATGATGGGGCCCTTATTCCTCTTCAATAATGCATGCTCTTTTGGTGCATGCTGAAAGT 541
QY 523 AGTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATAC 582
DB 542 AGTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTTATAC 601
QY 583 TCCTCTCAGAGTGCATTAATAAGGAAAGATTTGATGTTTGGTGCATGCTGTTTACAGCA 642
DB 602 TCCTCTCAGAGTGCATTAATAAGGAAAGATTTGATGTTTGGTGCATGCTGTTTACAGCA 661
QY 643 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 702
DB 662 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 721
QY 703 ATCTGCCAAAGCAGTGTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG 762
DB 722 ATCTGCCAAAGCAGTGTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG 781
QY 763 GAGTGGCAATGAAGAAATGATGGCTCTACTCACACCATTAATGTCAACTGCCAGC 822
DB 782 GAGTGGCAATGAAGAAATGATGGCTCTACTCACACCATTAATGTCAACTGCCAGC 841
QY 823 AAGTGATGGCAGAAAGTCAACTCCANTTACATTTGGCAGCAGATATAACAGAGTAAAGAT 882
DB 842 AAGTGATGGCAGAAAGTCAACTCCANTTACATTTGGCAGCAGATATAACAGAGTAAAGAT 901
QY 883 TGTACAGCTGTCTGCAACATGGAGCTGATGCTCATGCTTAAGATAAGGTGATCTGGT 942
DB 902 TGTACAGCTGTCTGCAACATGGAGCTGATGCTCATGCTTAAGATAAGGTGATCTGGT 961
QY 943 ACCATTACCAATGCTGTCTTATGTGTCATTATGAAGTAACTGAATCTTTTGGTCAAGCA 1002
DB 962 ACCATTACCAATGCTGTCTTATGTGTCATTATGAAGTAACTGAATCTTTTGGTCAAGCA 1021
QY 1003 TGGTGCTGTGTAATGCAATGGAGCTGTGGCAATTCATCTCTTTCATGAGGCGAGCTTC 1062
DB 1022 TGGTGCTGTGTAATGCAATGGAGCTGTGGCAATTCATCTCTTTCATGAGGCGAGCTTC 1081
QY 1063 TAAGAACAGGCTTGAAGTATGCTCTTCTTCTTAAAGTATGGTGCAGACCCCAACTGCT 1122
DB 1082 TAAGAACAGGCTTGAAGTATGCTCTTCTTCTTAAAGTATGGTGCAGACCCCAACTGCT 1141
QY 1123 CAATTTGTCAATAAAGTGTCTATAGACTTGGCTCCACACACAGTTTAAAGAAAGATT 1182
DB 1142 CAATTTGTCAATAAAGTGTCTATAGACTTGGCTCCACACACAGTTTAAAGAAAGATT 1201
QY 1183 AGCATATGAATTTAAAGGCCACTGTTGCTGCAAGCTGCACAGAGCTGATGTTACTCG 1242
DB 1202 AGCATATGAATTTAAAGGCCACTGTTGCTGCAAGCTGCACAGAGCTGATGTTACTCG 1261
QY 1243 AATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTGAAACACATGAAC 1302
DB 1262 AATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTGAAACACATGAAC 1321
QY 1303 AGCATGATGTTGCTGCTGCTGCTATCTCCATATCCCAAAAAAGCAATATGTGAATCTGTT 1362
DB 1322 AGCATGATGTTGCTGCTGCTGCTATCTCCATATCCCAAAAAAGCAATATGTGAATCTGTT 1381
QY 1363 GCTAAGAAAAAGGAGCAACATCAATGAAGAACTAAAGAAATCTTGAATCTCTGCAAGT 1422
DB 1382 GCTAAGAAAAAGGAGCAACATCAATGAAGAACTAAAGAAATCTTGAATCTCTGCAAGT 1441
QY 1423 GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT 1482
DB 1442 GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT 1501
QY 1483 TAATGCTCTGGATAATCTTTGGTGCAGACTTCTCTACACAGAGCTGCATATTTGGTGCATCT 1542

DB 1502 TAATGCTCTGGATAATCTTTGGTGCAGACTTCTCTACACAGAGCTGCATATTTGGTGCATCT 1561
QY 1543 ACAAACTGCGCGCTACTCTGAGCTATGGTGTGATGCTTAACATTTATATCCCTTCAGGG 1602
DB 1562 ACAAACTGCGCGCTACTCTGAGCTATGGTGTGATGCTTAACATTTATATCCCTTCAGGG 1621
QY 1603 CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGGCTATCTC 1662
DB 1622 CTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGGCTATCTC 1681
QY 1663 ATTAGGTAATTTACAGAGCAGACAGCAATTTGCTGGAAGCTGCAAAAGGCTGAGATGTCGA 1722
DB 1682 ATTAGGTAATTTACAGAGCAGACAGCAATTTGCTGGAAGCTGCAAAAGGCTGAGATGTCGA 1741
QY 1723 AACTGTAAAAAACTGTGTACTGTTTACAGAGTGTCAACTGTCAGAGACATTTGAAGGCGCTCA 1782
DB 1742 AACTGTAAAAAACTGTGTACTGTTTACAGAGTGTCAACTGTCAGAGACATTTGAAGGCGCTCA 1801
QY 1783 GTCTACACCACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT 1842
DB 1802 GTCTACACCACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT 1861
QY 1843 ACAGCATGGAGCTGATGCTATAAGATATAAGAGGCGCTTGTACTTTTGCACAATGC 1902
DB 1862 ACAGCATGGAGCTGATGCTATAAGATATAAGAGGCGCTTGTACTTTTGCACAATGC 1921
QY 1903 ATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTTGTTAAACATGAGGAGTAGTTAA 1962
DB 1922 ATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTTGTTAAACATGAGGAGTAGTTAA 1981
QY 1963 TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
DB 1982 TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2041
QY 2023 AATTTGCAAACTTCTGCTCCAGCATGTTGTCAGACCCCTACCAAAAAAAGCAGGATGGAAA 2082
DB 2042 AATTTGCAAACTTCTGCTCCAGCATGTTGTCAGACCCCTACCAAAAAAAGCAGGATGGAAA 2101
QY 2083 TACTCTTTTGGATCTTGTATAAGATGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA 2142
DB 2102 TACTCTTTTGGATCTTGTATAAGATGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA 2161
QY 2143 TGCAAGCTTGTGCTAGATCTGCCAAGAGGCTTGTGTAGCCAGAGTGAAGAGTGTCTTC 2202
DB 2162 TGCAAGCTTGTGCTAGATCTGCCAAGAGGCTTGTGTAGCCAGAGTGAAGAGTGTCTTC 2221
QY 2203 TCCTGATAATGTAAATTTGCCGCGATACCCAGGCGAGACATTTCAACACTTTTACATTTAGC 2262
DB 2222 TCCTGATAATGTAAATTTGCCGCGATACCCAGGCGAGACATTTCAACACTTTTACATTTAGC 2281
QY 2263 AGCTGGTTATTAATTTAGAGTTGAGAGTTGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA 2322
DB 2282 AGCTGGTTATTAATTTAGAGTTGAGAGTTGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA 2341
QY 2323 TGCCCAAGACAAAGGAGGAGCTTATTTCTTTTACATAATGTCAGCATCTTACGGGCAATGAGA 2382
DB 2342 TGCCCAAGACAAAGGAGGAGCTTATTTCTTTTACATAATGTCAGCATCTTACGGGCAATGAGA 2401
QY 2383 TGTAAGCAGCTCTACTAATAAAGTATAATGATGCTCAATGTCGAATGCCAGCAAAATGGGCTTT 2442
DB 2402 TGTAAGCAGCTCTACTAATAAAGTATAATGATGCTCAATGTCGAATGCCAGCAAAATGGGCTTT 2461
QY 2443 CACACCTTTGCAAGAGCGCCCAAGGAGGAGCAACAGCTTTGCTGCTTTGCTGCTAGC 2502
DB 2462 CACACCTTTGCAAGAGCGCCCAAGGAGGAGCAACAGCTTTGCTGCTTTGCTGCTAGC 2521
QY 2503 CCATGGAGCTGACCCGAGCTCTTAAATATCAGGAAGGAGCAACACTTTTAGATTTAGTTTC 2562
DB 2522 CCATGGAGCTGACCCGAGCTCTTAAATATCAGGAAGGAGCAACACTTTTAGATTTAGTTTC 2581
QY 2563 AGCGGATGATGTCAGCGCTCTTCTGACAGCAGCATGCCCCCATCTGCTGCTGCTCTG 2622

Db 2582 AGCGATGATGTCAGCGCTCTCTGACAGCAGCCATGCCCCCTCTGCTCTGCCCTCTTG 2641
Qy 2623 TTACAAGCCTCAAGTGTCTCAATGTGTGAGAGAGCCAGGAGCCACTCGAGATGCTCTCTC 2682
Db 2642 TTACAAGCCTCAAGTGTCTCAATGTGTGAGAGAGCCAGGAGCCACTCGAGATGCTCTCTC 2701
Qy 2683 TTCAAGTCCATAGCCCATCAAGCCCTTCTGACGACGACGATCTTGACAACTTATCTGG 2742
Db 2702 TTCAAGTCCATAGCCCATCAAGCCCTTCTGACGACGACGATCTTGACAACTTATCTGG 2761
Qy 2743 GAGTTTTTCAGAACTGTCTCAGTAGTGTAGTTCAGTGGAAACAGAGGCTCTCCAGTTT 2802
Db 2762 GAGTTTTTCAGAACTGTCTCAGTAGTGTAGTTCAGTGGAAACAGAGGCTCTCCAGTTT 2821
Qy 2803 GGAGAAAAGAGGTTCCAGGAGTAGATTTTTCAGATCACTCAATTCGTAAGGAATCTTGG 2862
Db 2822 GGAGAAAAGAGGTTCCAGGAGTAGATTTTTCAGATCACTCAATTCGTAAGGAATCTTGG 2881
Qy 2863 GATGGGACAAAGAGCTGAAGGAGATTGGAATCAATGCTTTATGGACATAGGCAAAACT 2922
Db 2882 ACTTGAGCACCCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGTTAGTTGA 2941
Qy 2923 GATGGGACAAAGAGCTGAAGGAGATTGGAATCAATGCTTTATGGACATAGGCAAAACT 2982
Db 2942 GATGGGACAAAGAGCTGAAGGAGATTGGAATCAATGCTTTATGGACATAGGCAAAACT 3001
Qy 2983 AATTAAAGGAGTCGAGAGACTTATCTCCGACAAACAAAGGCTTTAAACCATATTTAACTTT 3042
Db 3002 AATTAAAGGAGTCGAGAGACTTATCTCCGACAAACAAAGGCTTTAAACCATATTTAACTTT 3061
Qy 3043 GAACACCTCTGTTAGTGGAACTTCTATAGATGCTCTCTCTGATGATTAAGAGTTTCA 3102
Db 3062 GAACACCTCTGTTAGTGGAACTTCTATAGATGCTCTCTCTGATGATTAAGAGTTTCA 3121
Qy 3103 GTCTGTGGAGAAAGAGATGCAAGGTACAGTTCGAGAGCAGACAGATGGAGTCAATGAGG 3162
Db 3122 GTCTGTGGAGAAAGAGATGCAAGGTACAGTTCGAGAGCAGACAGATGGAGTCAATGAGG 3181
Qy 3163 TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAAACTATG 3222
Db 3182 TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAAACTATG 3241
Qy 3223 GGAAGATACACTCACCGGAGAAAGAGTTCTGAGAGAAACACACACCAATGCAATGA 3282
Db 3242 GGAAGATACACTCACCGGAGAAAGAGTTCTGAGAGAAACACACACCAATGCAATGA 3301
Qy 3283 ACGAATGCTATTTTCATGGGCTCTCTTTGTGAATGCAATTTATCCAAAGGCTTTGATGA 3342
Db 3302 ACGAATGCTATTTTCATGGGCTCTCTTTGTGAATGCAATTTATCCAAAGGCTTTGATGA 3361
Qy 3343 AAGCATGCGTACATAGTGGTATGTTTGGAGCTGGCAATTTATTTGCTGAAACTCTTC 3402
Db 3362 AAGCATGCGTACATAGTGGTATGTTTGGAGCTGGCAATTTATTTTGTGAAACTCTTC 3421
Qy 3403 CAAAAGCAATCAATATGATATGAAATGGAGAGGTACTGGGTCTCCAGTTCAACAAGA 3462
Db 3422 CAAAAGCAATCAATATGATATGAAATGGAGAGGTACTGGGTCTCCAGTTCAACAAGA 3481
Qy 3463 CAGATCTGTTTACATTTGCCACAGCAGCTGCTCTTTTCCGGGTAACTTTGGGAAAGTC 3522
Db 3482 CAGATCTGTTTACATTTGCCACAGCAGCTGCTCTTTTCCGGGTAACTTTGGGAAAGTC 3541
Qy 3523 TTTCTCGAGTTCAAGTGAATGAAATAGGACATCTCTCTCCAGGTATCACTCAGTCAAC 3582
Db 3542 TTTCTCGAGTTCAAGTGAATGAAATAGGACATCTCTCTCCAGGTATCACTCAGTCAAC 3601
Qy 3583 TGGTAGCCCACTGAATGCTAGATGCAATATGTTATTTTACAGAGAGAAC 3642
Db 3602 TGGTAGCCCACTGAATGCTAGATGCAATATGTTATTTTACAGAGAGAAC 3661
Qy 3643 GGCTTATCTCAGTATTTAAATTTACTTACCAATATGAGGCTCAAGGATGTCGATGG 3702
Db 3662 GGCTTATCTCAGTATTTAAATTTACTTACCAATATGAGGCTCAAGGATGTCGATGG 3721

Qy 3703 ATAAATAGTTATTTTAAGAACTAAATTCCTCACTGAACCTAAATCATCAAGACAGCTGG 3762
Db 3722 ATAAATAGTTATTTTAAGAACTAAATTCCTCACTGAACCTAAATCATCAAGACAGCTGG 3781
Qy 3763 CCTCTAGTTTACTCTCTTCTGCTGAAAAA 3797
Db 3782 CCTCTAGTTTACTCTCTTCTGCTGAAAAA 3816

RESULT 8
ID ADY97760 standard; cDNA; 3816 BP.
XX ADY97760;
XX AC
XX XX
DT 16-JUN-2005 (first entry)
XX Human tankyrase homologue isotype 2 encoding cDNA SEQ ID NO:2.
DE cell cycle; cancer; cytosstatic; tankyrase homologue isotype 2; gene; ss.
XX Homo sapiens.
XX OS
XX PH
XX Key Location/Qualifiers
XX CDS 3..3725
FT FT /*tag= a
FT FT /product= "tankyrase homologue isotype 2"
XX PN
XX US2005074825-A1.
XX PD
XX 07-APR-2005.
XX PF
XX 08-JUL-2003; 2003US-00616101.
XX PR
XX 25-OCT-1999; 99US-00427154.
XX PR
XX 25-OCT-2000; 2000US-00696668.
XX PR
XX 25-APR-2001; 2001US-00843159.
XX XX
XX (LUOY/) LUO Y.
XX (CHAN/) CHAN E.
XX (XUX/) XU X.
XX (HUAN/) HUANG B.
XX (OSSO/) OSSOVSKAYA V.
XX
XX Luo Y, Chan E, Xu X, Huang B, Ossovskaya V;
XX WPI; 2005-294737/30.
XX P-PSDB; ADY97762.
XX
XX Novel recombinant polypeptide such as cell cycle protein e.g. tankyrase
XX homolog, useful for screening its modulator.
XX
XX Claim 10; SEQ ID NO 2; 75pp; English.
XX
XX The invention relates to a recombinant polypeptide (I) such as cell cycle
XX protein e.g. tankyrase homologue (TaHo), comprising an amino acid
XX sequence having 85% or more sequence identity to the 1065 amino acid
XX sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also
XX described: (1) diagnosing cancer, which involves determining the activity
XX of (I) from a test sample of an individual and comparing the level with a
XX control with a control; (2) treating (M1) an individual with a cell cycle
XX related disorder, which involves administering to the individual an
XX inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (I),
XX comprising a nucleic acid that hybridizes under high stringent conditions
XX to a sequence complementary to the 3797 base pair sequence of ADY97759 or
XX the 3816 base pair sequence of ADY97760, or a nucleic acid having 85% or
XX more sequence identity to ADY97759 or ADY97760; (4) an expression vector
XX (III) comprising (II) operably linked to regulatory sequences recognized
XX by a host cell (IV) transformed with the nucleic acid; (5) a host cell
XX comprising (II) or (III); (6) producing (I); (7) a polypeptide that
XX specifically binds to (I); and (8) inhibiting (M2) growth of a tumor
XX cell, involves contacting the tumor with a bioactive agent capable of

CC inhibiting TaHo activity. (I) is useful for screening a bioactive agent
CC capable of modulating (I), or screening for agents capable of interfering
CC with the binding of (I) and P21. (M1) is useful for treating an
CC individual with a cell cycle related disorder. (M2) is useful for
CC inhibiting growth of a tumor cell by a bioactive agent e.g. antisense
CC oligonucleotide. The present sequence encodes the human tankyrase
CC homologue isotype 2.

XX SQ Sequence 3816 BP; 1097 A; 806 C; 949 G; 964 T; 0 U; 0 Other;

Query Match		89.4%;	Score 3393.4;	DB 14;	Length 3816;
Best Local Similarity		99.9%;	Pred. No. 0;		
Matches 3394;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	403	AGGTTTGGGGGAAAGACGCTAGTTGAATATTTGCTTCAGAAATGTCGCAAGTGTCCAAAGC	462		
Db	422	AGGTTTGGGGGAAAGACGCTAGTTGAATATTTGCTTCAGAAATGTCGCAAGTGTCCAAAGC	481		
Qy	463	ACGTGATGATGGGGCCCTTATTCCTCTTCATAATGCATGCTCTTTTGGTTCATGCTGAAAGT	522		
Db	482	ACGTGATGATGGGGCCCTTATTCCTCTTCATAATGCATGCTCTTTTGGTTCATGCTGAAAGT	541		
Qy	523	AGTCAATCTCTTTTGGACATGCTGACATGTCGACACCCCAATGCTGAGATAATTTGGAATATAC	582		
Db	542	AGTCAATCTCTTTTGGACATGCTGACATGTCGACACCCCAATGCTGAGATAATTTGGAATATAC	601		
Qy	583	TCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATTGATGTTTGCATGTTGCTGTACAGCA	642		
Db	602	TCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATTGATGTTTGCATGTTGCTGTACAGCA	661		
Qy	643	TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTAGCAGATCC	702		
Db	662	TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTAGCAGATCC	721		
Qy	703	ATCTGCCAAAGCAGTCTTACTGTTGAATATAAGAAAGATGAACTCTTTAGAAAGTGCCAG	762		
Db	722	ATCTGCCAAAGCAGTCTTACTGTTGAATATAAGAAAGATGAACTCTTTAGAAAGTGCCAG	781		
Qy	763	GAGTGGCAATGAAGAAATGATGGCTCTACTACACCATTTAAATGTCACATGCCACGC	822		
Db	782	GAGTGGCAATGAAGAAATGATGGCTCTACTACACCATTTAAATGTCACATGCCACGC	841		
Qy	823	AAGTGATGGCAGAAAGTCAATTCATTTACATTTGGCAGCAGGATATAACAGATTAAGAT	882		
Db	842	AAGTGATGGCAGAAAGTCAATTCATTTACATTTGGCAGCAGGATATAACAGATTAAGAT	901		
Qy	883	TGTACAGCTGTTCGCAACATGGAGCTGATGTCCATGCTAAAGATAAAGTGATCTGGT	942		
Db	902	TGTACAGCTGTTCGCAACATGGAGCTGATGTCCATGCTAAAGATAAAGTGATCTGGT	961		
Qy	943	ACCATTACCAATGCTGTTCTTATGGTTCATTTAGATTAAGTAAGTAACTTTTGGTCAAGCA	1002		
Db	962	ACCATTACCAATGCTGTTCTTATGGTTCATTTAGATTAAGTAACTTTTGGTCAAGCA	1021		
Qy	1003	TGGTCCCTGTGTAATGCAATGGACTGTGGCAATTCACCTCTCTTCATGAGGAGCTTC	1062		
Db	1022	TGGTCCCTGTGTAATGCAATGGACTGTGGCAATTCACCTCTCTTCATGAGGAGCTTC	1081		
Qy	1063	TAAAGAACAGGGTGAAGTATGTTCTCTCTTAAAGTTATGGTGAGACCCCAACATGCT	1122		
Db	1082	TAAAGAACAGGGTGAAGTATGTTCTCTCTTAAAGTTATGGTGAGACCCCAACATGCT	1141		
Qy	1123	CAATTTGTCACATTAAGTGTCTATAGACTTGGCTCCGACACACAGTTAAAGAAAGNTT	1182		
Db	1142	CAATTTGTCACATTAAGTGTCTATAGACTTGGCTCCGACACACAGTTAAAGAAAGNTT	1201		
Qy	1183	AGCATATGAAATTTAAAGGCCACTCGTGTCTGCAAGCTGACAGAGCTGATTTACTCG	1242		
Db	1202	AGCATATGAAATTTAAAGGCCACTCGTGTCTGCAAGCTGACAGAGCTGATTTACTCG	1261		
Qy	1243	AATCAAAAAACATCTCTCTCTGGAAATGGTGAATTTCAAGCATCTTCAACACATGAAC	1302		
Db	1262	AATCAAAAAACATCTCTCTCTGGAAATGGTGAATTTCAAGCATCTTCAACACATGAAC	1321		

Qy	1303	AGCATTGCATTGTGCTGCTCATCTCCATATCCCAAAAGAAAGCAAAATATCTGAACCTGT	1362		
Db	1322	AGCATTGCATTGTGCTGCTCATCTCCATATCCCAAAAGAAAGCAAAATATCTGAACCTGT	1381		
Qy	1363	GCTAAGAAAAAGGACCAACATCAATGAAGAAAGCTTAAAGAAATTTCTTGACCTCTTCGACGT	1422		
Db	1382	GCTAAGAAAAAGGACCAACATCAATGAAGAAAGCTTAAAGAAATTTCTTGACCTCTTCGACGT	1441		
Qy	1423	GGCATCTGAGNAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAAAGGT	1482		
Db	1442	GGCATCTGAGNAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAAAGGT	1501		
Qy	1483	TAAATGCTCTGGATAATCTTTGGTTCAGACTTCTCTACACAGAGCTGCATATTTGGTTCATCT	1542		
Db	1502	TAAATGCTCTGGATAATCTTTGGTTCAGACTTCTCTACACAGAGCTGCATATTTGGTTCATCT	1561		
Qy	1543	ACAAACCTGCCGCCCTACTCTCTGAGCTATGGGTGTGATCTTAACATTAATATATCCCTTCAGGG	1602		
Db	1562	ACAAACCTGCCGCCCTACTCTCTGAGCTATGGGTGTGATCTTAACATTAATATATCCCTTCAGGG	1621		
Qy	1603	CTTTACTGCTTTACAGATGGGAAATGAAATGTTACAGCAACTCTCTCCAAAGAGGTATCTC	1662		
Db	1622	CTTTACTGCTTTACAGATGGGAAATGAAATGTTACAGCAACTCTCTCCAAAGAGGTATCTC	1681		
Qy	1663	ATTAGGTAAATTCAGAGGCAGACAGCAATTCCTGGAAGCTGCAAGGCTGGAGATGTGCA	1722		
Db	1682	ATTAGGTAAATTCAGAGGCAGACAGCAATTCCTGGAAGCTGCAAGGCTGGAGATGTGCA	1741		
Qy	1723	AACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGTCAGAGACATTTGAAGGCGCTCA	1782		
Db	1742	AACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGTCAGAGACATTTGAAGGCGCTCA	1801		
Qy	1783	GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT	1842		
Db	1802	GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT	1861		
Qy	1843	ACAGCATGGAGCTCATGTGCATGCTTAAAGTAAAGGAGGCTCTTACCTTTGCAACAATGC	1902		
Db	1862	ACAGCATGGAGCTCATGTGCATGCTTAAAGTAAAGGAGGCTCTTACCTTTGCAACAATGC	1921		
Qy	1903	ATGTTCTTTATGGACATTTATGAAGTTGCAGAACTTTCTTTTAAACATGGAGCAGTAGTTAA	1962		
Db	1922	ATGTTCTTTATGGACATTTATGAAGTTGCAGAACTTTCTTTTAAACATGGAGCAGTAGTTAA	1981		
Qy	1963	TGTAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGAAATATGA	2022		
Db	1982	TGTAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGAAATATGA	2041		
Qy	2023	AAATTTGCAAACTTCTGCTCCAGCATGCTGCAGACCCCTACCAAAAAACACGGATGGAAA	2082		
Db	2042	AAATTTGCAAACTTCTGCTCCAGCATGCTGCAGACCCCTACCAAAAAACACGGATGGAAA	2101		
Qy	2083	TACTCTTTTGGATCTTGTTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA	2142		
Db	2102	TACTCTTTTGGATCTTGTTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA	2161		
Qy	2143	TGCAGCTTTGCTAGATGCTGCCAAAGAGGGTGTGTTTACGACAGTGAAGAGTTGCTCTTC	2202		
Db	2162	TGCAGCTTTGCTAGATGCTGCCAAAGAGGGTGTGTTTACGACAGTGAAGAGTTGCTCTTC	2221		
Qy	2203	TCCTGATAATGTAATTTGCCGCGATACCCAGGCGAGACATTTCAACCTTTTACATTTAGC	2262		
Db	2222	TCCTGATAATGTAATTTGCCGCGATACCCAGGCGAGACATTTCAACCTTTTACATTTAGC	2281		
Qy	2263	AGCTGGTTATAATTTAGAAAGTTGAGAGTATTTGTTTACAAACACGAGCTGATGTGAA	2322		
Db	2282	AGCTGGTTATAATTTAGAAAGTTGAGAGTATTTGTTTACAAACACGAGCTGATGTGAA	2341		
Qy	2323	TGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATATGACGATCTTACGGGCGATGTAGA	2382		
Db	2342	TGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATATGACGATCTTACGGGCGATGTAGA	2401		

QY 2393 TGTAGCAGCTCTACTAATAAAGTATATATGCGATGTGTCAATGCCACGACCAAAATGGGCTTT 2442
Db 2402 TGTAGCAGCTCTACTAATAAAGTATATATGCGATGTGTCAATGCCACGACCAAAATGGGCTTT 2461
QY 2443 CACACCTTTGACAGAGCAGCCCAAAAGGAGCAGAACACAGCTTTGTGTCTTTGTTGCTAGC 2502
Db 2462 CACACCTTTGACAGAGCAGCCCAAAAGGAGCAGAACACAGCTTTGTGTCTTTGTTGCTAGC 2521
QY 2503 CCATGGAGCTGACCCGACTCTTAAATAATCAGGAAGGACAAAACACCTTTAGATTGTTTC 2562
Db 2522 CCATGGAGCTGACCCGACTCTTAAATAATCAGGAAGGACAAAACACCTTTAGATTGTTTC 2581
QY 2563 AGCGGATGATGTCAGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTGCCCTCTTG 2622
Db 2582 AGCGGATGATGTCAGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTGCCCTCTTG 2641
QY 2623 TTACAAGGCTCAAGTGCTCAATGGTGTGAGAAGCCAGGAGCCACTGCAGATGCTCTCTC 2682
Db 2642 TTACAAGGCTCAAGTGCTCAATGGTGTGAGAAGCCAGGAGCCACTGCAGATGCTCTCTC 2701
QY 2683 TTCAGGCTCCATCTAGCCCATCAAGCCTTTCTGACGCCAGAGCTTTGACAACTTATCTGG 2742
Db 2702 TTCAGGCTCCATCTAGCCCATCAAGCCTTTCTGACGCCAGAGCTTTGACAACTTATCTGG 2761
QY 2743 GAGTTTTTTCAGAACTGCTCTCAGTAGTTAGTTTCAAGTGGACAGAGGCTGCTCCAGTTT 2802
Db 2762 GAGTTTTTTCAGAACTGCTCTCAGTAGTTAGTTTCAAGTGGACAGAGGCTGCTCCAGTTT 2821
QY 2803 GGAGAAAAGAGAGGTTCCAGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGG 2862
Db 2822 GGAGAAAAGAGAGGTTCCAGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGG 2881
QY 2863 ACTTGAGCACCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGATTAGTTGA 2922
Db 2882 ACTTGAGCACCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGATTAGTTGA 2941
QY 2923 GATGGGACAAAGAGCTGAAGGATTTGGATCAATGCTTATGGACATAGGCACAACT 2982
Db 2942 GATGGGACAAAGAGCTGAAGGATTTGGATCAATGCTTATGGACATAGGCACAACT 3001
QY 2983 AATTAAAGAGTTCGAGAGACTTATCTCCGACAAACAGAGTCTTAACCCATATTTAACTTT 3042
Db 3002 AATTAAAGAGTTCGAGAGACTTATCTCCGACAAACAGAGTCTTAACCCATATTTAACTTT 3061
QY 3043 GAACACCTCTGGTAGTGAACAAATCTTATAGATCTGTCTCTGATGATAAGAGTTTCA 3102
Db 3062 GAACACCTCTGGTAGTGAACAAATCTTATAGATCTGTCTCTGATGATAAGAGTTTCA 3121
QY 3103 GTCTGTGGAGGAGATGCAAGTACAGTTTCGAGAGCAGAGATGGAGTCAATGAGG 3162
Db 3122 GTCTGTGGAGGAGATGCAAGTACAGTTTCGAGAGCAGAGATGGAGTCAATGAGG 3181
QY 3163 TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTATG 3222
Db 3182 TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTATG 3241
QY 3223 GGAAGATACACTCAACCGAGAAAGAGTTTCTGAAGAAACCAACACCATGCAATGA 3282
Db 3242 GGAAGATACACTCAACCGAGAAAGAGTTTCTGAAGAAACCAACACCATGCAATGA 3301
QY 3283 ACGAATGCTATTTCAATGGGCTCTCTTTTGTGATGCAATTTCCACAAAGGCTTTGATGA 3342
Db 3302 ACGAATGCTATTTCAATGGGCTCTCTTTTGTGATGCAATTTCCACAAAGGCTTTGATGA 3361
QY 3343 AAGGCATCGGTACATAGTGGTGTATGTTTGGAGCTGGCACTTTATTTGCTGAAAACCTCTTC 3402
Db 3362 AAGGCATCGGTACATAGTGGTGTATGTTTGGAGCTGGCACTTTATTTGCTGAAAACCTCTTC 3421
QY 3403 CAAAAGCAATCAATATGATATATGGAATTTGGAGGAGGTACTGGGTGTCAGTTTCAAGA 3462
Db 3422 CAAAAGCAATCAATATGATATATGGAATTTGGAGGAGGTACTGGGTGTCAGTTTCAAGA 3481
QY 3463 CAGATCTTGTGTACATTGCCACAGCAGCTGCTCTTTTGGCGGGGTAACTTTGGGGAAGTC 3522

Db 3482 CAGATCTTGTGTACATTGGCCACAGCAGCTGCTCTTTTGGCGGTAACCTTTGGGAAGTC 3541
QY 3523 TTTCTCAGCTTCAGTGCAATGAAATGGCACATTTCTCTCCAGGTCATCACTCAGTCAC 3582
Db 3542 TTTCTCAGCTTCAGTGCAATGAAATGGCACATTTCTCTCCAGGTCATCACTCAGTCAC 3601
QY 3583 TGGTAGCCAGCTGTAAATGGCCCTAGCATTTAGCTGAATATGTTATTTACAGAGAGAAC 3642
Db 3602 TGGTAGCCAGCTGTAAATGGCCCTAGCATTTAGCTGAATATGTTATTTACAGAGAGAAC 3661
QY 3643 GGCTTATCTCAGTATTTAAATTTACTTACCAGATTTATGAGGCCTGAAGGTATGGTCGATGG 3702
Db 3662 GGCTTATCTCAGTATTTAAATTTACTTACCAGATTTATGAGGCCTGAAGGTATGGTCGATGG 3721
QY 3703 ATAAATAGTATTTTAAAGAACTAAATTTCCACTGAACCTAAATAATCATCAAGCAGCAGTGG 3762
Db 3722 ATAAATAGTATTTTAAAGAACTAAATTTCCACTGAACCTAAATAATCATCAAGCAGCAGTGG 3781
QY 3763 CCTCTAGCTTTTACTCTCTTTGCTGAAAAA 3797
Db 3782 CCTCTAGCTTTTACTCTCTTTGCTGAAAAA 3816

RESULT 9
AAC66825
ID AAC66825 standard; cDNA; 4275 BP.
XX
AC AAC66825;
XX
DT 27-FEB-2001 (first entry)
XX
DE Human tankyrase II coding sequence SEQ ID NO: 5.
XX
KW Human; tankyrase II; telomere length; signal transduction; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 284..3784
FT /*tag= a
FT /product= "tankyrase II"
FT /tranel_except= (pos:655..660,aa:TyrThr)
XX
PN WO200061813-A1.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US009558.
XX
PR 09-APR-1999; 99US-0128577P.
PR 13-APR-1999; 99US-0129123P.
XX
PA (GERO-) GERON CORP.
XX
PI Morin GB, Funk WD, Piatyszek MA;
XX
DR WPI; 2000-679503/66.
DR P-PSDB; AAB27211.
XX
PT Novel mammalian Tankyrase II polypeptide and the polynucleotide encoding
PT the polypeptide useful for modulating or maintaining telomere length,
PT replicative capacity, apoptosis, chromosome packing or gene expression.
XX
PS Claim 1; Fig 4; 52pp; English.
XX
CC The present sequence is a version of the human tankyrase II coding
CC sequence. Its protein is thought to be involved in signal transduction in
CC the cell, and to have binding activity for other telomere-associated
CC proteins. It is possible that it plays a role in the regulation of
CC telomere length, thus affecting the replicative ability of the cell. The
CC protein is useful for ribosylating target proteins, for determining
CC tankyrase II binding activity in a sample, and for modulating telomere

CC	length in a cell	
XX	Sequence 4275 BP; 1247 A; 889 C; 1025 G; 1114 T; 0 U; 0 Other;	
SQ	Query Match 89.2%; Score 3388.8; DB 3; Length 4275; Best Local Similarity 99.9%; Pred. No. 0; Matches 3390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	403 AGGTTTGGGCGGAAGACGTAGTTGAATATTTGCTTCAGATGTCGCAAGTGTCCRAAGC 462	Db
DB	481 AGGTTTGGGCGGAAGACGTAGTTGAATATTTGCTTCAGATGTCGCAAGTGTCCRAAGC 540	QY
QY	463 ACGTGATGATGGGGCCCTATTCTCTTCATAATGCATGCTCTTTTGGTCTATGCTGAAGT 522	Db
DB	541 ACGTGATGATGGGGCCCTATTCTCTTCATAATGCATGCTCTTTTGGTCTATGCTGAAGT 600	QY
QY	523 AGTCAATCTCTTTTGGGACATGTTGCGACAGACCCCAATGCTCGAGATAATTTGAATTTATAC 582	Db
DB	601 AGTCAATCTCTTTTGGGACATGTTGCGACAGACCCCAATGCTCGAGATAATTTGAATTTATAC 660	QY
QY	583 TCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATTGATGTTTGCAATGCTGCTGTTACAGCA 642	Db
DB	661 TCCTCTCCATGAAGCTGCAATTTAAAGGAAAGATTGATGTTTGCAATGCTGCTGTTACAGCA 720	QY
QY	643 TGGAGCTGAGGCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGCAATTTAGCAGATCC 702	Db
DB	721 TGGAGCTGAGGCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGCAATTTAGCAGATCC 780	QY
QY	703 ATCTGCCAAAGCAGTGTCTTACTGTGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG 762	Db
DB	781 ATCTGCCAAAGCAGTGTCTTACTGTGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG 840	QY
QY	763 GAGTGGCAATGAAGAAATGATGGCTCTACTCACACCATTAATGTCRACTGCCAGC 822	Db
DB	841 GAGTGGCAATGAAGAAATGATGGCTCTACTCACACCATTAATGTCRACTGCCAGC 900	QY
QY	823 AAGTGATGCGAAGATCAATCCATTACATTTGGCAGCAGGATATACAGATGAAGAT 882	Db
DB	901 AAGTGATGCGAAGATCAATCCATTACATTTGGCAGCAGGATATACAGATGAAGAT 960	QY
QY	883 TGTACAGCTGTATCGCAACATGAGAGCTGATGTCATGCTAAAGATAAAGTGATCTGGT 942	Db
DB	961 TGTACAGCTGTATCGCAACATGAGAGCTGATGTCATGCTAAAGATAAAGTGATCTGGT 1020	QY
QY	943 ACCATTACACATGCTCTCTTATGTCATTATGAAGTAACTGAATTTTGGTCAAGCA 1002	Db
DB	1021 ACCATTACACATGCTCTCTTATGTCATTATGAAGTAACTGAATTTTGGTCAAGCA 1080	QY
QY	1003 TGGTGCTGTGTAAATGCAATGGACTTGTGGCAATTCACCTCTTCTATGAGGCGAGCTTC 1062	Db
DB	1081 TGGTGCTGTGTAAATGCAATGGACTTGTGGCAATTCACCTCTTCTATGAGGCGAGCTTC 1140	QY
QY	1063 TAAGAACAGGGTTGAAGTATGTTCTTTCTTTAAGTTATGGTGAGACCCCAACACTGCT 1122	Db
DB	1141 TAAGAACAGGGTTGAAGTATGTTCTTTCTTTAAGTTATGGTGAGACCCCAACACTGCT 1200	QY
QY	1123 CAATTTGTCATATAAGTCTATAGACTTGGCTCCACACACACAGTTAAAGAAAGATT 1182	Db
DB	1201 CAATTTGTCATATAAGTCTATAGACTTGGCTCCACACACACAGTTAAAGAAAGATT 1260	QY
QY	1183 AGCATATGAATTTAAAGGCCACTCGTGTGTCAGCTGCAGAGAGCTGATTTACTCG 1242	Db
DB	1261 AGCATATGAATTTAAAGGCCACTCGTGTGTCAGCTGCAGAGAGCTGATTTACTCG 1320	QY
QY	1243 AATCAAAAACATCTCTCTCTGGAAATGGTGAATTTCAAGCATCTCAACACATGAAC 1302	Db
DB	1321 AATCAAAAACATCTCTCTCTGGAAATGGTGAATTTCAAGCATCTCAACACATGAAC 1380	QY
QY	1303 AGCATTTGATTTGTGCTGTGATCTCCATATCCCAAAAGAAAGCAATATGTGAATGTT 1362	Db
DB	1381 AGCATTTGATTTGTGCTGTGATCTCCATATCCCAAAAGAAAGCAATATGTGAATGTT 1440	QY
QY	1363 GCTAAGAAAAGGAGCAACATCAATGAAAAGACTTAAAGAAATTTCTTGACTCTCTGCAAGT 1422	Db
QY	1441 GCTAAGAAAAGGAGCAACATCAATGAAAAGACTTAAAGAAATTTCTTGACTCTCTGCAAGT 1500	Db
QY	1423 GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAGCAAGGT 1482	Db
DB	1501 GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAGCAAGGT 1560	QY
QY	1483 TAATGCTCTGATATAATCTTGGTCTGAGACTTCTCTACACAGAGCTGCATATTTGGTCTATCT 1542	Db
DB	1561 TAATGCTCTGATATAATCTTGGTCTGAGACTTCTCTACACAGAGCTGCATATTTGGTCTATCT 1620	QY
QY	1543 ACAAACCTGCGGCTACTCTGAGCTATGGGTGTGATCTCTAAACATTTATATCCCTTCAGGG 1602	Db
DB	1621 ACAAACCTGCGGCTACTCTGAGCTATGGGTGTGATCTCTAAACATTTATATCCCTTCAGGG 1680	QY
QY	1603 CTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCTCCAAAGGGGTATCTC 1662	Db
DB	1681 CTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCTCCAAAGGGGTATCTC 1740	QY
QY	1663 ATTAGGTAATTCAGAGGACAGACAGCAATTTGCTGGAAGCTGCAAGGCTGGAGATGTGCA 1722	Db
DB	1741 ATTAGGTAATTCAGAGGACAGACAGCAATTTGCTGGAAGCTGCAAGGCTGGAGATGTGCA 1800	QY
QY	1723 AACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGTCAGAGACATTTGAAGGCGGTCA 1782	Db
DB	1801 AACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGTCAGAGACATTTGAAGGCGGTCA 1860	QY
QY	1783 GTCTACACCACTTCATTTTGCAGCTGGGTATACAGAGTGTCCGTGGTGGAAATATCTGCT 1842	Db
DB	1861 GTCTACACCACTTCATTTTGCAGCTGGGTATACAGAGTGTCCGTGGTGGAAATATCTGCT 1920	QY
QY	1843 ACAGCATGGAGCTGATGTCATGCTAAAGATAAAGGAGGCTCTGTACTTTGCAACAATGC 1902	Db
DB	1921 ACAGCATGGAGCTGATGTCATGCTAAAGATAAAGGAGGCTCTGTACTTTGCAACAATGC 1980	QY
QY	1903 ATGTTCTTATGGACATTTATGAAGTTGCAGAACTCTTTGTTTAAACATGGAGCAGTAGTTAA 1962	Db
DB	1981 ATGTTCTTATGGACATTTATGAAGTTGCAGAACTCTTTGTTTAAACATGGAGCAGTAGTTAA 2040	QY
QY	1963 TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022	Db
DB	2041 TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2100	QY
QY	2023 AATTTGCAAACTTCTGCTCCAGCATGCTGCAGACCCCTACCAAAAAAACAAGGATGGAAA 2082	Db
DB	2101 AATTTGCAAACTTCTGCTCCAGCATGCTGCAGACCCCTACCAAAAAAACAAGGATGGAAA 2160	QY
QY	2083 TACTCTTTGGATCTTGTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGAGA 2142	Db
DB	2161 TACTCTTTGGATCTTGTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGAGA 2220	QY
QY	2143 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGATGTTGCTTTC 2202	Db
DB	2221 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGATGTTGCTTTC 2280	QY
QY	2203 TCCTGATAATGTAATTTGCGCGATACCAAGGACAGACATTTCAACACTTTTACATTTAGC 2262	Db
DB	2281 TCCTGATAATGTAATTTGCGCGATACCAAGGACAGACATTTCAACACTTTTACATTTAGC 2340	QY
QY	2263 AGCTGGTTATAAATTTAGAGTTGAGAGTATTTGTTTACCAACCGAGCTGATGTAA 2322	Db
DB	2341 AGCTGGTTATAAATTTAGAGTTGAGAGTATTTGTTTACCAACCGAGCTGATGTAA 2400	QY
QY	2323 TGCCCAAGACAAAGGAGACTTATTCCTTTTACATAATGTCAGCATCTTACGGGCATGTAGA 2382	Db
DB	2401 TGCCCAAGACAAAGGAGACTTATTCCTTTTACATAATGTCAGCATCTTACGGGCATGTAGA 2460	QY
QY	2383 TGTAGCAGCTCTACTATAAAGTATAATGATGTGTCAATGCCACGACAAATGGGCTTT 2442	Db
DB	2461 TGTAGCAGCTCTACTATAAAGTATAATGATGTGTCAATGCCACGACAAATGGGCTTT 2520	QY
QY	2443 CACACCTTTGCAAGGAGCGCCCAAGGAGCGAACACAGCTTTGTGCTTTGTTGCTAGC 2502	Db

2521	Db	CACACCTTTGCGACGAGCAGCCCAAAAGGAGCGAACACAGCTTTGTGCTTTGTGTGCTAGC	2588
2503	Qy	CCATGGAGCTGACCCCGACTCTTAAAAATCAGGAAGGACAAACACCTTTAGATTAGTTTC	2562
2581	Db	CCATGGAGCTGACCCCGACTCTTAAAAATCAGGAAGGACAAACACCTTTAGATTAGTTTC	2640
2563	Qy	AGCGGATGATGTGAGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCTCTTG	2622
2641	Db	AGCGGATGATGTGAGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCTCTTG	2700
2623	Qy	TTACAAGCCTCAAGTGTCTCAATGGTGTGAGAAGCCAGAGGCCACTGCGATGCTCTCTC	2682
2701	Db	TTACAAGCCTCAAGTGTCTCAATGGTGTGAGAAGCCAGAGGCCACTGCGATGCTCTCTC	2760
2683	Qy	TTCAAGTCCCATCTAGCCCATCAAGCCCTTCTGCAGCCAGCAGCTCTTGACAACCTTATCTGG	2742
2761	Db	TTCAAGTCCCATCTAGCCCATCAAGCCCTTCTGCAGCCAGCAGCTCTTGACAACCTTATCTGG	2820
2743	Qy	GAGTTTTTCAAGACTGTCTTTCAGTAGTTAGTTCAAGTGGAAACAGAGGGTGTCTTCCAGTTT	2802
2821	Db	GAGTTTTTCAAGACTGTCTTTCAGTAGTTAGTTCAAGTGGAAACAGAGGGTGTCTTCCAGTTT	2880
2803	Qy	GGAGAAAAGAGGGTTCACGAGTAGATTTTACGATCACTCAATTCGTAAAGGAATCTTGG	2862
2881	Db	GGAGAAAAGAGGGTTCACGAGTAGATTTTACGATCACTCAATTCGTAAAGGAATCTTGG	2940
2863	Qy	ACTTGAGCACTTAATGGATATATTGTAGAGAGAAACAGATCACTTGGATGTATTTAGTTGA	2922
2941	Db	ACTTGAGCACTTAATGGATATATTGTAGAGAGAAACAGATCACTTGGATGTATTTAGTTGA	3000
2923	Qy	GATGGGSCAACAGGAGCTGAAGGAGATTGGAATCAATGCTTATGACATAGGCACAAACT	2982
3001	Db	GATGGGSCAACAGGAGCTGAAGGAGATTGGAATCAATGCTTATGACATAGGCACAAACT	3060
2983	Qy	AATTAAGGAGTGGAGACTTATCTCCGAGACAAAGAGTCTTAAACCATTTTAACCTTT	3042
3061	Db	AATTAAGGAGTGGAGACTTATCTCCGAGACAAAGAGTCTTAAACCATTTTAACCTTT	3120
3043	Qy	GAACACCTCTGGTAGTGGAAACAATCTTATAGATCTGTCTCTGATGATAAGAGTTTCA	3102
3121	Db	GAACACCTCTGGTAGTGGAAACAATCTTATAGATCTGTCTCTGATGATAAGAGTTTCA	3180
3103	Qy	GTCTGTGGAGGAAGAGATGCAAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCAATGCAGG	3162
3181	Db	GTCTGTGGAGGAAGAGATGCAAAAGTACAGTTCGAGAGCACAGAGATGGAGGTCAATGCAGG	3240
3163	Qy	TGGAATCTTCAACAGATACAAATATTTCTCAAGATTCAGAGGTTTGTAAACAAGAAACTATG	3222
3241	Db	TGGAATCTTCAACAGATACAAATATTTCTCAAGATTCAGAGGTTTGTAAACAAGAAACTATG	3300
3223	Qy	GGAAAGATACACTCACCGGAGAAAGAGTTTCTGAGAGAAACCAACCATGCCAATGA	3282
3301	Db	GGAAAGATACACTCACCGGAGAAAGAGTTTCTGAGAGAAACCAACCATGCCAATGA	3360
3283	Qy	ACGAATCTATTTTCATGGGTCTCCTTTGTGAAATGCAATTTATCCAAAAGGCTTTGATGA	3342
3361	Db	ACGAATCTATTTTCATGGGTCTCCTTTGTGAAATGCAATTTATCCAAAAGGCTTTGATGA	3420
3343	Qy	AAGGCATGCGTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTTGTGAAAACCTTTC	3402
3421	Db	AAGGCATGCGTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTTGTGAAAACCTTTC	3480
3403	Qy	CAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTTGGGTGTCAGTTTCAAAAGA	3462
3481	Db	CAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTTGGGTGTCAGTTTCAAAAGA	3540
3463	Qy	CAGATCTTGTATCAATTTGCCACAGGAGCTGTCTTTTGTGCGGGTAACTTTGGGAAAGTC	3522
3541	Db	CAGATCTTGTATCAATTTGCCACAGGAGCTGTCTTTTGTGCGGGTAACTTTGGGAAAGTC	3600
3523	Qy	TTTCTCGAGTTCAGTGCATATGAAAATGGCAATTTCTCTCCAGGTCAATCACTCAGTCAAC	3582
3601	Db	TTTCTCGAGTTCAGTGCATATGAAAATGGCAATTTCTCTCCAGGTCAATCACTCAGTCAAC	3660

Qy	3583	TGGTAGGCCCCAGTGTAAATGGCTAGCAATTTAGCTGAATATGTTATTATACAGAGGAGAAC	3641
Db	3661	TGGTAGGCCCCAGTGTAAATGGCTAGCAATTTAGCTGAATATGTTATTATACAGAGGAGAAC	3720
Qy	3643	GGCTTATCCTCGAGTATTAAATTAATTTACTTACCAGATTTATGAGGCCCTGAAGGTATGGTCCGATGG	3702
Db	3721	GGCTTATCCTCGAGTATTAAATTTACTTACCAGATTTATGAGGCCCTGAAGGTATGGTCCGATGG	3780
Qy	3703	ATAAATAGTATTATTTTAAGAAACTAATTTCCACTGAACCTCAAAATCATCAAAAGCAGCAGTGG	3762
Db	3781	ATAAATAGTATTATTTTAAGAAACTAATTTCCACTGAACCTCAAAATCATCAAAAGCAGCAGTGG	3840
Qy	3763	CCTCTAGCTTTTACTCTCTTTCGTAAGAAAAA	3794
Db	3841	CCTCTAGCTTTTACTCTCTTTCGTAAGAAAAA	3872
RESULT 10			
AAC85294			
ID	AAC85294	standard; cDNA; 6019 BP.	
XX	AC	AAC85294;	
XX	AC		
XX	XX		
DT	29-MAR-2001	(first entry)	
XX	XX		
DE	Human SPANK cDNA.		
XX			
KW	SPANK; SAM; sterile alpha motif; PAPP; insulin resistance;		
KW	poly adenosine diphosphate-ribose polymerase; catalytic domain; ANK;		
KW	ankyrin repeat; cytosol; insulin-responsive aminopeptidase; IRAP; GLUT4;		
KW	adipocyte; insulin signalling pathway; hyperlipidaemia;		
KW	glucose intolerance; atheromatous disease; atherosclerosis; obesity;		
KW	cardiac insufficiency; coronary insufficiency; stroke;		
KW	high blood pressure; non-insulin dependent diabetes; hypertension;		
KW	hyperuricemia; Syndrome X; muscular dystrophy; muscle atrophy; ds.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
PH	252..3735		
CDS	/*tag= a		
FT	/product= "Human SPANK"		
FT	/transl_except= (pos:768..878,aa:173..209)		
FT	/transl_except= (pos:1230..1337,aa:327..362)		
FT	/transl_except= (pos:1374..1445,aa:375..398)		
FT	/transl_except= (pos:1695..1823,aa:482..524)		
FT	/transl_except= (pos:2172..2282,aa:641..677)		
XX			
PN	WO200077225-A1.		
XX			
PD	21-DEC-2000.		
XX			
PF	09-JUN-2000; 2000WO-US015926.		
XX			
PR	11-JUN-1999; 99US-0138957P.		
XX			
FA	(WHED) WHITEHEAD INST BIOMEDICAL RES.		
PA	(GHEO) GEN HOSPITAL CORP.		
XX			
PI	Chi N, Lodish HF;		
XX			
DR	WPI; 2001-091404/10.		
DR	P-PSDB; AAB47022.		
XX			
PT	New insulin signaling protein SPANK, useful for reducing body mass,		
PT	glucose intolerance or insulin resistance and for preventing or treating		
PT	obesity-related and muscle-related diseases.		
XX			
ES	Claim 3; Fig 4; 65pp; English.		
XX			
CC	This sequence represents the human SPANK cDNA. The SPANK protein		
CC	comprises 3 domains:(a) a SAM (sterile alpha motif) domain;(b) a PAPP		

403	Qy	AGTTTTGGCGGCGAAGACGCTAGTTGAATATTTGCTTCAGAAATGGTGCAAGTGTCCCAAGC	462
449	Db	AGGTTTTGGGCGGCGAAGACGCTAGTTGAATATTTGCTTCAGAAATGGTGCAAAATGTCCCAAGC	508
463	Qy	ACGTGATGATGGGGGCGCTTATTCCTCTTCATAAATGCATGCTCTTTTGGTCATGCTGGAAGT	522
509	Db	ACGTGATGATGGGGGCGCTTATTCCTCTTCATAAATGCATGCTCTTTTGGTCATGCTGGAAGT	568
523	Qy	AGTCAATCTCCTTTTGGGACATGGTGCGAGACCCCAATGCTCGAGATAATTTGGAATTTATAC	582
569	Db	AGTCAATCTCCTTTTGGGACATGGTGCGAGACCCCAATGCTCGAGATAATTTGGAATTTATAC	628
583	Qy	TCCTCTCCATGAGACTGCAATTAAGAGAAAGATTGATGTTTGGCATTTGCTGTGTACAGGA	642
629	Db	TCCTCTCCATGAGACTGCAATTAAGAGAAAGATTGATGTTTGGCATTTGCTGTGTACAGGA	688
643	Qy	TGGAGCTGAGCCCAACCATCCCGAAATACAGATGGAGGACAGCATTTGGATTTTAGCAGATCC	702
689	Db	TGGAGCTGAGCCCAACCATCCCGAAATACAGATGGAGGACAGCATTTGGATTTTAGCAGATCC	748
703	Qy	ATCTGCCAAAGCAGTGTCTTACTGGTGAAATATAAGAAAGATGAACTCTTTAGAAAGTGCACG	762
749	Db	ATCTGCCAAAGCAGTGTCTTACTGGTGAAATATAAGAAAGATGAACTCTTTAGAAAGTGCACG	808
763	Qy	GAGTGGCAATGAAGAAAATAATGATGGCTCTACTCACACATTAATAATGTCAAATGTCGACGC	822
809	Db	GAGTGGCAATGAAGAAAATAATGATGGCTCTACTCACACATTAATAATGTCAAATGTCGACGC	868
823	Qy	AACTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATACAGAGTAAAGAT	882
869	Db	AACTGATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATACAGAGTAAAGAT	928
883	Qy	TGTACAGCTGTTACTTGCACCAATGGAGCTGATGTCATGCTTAAAGATAAAGGTGATCTCGT	942
929	Db	TGTACAGCTGTTACTTGCACCAATGGAGCTGATGTCATGCTTAAAGATAAAGGTGATCTCGT	988
943	Qy	ACCAATTACAATGCCTGTTCTTTATGGTCAATATGAAGTAACTGTAACCTTTTGGTCAAGCA	1002
989	Db	ACCAATTACAATGCCTGTTCTTTATGGTCAATATGAAGTAACTGTAACCTTTTGGTCAAGCA	1048
1003	Qy	TGGTGCCGTGTAAATGCAATGGACTGTGGCAATTCACCTCTTTCATGAGGCGAGCTTC	1062
1049	Db	TGGTGCCGTGTGTAAATGCAATGGACTGTGGCAATTCACCTCTTTCATGAGGCGAGCTTC	1108
1063	Qy	TAAGAACAGGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGAGACCCCAACACTGCT	1122
1109	Db	TAAGAACAGGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGAGACCCCAACACTGCT	1168
1123	Qy	CAATTGTCACAATAAAAAGTGTCTATAGACTTGGCTCCCAACACAGTTTAAAGAAGAATT	1182
1169	Db	CAATTGTCACAATAAAAAGTGTATAGACTTGGCTCCCAACACAGTTTAAAGAAGAATT	1222

CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
XX disorders

QQ	Sequence	4127 BP; 1245 A; 813 C; 934 G; 1135 T; 0 U; 0 Other;	
QY	Query Match	89.2%; Score 3387.2; DB 5; Length 4127;	
DB	Best Local Similarity	99.9%; Pred. No. 0;	
DB	Matches 3389; Conservative	0; Mismatches 3; Indels 0; Gaps 0;	
QY	403	AGGTTTGGGCGGAAAGACGAGTAGTTGAATATTTGCTTCAGAAATGGTGCAAGTGCACAGC	462
DB	208	AGGTTTGGGCGGAAAGACGAGTAGTTGAATATTTGCTTCAGAAATGGTGCAAGTGCACAGC	267
QY	463	ACGTGATGATGGGGCCCTTATCTCTTCAATAAGCATGCTCTTTTGGTGTATGCTGAAGT	522
DB	268	ACGTGATGATGGGGCCCTTATCTCTTCAATAAGCATGCTCTTTTGGTGTATGCTGAAGT	327
QY	523	AGTCAATCTCTTTTGGGACATGGTGACAGACCCCAATGCTCGAGATAATTTGGAATTATAC	582
DB	328	AGTCAATCTCTTTTGGGACATGGTGACAGACCCCAATGCTCGAGATAATTTGGAATTATAC	387
QY	583	TCCTCTCATGAAGTGCATTAAGAAAGATGATGATTTTGCATGTGCTGTGTACAGCA	642
DB	388	TCCTCTCATGAAGTGCATTAAGAAAGATGATGATTTTGCATGTGCTGTGTACAGCA	447
QY	643	TGGAGCTGAGCCACCACTCCGAAATACAGATGGAGGACAGCATTTGGATTAGCAGATCC	702
DB	448	TGGAGCTGAGCCACCACTCCGAAATACAGATGGAGGACAGCATTTGGATTAGCAGATCC	507
QY	703	ATCTGCCAAAGCAGTGCTTACTTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCCAG	762
DB	508	ATCTGCCAAAGCAGTGCTTACTTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCCAG	567
QY	763	GAGTGGCAATGAAGAAATATGATGGCTCTACTCACACCATTAATGTCACATGCCAGC	822
DB	568	GAGTGGCAATGAAGAAATATGATGGCTCTACTCACACCATTAATGTCACATGCCAGC	627
QY	823	AAAGTATGGCAGAAAGTCAATCCATTAATTTGGCAGCAGATATACAGATTAAGAT	882
DB	628	AAAGTATGGCAGAAAGTCAATCCATTAATTTGGCAGCAGATATACAGATTAAGAT	687
QY	883	TGTACAGCTGTACTGCAACATGAGCTGATGCTCCATGCTAAAGATAAGGTGATCTGGT	942
DB	688	TGTACAGCTGTACTGCAACATGAGCTGATGCTCCATGCTAAAGATAAGGTGATCTGGT	747
QY	943	ACCATTAACAATGCTGCTTTATGCTGATTAAGTAACTGAACTGTTTGGTCAAGCA	1002
DB	748	ACCATTAACAATGCTGCTTTATGCTGATTAAGTAACTGAACTGTTTGGTCAAGCA	807
QY	1003	TGGTGCCTGTGAATGAAGTGGCTTGGCAATTTCACTCTTCAATGAGGCGCTTC	1062
DB	808	TGGTGCCTGTGAATGAAGTGGCTTGGCAATTTCACTCTTCAATGAGGCGCTTC	867
QY	1063	TAAGAAACAGGGTGAAGTATGTTCTTCTTAAAGTATGTTGTCAGACCCCAACACTGCT	1122
DB	868	TAAGAAACAGGGTGAAGTATGTTCTTCTTAAAGTATGTTGTCAGACCCCAACACTGCT	927
QY	1123	CAATTTGTCACAAATAAGTGTATAGACTTGGCTCCCAACACACAGTTTAAAGAAAGATT	1182
DB	928	CAATTTGTCACAAATAAGTGTATAGACTTGGCTCCCAACACACAGTTTAAAGAAAGATT	987
QY	1183	AGCATATGAATTAAGGCGCACTGTTGCTGCAAGCTGCAAGAGCTGATGTTACTCG	1242
DB	988	AGCATATGAATTAAGGCGCACTGTTGCTGCAAGCTGCAAGAGCTGATGTTACTCG	1047
QY	1243	AATCAAAAAACATCTCTCTGGAATAGTGAATTTCAAGCATCTCCAAACACATGAAAC	1302
DB	1048	AATCAAAAAACATCTCTCTGGAATAGTGAATTTCAAGCATCTCCAAACACATGAAAC	1107
QY	1303	AGCATTTGATTTGCTGCTGATCTCCATATCCCAAAAAAGAAAGCAATATGTAAGTGT	1362
DB	1108	AGCATTTGATTTGCTGCTGATCTCCATATCCCAAAAAAGAAAGCAATATGTAAGTGT	1167

QY	1363	GCTAAGAAAAAGGACCAACATCAATGAAAAAGACTTAAAGAAATTTCTTGACTCTCTGACGCT	1422
DB	1168	GCTAAGAAAAAGGACCAACATCAATGAAAAAGACTTAAAGAAATTTCTTGACTCTCTGACGCT	1227
QY	1423	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT	1482
DB	1228	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT	1287
QY	1483	TAATGCTCTGGATTAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTCGTGCTCATCT	1542
DB	1288	TAATGCTCTGGATTAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTCGTGCTCATCT	1347
QY	1543	ACAAACCTGCGGCTACTCTCTGAGCTATGGGTGATGCTTAAACATTTATATCCCTTCAGGG	1602
DB	1348	ACAAACCTGCGGCTACTCTCTGAGCTATGGGTGATGCTTAAACATTTATATCCCTTCAGGG	1407
QY	1603	CTTTTACCTGCTTTACAGATGGGAAATGAAATGTAACAGAACTCTCTCCAAAGAGGTATCTC	1662
DB	1408	CTTTTACCTGCTTTACAGATGGGAAATGAAATGTAACAGAACTCTCTCCAAAGAGGTATCTC	1467
QY	1663	ATTAGGTAATTCAGAGGACAGACAGCAATTTGCTTGAAGCTGCAAGGCTGAGATGTCGA	1722
DB	1468	ATTAGGTAATTCAGAGGACAGACAGCAATTTGCTTGAAGCTGCAAGGCTGAGATGTCGA	1527
QY	1723	AACGTGTAATAAACTGTTGTTACTGTTTACAGAGTGTCAACTGACAGACATTTGAAGGCGCTCA	1782
DB	1528	AACGTGTAATAAACTGTTGTTACTGTTTACAGAGTGTCAACTGACAGACATTTGAAGGCGCTCA	1587
QY	1783	GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT	1842
DB	1588	GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT	1647
QY	1843	ACAGCATGGAGCTGATGTCATGCTTAAAGATAAGAGGAGGCTTGTACCTTTGCAATGTC	1902
DB	1648	ACAGCATGGAGCTGATGTCATGCTTAAAGATAAGAGGAGGCTTGTACCTTTGCAATGTC	1707
QY	1903	ATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTGTAAACATGGAGCAGTAGTTAA	1962
DB	1708	ATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTGTAAACATGGAGCAGTAGTTAA	1767
QY	1963	TGTAGCTGATTTATGGAAATTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2022
DB	1768	TGTAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA	1827
QY	2023	AATTTGCAAACTTCTGCTCCAGCATGTCAGACCCCTACCAAAACACAGGATGGAA	2082
DB	1828	AATTTGCAAACTTCTGCTCCAGCATGTCAGACCCCTACCAAAACACAGGATGGAA	1887
QY	2083	TACTCTTTGGATCTGTTAAAGATGGAGATACAGATATTTCAAGATCTGTTAGGGGAGA	2142
DB	1888	TACTCTTTGGATCTGTTAAAGATGGAGATACAGATATTTCAAGATCTGTTAGGGGAGA	1947
QY	2143	TGCAGCTTTGCTAGATGCTGCCAAAGAGGTTGTTTATGCCAGAGTGAAGAGTTGCTTTC	2202
DB	1948	TGCAGCTTTGCTAGATGCTGCCAAAGAGGTTGTTTATGCCAGAGTGAAGAGTTGCTTTC	2007
QY	2203	TCCTGATTAATGTAATTTGCCGCGATACCCAGGACAGATTTCAACCTTTTACATTTAGC	2262
DB	2008	TCCTGATTAATGTAATTTGCCGCGATACCCAGGACAGATTTCAACCTTTTACATTTAGC	2067
QY	2263	AGCTGGTTTATAATTTAGAAAGTTGCAGAGTATTTGTTTACAAACCGAGCTGATGTGA	2322
DB	2068	AGCTGGTTTATAATTTAGAAAGTTGCAGAGTATTTGTTTACAAACCGAGCTGATGTGA	2127
QY	2323	TGCCCAAGCAAAAGGAGGACTTATTTCTTTTACATAATTCAGCATCTTACCGGCAATGTA	2382
DB	2128	TGCCCAAGCAAAAGGAGGACTTATTTCTTTTACATAATTCAGCATCTTACCGGCAATGTA	2187
QY	2383	TGTAGCAGCTCTACTTAATAAGTATTAATGCTGCTCAATGCCACGCAAAATGGGCTTT	2442
DB	2188	TGTAGCAGCTCTACTTAATAAGTATTAATGCTGCTCAATGCCACGCAAAATGGGCTTT	2247

487	Db	AGTTTTGGCGGGAAGACGCTAGTGTGAATATTTGCTCTTCAGAAATGGTGCAAAATGTCOAAGC	546
463	Qy	ACGTGATGATGGGGCCCTTATTCCTCTTTCATAATGCAATGCTCTTTTGGTCAATGCTGAAGT	522
547	Db	ACGTGATGATGGGGCCCTTATTCCTCTTCATAATGCAATGCTCTTTTGGTCAATGCTGAAGT	606
523	Qy	AGTCAATCTCTTTTGGGACANATGGTGAGACCCCAATGCTTCGAGATAAATTTGGAATTTATAC	582
607	Db	AGTCAATCTCTTTTGGGACANATGGTGAGACCCCAATGCTTCGAGATAAATTTGGAATTTATAC	666
583	Qy	TCCTCTCCATGAGCTCAATTAAAGGAAAGATTGATGTTTGGCATTTGCTGTCTGTTTACAGCA	642
667	Db	TCCTCTCCATGAGCTCAATTAAAGGAAAGATTGATGTTTGGCATTTGCTGTCTGTTTACAGCA	726
643	Qy	TGGAGCTGAGCCAACCATCCGAATAACAGATGGAAGCAGCAGCATTTGATTTAGCAGATCC	702
727	Db	TGGAGCTGAGCCAACCATCCGAATAACAGATGGAAGCAGCAGCATTTGATTTAGCAGATCC	786
703	Qy	ATCTGCCAAAGCAGTGCTTACTGCTGTAATATAGAAAGATGAACTCTTTAGAAAGTGCCAG	762
787	Db	ATCTGCCAAAGCAGTGCTTACTGCTGTAATATAGAAAGATGAACTCTTTAGAAAGTGCCAG	846
763	Qy	GAGTGGCAATGAAGAAAATGATGGCTCTACTTCACACCAATTAATATGTCACCTGCCACGC	822
847	Db	GAGTGGCAATGAAGAAAATGATGGCTCTACTTCACACCAATTAATATGTCACCTGCCACGC	906
823	Qy	AAATGATGGCAAGAAATGCAACTCCATTCACATTTGGCAGCAGGATATAACAGAGTAAAGAT	882
907	Db	AAATGATGGCAAGAAATGCAACTCCATTCACATTTGGCAGCAGGATATAACAGAGTAAAGAT	966
883	Qy	TGTACAGCTGTTACTGCAACATGAGGCTGATGTCATGCTTAAAGATAAAGGTGATCTGGT	942
967	Db	TGTACAGCTGTTACTGCAACATGAGGCTGATGTCATGCTTAAAGATAAAGGTGATCTGGT	1026
943	Qy	ACCAATACAAATGCCCTGTTCTTATGCTCAATATAGAGTAACTTGAACCTTTTGGTCAAGCA	1002
1027	Db	ACCAATACAAATGCCCTGTTCTTATGCTCAATATAGAGTAACTTGAACCTTTTGGTCAAGCA	1086
1003	Qy	TGGTGCCCTGTGTAATGCAATGGACTTTGGCAATTCACCTCTTTCATGAGCAGCTTC	1062
1087	Db	TGGTGCCCTGTGTAATGCAATGGACTTTGGCAATTCACCTCTTTCATGAGCAGCTTC	1146
1063	Qy	TAAGAACAGGGTTGAAGTATGTTCTCTTCTTTAAGTTATGGTGCAAGCCCAACACTGCT	1122
1147	Db	TAAGAACAGGGTTGAAGTATGTTCTCTTCTTCTTTAAGTTATGGTGCAAGCCCAACACTGCT	1206
1123	Qy	CAATTTGTCAATAAAAGTGCTATAGACTTTGGCTCCCAACCAACAGTTTAAAGAAAGATT	1182
1207	Db	CAATTTGTCAATAAAAGTGCTATAGACTTTGGCTCCCAACCAACAGTTTAAAGAAAGATT	1266
1183	Qy	AGCATATGAATTTAAAGCCCACTCGTTGTGCAAGCTGCAAGAGAGCTCATGTTACTCG	1242
1267	Db	AGCATATGAATTTAAAGCCCACTCGTTGTGCAAGCTGCAAGAGAGCTCATGTTACTCG	1326
1243	Qy	AATCAAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCTCTCAACACATGAAAC	1302
1327	Db	AATCAAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCTCTCAACACATGAAAC	1386
1303	Qy	AGCAATGCAATTTGCTGCTGATCTCCATATCCCAAAAGAAAGCAATATGTAAGCTGTT	1362
1387	Db	AGCAATGCAATTTGCTGCTGATCTCCATATCCCAAAAGAAAGCAATATGTAAGCTGTT	1446
1363	Qy	GCTAAGAAAAGGAGCAACATCAATGAAAGACTTAAAGAAATCTTGACTCTCTGACAGT	1422
1447	Db	GCTAAGAAAAGGAGCAACATCAATGAAAGACTTAAAGAAATCTTGACTCTCTGACAGT	1506
1423	Qy	GGCATCTGAGAAAGCTCATATGATGTTGTTTGAAGTAGTGGTGAAACATGAAGCAAGGT	1482
1507	Db	GGCATCTGAGAAAGCTCATATGATGTTGTTTGAAGTAGTGGTGAAACATGAAGCAAGGT	1566
1483	Qy	TAATGCTCTGGAATTAATCTTTGGTGAGACTTCTCTTACACAGAGCTGCATATTTGGTGATCT	1542
1567	Db	TAATGCTCTGGAATTAATCTTTGGTGAGACTTCTCTTACACAGAGCTGCATATTTGGTGATCT	1626

Qy 2623 TTCAAGCCTCAAGTGTCTCAATGTGTGAGNAGCCAGGAGCCACTGCAGATGCTCTCTC 2682
Db 2707 TTCAAGCCTCAAGTGTCTCAATGTGTGAGNAGCCAGGAGCCACTGCAGATGCTCTCTC 2766
Qy 2683 TTCAAGTCCATCTAGCCCATCAAGCCTTTCTGAGCCAGCAGTCTTGACAACTTATCTGG 2742
Db 2767 TTCAAGTCCATCTAGCCCATCAAGCCTTTCTGAGCCAGCAGTCTTGACAACTTATCTGG 2826
Qy 2743 GAGTTTTTTCAGAACTGTCTTTCAGTAGTGTAGTTCAGTGGAAACAGAGGCTCTCCAGTTT 2802
Db 2827 GAGTTTTTTCAGAACTGTCTTTCAGTAGTGTAGTTCAGTGGAAACAGAGGCTCTCCAGTTT 2886
Qy 2803 GGAGAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAAGGATCTTGG 2862
Db 2887 GGAGAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAAGGATCTTGG 2946
Qy 2863 ACTTGAGCACCCTAATGATATATTTTGAGAGAGACAGATCACTTTGGATGTATTAGTTGA 2922
Db 2947 ACTTGAGCACCCTAATGATATATTTTGAGAGAGACAGATCACTTTGGATGTATTAGTTGA 3006
Qy 2923 GATGGGCACAAGAGCTGAAGAGATTTGGAATCAATGCTTTATGGAATAGGCAAACT 2982
Db 3007 GATGGGCACAAGAGCTGAAGAGATTTGGAATCAATGCTTTATGGAATAGGCAAACT 3066
Qy 2983 AATTAAAGGAGTCCAGAGACTTATCTCGGACAAAGGCTTTAAACCATATTTAACTTT 3042
Db 3067 AATTAAAGGAGTCCAGAGACTTATCTCGGACAAAGGCTTTAAACCATATTTAACTTT 3126
Qy 3043 GAACACCTCTGGTAGTGGAACTTTCTTATAGATCTGTCTCTGATGATAAGAGTTTCA 3102
Db 3127 GAACACCTCTGGTAGTGGAACTTTCTTATAGATCTGTCTCTGATGATAAGAGTTTCA 3186
Qy 3103 GTCTGTGGAGAAAGATGCAAGATACAGTTTCGAGACACAGATGGAGTCAATGAGG 3162
Db 3187 GTCTGTGGAGAAAGATGCAAGATACAGTTTCGAGAGACACAGATGGAGTCAATGAGG 3246
Qy 3163 TGGAACTTCAACAGATACAAATTTCTCAAGATTCAGAGTTTGTAAACAGAACTATG 3222
Db 3247 TGGAACTTCAACAGATACAAATTTCTCAAGATTCAGAGTTTGTAAACAGAACTATG 3306
Qy 3223 GGAAGATATACACTCACCGGAGAAAAGTTCTTGAAGAAAACCAACCAATGCAATGA 3282
Db 3307 GGAAGATATACACTCACCGGAGAAAAGTTCTTGAAGAAAACCAACCAATGCAATGA 3366
Qy 3283 ACGAATGCTATTTTCATGGTCTCTTTTGTGAATGCAATATTCACAAAGCTTTGATGA 3342
Db 3367 ACGAATGCTATTTTCATGGTCTCTTTTGTGAATGCAATATTCACAAAGCTTTGATGA 3426
Qy 3343 AAGGCATGCGTACATAGTGTGTTTGGAGCTGGCATTTATTTTCTGAAAACCTCTTC 3402
Db 3427 AAGGCATGCGTACATAGTGTGTTTGGAGCTGGCATTTATTTTCTGAAAACCTCTTC 3486
Qy 3403 CAAAAGCAATCAATATGTATATGAAATTTGGAGGAGTACTGGGTGTCCAGTTCAACAAGA 3462
Db 3487 CAAAAGCAATCAATATGTATATGAAATTTGGAGGAGTACTGGGTGTCCAGTTCAACAAGA 3546
Qy 3463 CAGATCTGTGTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACTTTGGGAAAGTC 3522
Db 3547 CAGATCTGTGTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAACTTTGGGAAAGTC 3606
Qy 3523 TTTCTCGAGTTCAAGTCAATGAAATGGCCATAGCATTTCTCTCCAGGTCACTCAGTCAAC 3582
Db 3607 TTTCTCGAGTTCAAGTCAATGAAATGGCCATAGCATTTCTCTCCAGGTCACTCAGTCAAC 3666
Qy 3583 TGGTAGGCCAGTGTAAATGGCCATAGCATTTCTCTCCAGGTCACTCAGTCAAC 3642
Db 3667 TGGTAGGCCAGTGTAAATGGCCATAGCATTTCTCTCCAGGTCACTCAGTCAAC 3726
Qy 3643 GGCATTATCTGAGTATTTAATTAATTACAGATTTAGAGGCTGAAGGTATGTCGATGG 3702
Db 3727 GGCATTATCTGAGTATTTAATTAATTACAGATTTAGAGGCTGAAGGTATGTCGATGG 3786
Qy 3703 ATAAATAGTTATTTAAGAACTAATTTCCACTGAACCTAAATCATCAAGCAGCAGTGG 3762

Db 3787 ATAAATAGTTATTTAAGAACTAATTTCCACTGAACCTAAATCATCAAGCAGCAGTGG 3846
Qy 3763 CCTCTAGCTTTTACTCCTTTTGTGCTGAAAAAAA 3794
Db 3847 CCTCTAGCTTTTACTCCTTTTGTGCTGAAAAAAA 3878
RESULT 13
AAF63953
ID AAF63953 standard; DNA; 4992 BP.
XX
AC AAF63953;
XX
XX 05-APR-2001 (first entry)
XX Human tankyrase2 TANK2-SHORT coding sequence SEQ ID NO: 134.
XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
XX inflammatory disorder; ds.
XX Homo sapiens.
XX
XX WO200100849-A1.
XX
XX 04-JAN-2001.
XX
XX 28-JUN-2000; 2000WO-US017827.
XX
XX 29-JUN-1999; 99US-0141582P.
XX
XX (ICOS-) ICOS CORP.
XX
XX Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
XX WPI; 2001-102896/11.
XX
XX P-PSDB; AAB66295.
XX
XX New tankyrase2 polypeptides, useful for treating conditions mediated by
XX poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
XX inflammatory and autoimmune disorders.
XX
XX Claim 6; Page 195-200; 242pp; English.
XX
XX The present invention provides the protein and coding sequence for the
XX human tankyrase2 protein. This is found in two different versions,
XX designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
XX ribosylation activity and is involved in the modification of TRF1, which
XX is a telomere-specific binding protein. The regulation of telomere
XX length, in which TRF1 has a role, is linked to ageing and cancer. The
XX sequences are useful in the treatment of cancers and inflammatory
XX disorders
XX
SQ Sequence 4992 BP; 1454 A; 1064 C; 1191 G; 1283 T; 0 U; 0 Other;
Query Match 89.28; Score 3387.2; DB 5; Length 4992;
Best Local Similarity 99.94; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 403 AGGTTTTTGGCGGAAAGACCTAGTTGAATATTTGCTTCAGAAATGGTGCAGTGTCCCAAGC 462
Db 1073 AGGTTTTTGGCGGAAAGACCTAGTTGAATATTTGCTTCAGAAATGGTGCAGTGTCCCAAGC 1132
Qy 463 ACGTGATGATGGGGCCCTTATCTCTTCATATATGATGCTCTTTTGGTCAATGCTGAAGT 522
Db 1133 ACGTGATGATGGGGCCCTTATCTCTTCATATATGATGCTCTTTTGGTCAATGCTGAAGT 1192
Qy 523 AGTCATCTCTTTTGGAGATGTCGACATGTCAGACCCCAATGCTCGAGATATGGAAATTATAC 582
Db 1193 AGTCATCTCTTTTGGAGATGTCGACATGTCGACACCCCAATGCTCGAGATATGGAAATTATAC 1252
Qy 583 TCCTCTCCATGAAGCTGCAATTAAGGAAAGATGTGTTTGGCATTTGCTGTTTACAGCA 642

Db 1253 TCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATGTTTGCAATGTTGCTGTTACAGCA 1312
Qy 643 TGGAGCTGAGCCCAACCACTCCGAATACAGATGGAAGGACAGCATTTGGATTAGCAGATCC 702
Db 1313 TGGAGCTGAGCCCAACCACTCCGAATACAGATGGAAGGACAGCATTTGGATTAGCAGATCC 1372
Qy 703 ATCTGCCAAAGCAGTGTCTACTGTGGTAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG 762
Db 1373 ATCTGCCAAAGCAGTGTCTACTGTGGTAATATAAGAAAGATGAATCTTTAGAAAGTGCCAG 1432
Qy 763 GAGTGGCAATGAAGAAATAATGATGGCTCTACTCAACATTAATGAATGCAATGCGCAGC 822
Db 1433 GAGTGGCAATGAAGAAATAATGATGGCTCTACTCAACATTAATGAATGCAATGCGCAGC 1492
Qy 823 AAGTCATGCGCAGAAAGTCAATCCCAATACATTTGCGCAGCAGATATACAGATGAAGAT 882
Db 1493 AAGTCATGCGCAGAAAGTCAATCCCAATACATTTGCGCAGCAGATATACAGATGAAGAT 1552
Qy 883 TGTCAGCTGTTTACTGCAACATGAGCTGATGTCATGCTAAAGATAAAGGTGATCTGGT 942
Db 1553 TGTCAGCTGTTTACTGCAACATGAGCTGATGTCATGCTAAAGATAAAGGTGATCTGGT 1612
Qy 943 ACCATTACAAATGCTGTTCTTATGTCATTAATGAAGTAACTGAATTTGGTCAAGCA 1002
Db 1613 ACCATTACAAATGCTGTTCTTATGTCATTAATGAAGTAACTGAATTTGGTCAAGCA 1672
Qy 1003 TGGTCCCTGTGAATGCAATGGACTTGTGGCAATTTCACTCTTTCATGAGGAGCTTC 1062
Db 1673 TGGTCCCTGTGAATGCAATGGACTTGTGGCAATTTCACTCTTTCATGAGGAGCTTC 1732
Qy 1063 TAAGAAACAGGGTGTGAAGTATGTTCTTCTTTAAGTTATGTCGAGACCCAACTGCT 1122
Db 1733 TAAGAAACAGGGTGTGAAGTATGTTCTTCTTTAAGTTATGTCGAGACCCAACTGCT 1792
Qy 1123 CAATTTGTCAATAAAGTGTATAGACTTGGCTCCCAACACACAGTTTAAAGAAAGATT 1182
Db 1793 CAATTTGTCAATAAAGTGTATAGACTTGGCTCCCAACACACAGTTTAAAGAAAGATT 1852
Qy 1183 AGCATATGAATTAAGGCCACTGTTGCTGCAAGCTGCGAGAGCTGATGTTACTCG 1242
Db 1853 AGCATATGAATTAAGGCCACTGTTGCTGCAAGCTGCGAGAGCTGATGTTACTCG 1912
Qy 1243 AATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTCAAAACACATGAAC 1302
Db 1913 AATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTCAAAACACATGAAC 1972
Qy 1303 AGCATGCTGCTGCTGCTATCCATATCCCAAAAGAAAGCAATATGGAATGTT 1362
Db 1973 AGCATGCTGCTGCTGCTATCCATATCCCAAAAGAAAGCAATATGGAATGTT 2032
Qy 1363 GCTAAGAAAGGAGCAACATCAATGAAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1422
Db 2033 GCTAAGAAAGGAGCAACATCAATGAAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2092
Qy 1423 GGCATCTGAGAAAGTCAATATGATGTTGTTGAAGTGGTGAAGCAAGGATGAAGG 1482
Db 2093 GGCATCTGAGAAAGTCAATATGATGTTGTTGAAGTGGTGAAGCAAGGATGAAGG 2152
Qy 1483 TAATGCTCTGGTAATCTTTGGTGCAGACTTCTTACACAGAGCTGCATATTTGGTGCATCT 1542
Db 2153 TAATGCTCTGGTAATCTTTGGTGCAGACTTCTTACACAGAGCTGCATATTTGGTGCATCT 2212
Qy 1543 ACAACCTGCGCCCTACTCTGAGCTATGGGTGATGCTTAACATATATCTCTTCAGGG 1602
Db 2213 ACAACCTGCGCCCTACTCTGAGCTATGGGTGATGCTTAACATATATCTCTTCAGGG 2272
Qy 1603 CTTTACTCTTTACAGATGGGAAATGAATAATGATGATGATGATGATGATGATGATGATG 1662
Db 2273 CTTTACTCTTTACAGATGGGAAATGAATAATGATGATGATGATGATGATGATGATGATG 2332
Qy 1663 ATTAGGTAATTCAGAGGAGACAGACAAATGCTGGAAGCTGCAAAAGGCTGGAGATGTCGA 1722
Db 2333 ATTAGGTAATTCAGAGGAGACAGACAAATGCTGGAAGCTGCAAAAGGCTGGAGATGTCGA 2392

Qy 1723 AACTGTAAAAAACTGTGTACTGTTTCAAGTGTCAACTGCAGAGACATTTGAAGGCGGTCA 1782
Db 2393 AACTGTAAAAAACTGTGTACTGTTTCAAGTGTCAACTGCAGAGACATTTGAAGGCGGTCA 2452
Qy 1783 GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT 1842
Db 2453 GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT 2512
Qy 1843 ACAGCATGGAGCTGATGTCATGCTAAAGATAAAGGAGGCCCTTTACCTTTGCACAATGC 1902
Db 2513 ACAGCATGGAGCTGATGTCATGCTAAAGATAAAGGAGGCCCTTTACCTTTGCACAATGC 2572
Qy 1903 ATGTTCTTATGCAATTAATGAAGTTGCAAGACTTCTTGTAAACATGAGCAGTAGTTAA 1962
Db 2573 ATGTTCTTATGCAATTAATGAAGTTGCAAGACTTCTTGTAAACATGAGCAGTAGTTAA 2632
Qy 1963 TGTAAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
Db 2633 TGTAAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2692
Qy 2023 AATTTGCAAACTTCTGCTCCAGCATGTCGAGACCTTACCAAAAAACACAGGATGGAA 2082
Db 2693 AATTTGCAAACTTCTGCTCCAGCATGTCGAGACCTTACCAAAAAACACAGGATGGAA 2752
Qy 2083 TACTCCTTTGGATCTTGTAAAGATGAGATACAGATATTTCAAGATCTGTTAGGGGAGA 2142
Db 2753 TACTCCTTTGGATCTTGTAAAGATGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA 2812
Qy 2143 TGCAAGCTTTGCTAGATGCTGCAAGAGGGTGTTTAGCCAGAGTGAAGAGTTGTCTTC 2202
Db 2813 TGCAAGCTTTGCTAGATGCTGCAAGAGGGTGTTTAGCCAGAGTGAAGAGTTGTCTTC 2872
Qy 2203 TCCTGATTAATGTAATTTGCGCGATACCCAAAGGAGACATTTCAACACTTTTACATTTAGC 2262
Db 2873 TCCTGATTAATGTAATTTGCGCGATACCCAAAGGAGACATTTCAACACTTTTACATTTAGC 2932
Qy 2263 AGCTGGTTTATAATTTTAGAAGTTGAGAGTATTTGTTTACAACACGAGCTGATGTCAA 2322
Db 2933 AGCTGGTTTATAATTTTAGAAGTTGAGAGTATTTGTTTACAACACGAGCTGATGTCAA 2992
Qy 2323 TGCCCAAGACAAAGGAGGACTTATTTCTTTTACATAATGACAGCATCTTACGGGCAATGTAGA 2382
Db 2993 TGCCCAAGACAAAGGAGGACTTATTTCTTTTACATAATGACAGCATCTTACGGGCAATGTAGA 3052
Qy 2383 TGTAGCAGCTCTACTAATAAGATATATGATGTCATGTCATGTCGACGCAAGCAATGGGCTTT 2442
Db 3053 TGTAGCAGCTCTACTAATAAGATATATGATGTCATGTCATGTCGACGCAAGCAATGGGCTTT 3112
Qy 2443 CACACCTTTGCAACAGCAGCCCAAAAGGAGCAACACAGCTTTTGTGCTTTGTTGCTAGC 2502
Db 3113 CACACCTTTGCAACAGCAGCCCAAAAGGAGCAACACAGCTTTTGTGCTTTGTTGCTAGC 3172
Qy 2503 CCATGGAGCTGACCCGACTCTTTAAAAATCAGAAAGGAGCAACACCTTTTAGATTTAGTTTC 2562
Db 3173 CCATGGAGCTGACCCGACTCTTTAAAAATCAGAAAGGAGCAACACCTTTTAGATTTAGTTTC 3232
Qy 2563 AGCGATGATGTGACGGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCTCTTG 2622
Db 3233 AGCAGATGATGTGACGGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCTCTTG 3292
Qy 2623 TTACAAGCCTCAAGTGTCAATGTCGTAAGAGCCAGAGGCCCTGAGATGCTCTCTC 2682
Db 3293 TTACAAGCCTCAAGTGTCAATGTCGTAAGAGCCAGAGGCCCTGAGATGCTCTCTC 3352
Qy 2683 TTTAGGCTCCATCTAGCCCATCAAGCCTTTCTGACGAGCAGTCTTGAACACTTATCTGG 2742
Db 3353 TTTAGGCTCCATCTAGCCCATCAAGCCTTTCTGACGAGCAGTCTTGAACACTTATCTGG 3412
Qy 2743 GAGTTTTTCAAGACTGTCTTTCAGTAGTTAGTTTCAAGTGAAGCAGAGGCTGCTTCAGTTT 2802
Db 3413 GAGTTTTTCAAGACTGTCTTTCAGTAGTTAGTTTCAAGTGAAGCAGAGGCTGCTTCAGTTT 3472

QY 2803 GGAGAAAAGGAGGTTCCAGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGG 2862
Db 3473 GGAGAAAAGGAGGTTCCAGAGTAGATTTTAGCATAACTCAATTCGTAAGGAATCTTGG 3532
QY 2863 ACTTGAGCACCTAATGGATATATTTTGAGAGAGAAGACAGATCACTTTGGATGTATTAGTTGA 2922
Db 3533 ACTTGAGCACCTAATGGATATATTTTGAGAGAGAAGACAGATCACTTTGGATGTATTAGTTGA 3592
QY 2923 GATGGGCACAAGAGCTGAAGAGATTTGGAATCAATGCTTTATCGACATAGGCACAACT 2982
Db 3593 GATGGGCACAAGAGCTGAAGAGATTTGGAATCAATGCTTTATCGACATAGGCACAACT 3652
QY 2983 AATTAAAGGAGTCAGAGACTTATCTCCGGACAACAGAGTCTTAAACCATATTTAACTTT 3042
Db 3653 AATTAAAGGAGTCAGAGACTTATCTCCGGACAACAGAGTCTTAAACCATATTTAACTTT 3712
QY 3043 GAACACCTCTGCTAGTGGAACAATTTCTTATAGATCTGCTCTGATGATTAAGAGTTTCA 3102
Db 3713 GAACACCTCTGCTAGTGGAACAATTTCTTATAGATCTGCTCTGATGATTAAGAGTTTCA 3772
QY 3103 GTCTGTGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTCAATGAGG 3162
Db 3773 GTCTGTGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTCAATGAGG 3832
QY 3163 TGGAAATCTTCAACAGATCAATATTTCTCAAGATTCAGAGGTTTGTAAAGAAACTATG 3222
Db 3833 TGGAAATCTTCAACAGATCAATATTTCTCAAGATTCAGAGGTTTGTAAAGAAACTATG 3892
QY 3223 GGAAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACACCATGCCAATGA 3282
Db 3893 GGAAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACACCATGCCAATGA 3952
QY 3283 ACGAATGCTATTTTCATGGGTCCTCTTTTGTGAATGCAATATTCACAAAGGCTTTGATGA 3342
Db 3953 ACGAATGCTATTTTCATGGGTCCTCTTTTGTGAATGCAATATTCACAAAGGCTTTGATGA 4012
QY 3343 AAGGATCGGTACATAGTGGTATGTTTGGAGCTGGCAATTTATTTTGTCTGAAAACCTCTTC 3402
Db 4013 AAGGATCGGTACATAGTGGTATGTTTGGAGCTGGCAATTTATTTTGTCTGAAAACCTCTTC 4072
QY 3403 CAAGAAGCAATCAATATGATATGAAATGGAGGAGGTACTGGGTGCCAGTTCCAAAGA 3462
Db 4073 CAAGAAGCAATCAATATGATATGAAATGGAGGAGGTACTGGGTGCCAGTTCCAAAGA 4132
QY 3463 CAGATCTTTGTATCAATTTGCCACAGCAGCTGCTCTTTTGGCGGTAACCTTTGGGAAAGTC 3522
Db 4133 CAGATCTTTGTATCAATTTGCCACAGCAGCTGCTCTTTTGGCGGTAACCTTTGGGAAAGTC 4192
QY 3523 TTTCTCGAGTTTCAAGTGAATGAAAATGGACATCTCTCTCAGGTGATCACTCAGTCAC 3582
Db 4193 TTTCTCGAGTTTCAAGTGAATGAAAATGGACATCTCTCTCAGGTGATCACTCAGTCAC 4252
QY 3583 TGGTAGGCCAGGTGAAATGCGCTAGCAATAGCTGAATATGTTATTTACAGAGGAGAAC 3642
Db 4253 TGGTAGGCCAGGTGAAATGCGCTAGCAATAGCTGAATATGTTATTTACAGAGGAGAAC 4312
QY 3643 GGCCTTATCTGAGTATTTAAATTTACTTACAGATATGAGGCTGAAAGTATGGTCGATGG 3702
Db 4313 GGCCTTATCTGAGTATTTAAATTTACTTACAGATATGAGGCTGAAAGTATGGTCGATGG 4372
QY 3703 ATAAATAGTATTTTAAAGAACTAAATTCACCTGAACCTTAAATCATCAAGCAGCAGTGG 3762
Db 4373 ATAAATAGTATTTTAAAGAACTAAATTCACCTGAACCTTAAATCATCAAGCAGCAGTGG 4432
QY 3763 CCTCTACGTTTTTACTCCTTTGCTGAAAAAAA 3794
Db 4433 CCTCTACGTTTTTACTCCTTTGCTGAAAAAAA 4464

RESULT 14
ID AAF63952
XX AAF63952 standard; DNA; 5002 BP.

AAAF63952;
05-APR-2001 (first entry)
Human tankyrase2 TANK2-LONG coding sequence SEQ ID NO: 132.
Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
inflammatory disorder; ds.
Homo sapiens.
WO200100849-A1.
04-JAN-2001.
28-JUN-2000; 2000WO-US017827.
29-JUN-1999; 99US-0141582P.
(ICOS-) ICOS CORP.
Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
WPI; 2001-102896/11.
P-PSDB; AAB66294.
New tankyrase2 polypeptides, useful for treating conditions mediated by
poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
inflammatory and autoimmune disorders.
Claim 5; Page 185-190; 242pp; English.
The present invention provides the protein and coding sequence for the
human tankyrase2 protein. This is found in two different versions,
designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
ribosylation activity and is involved in the modification of TRF1, which
is a telomere-specific binding protein. The regulation of telomere
length, in which TRF1 has a role, is linked to ageing and cancer. The
sequences are useful in the treatment of cancers and inflammatory
disorders
SQ Sequence 5002 BP; 1456 A; 1065 C; 1196 G; 1285 T; 0 U; 0 Other;
Query Match 89.2%; Score 3387.2; DB 5; Length 5002;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 403 AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTCAAGTGTCCAAGC 462
Db 1083 AGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTCAAGTGTCCAAGC 1142
QY 463 ACGTGATGATGGGGCCCTTATCTCTTCAATAATGCAATGCTCTTTGGTCATGCTGAAGT 522
Db 1143 ACGTGATGATGGGGCCCTTATCTCTTCAATAATGCAATGCTCTTTGGTCATGCTGAAGT 1202
QY 523 AGTCAATCTCTTTTGGACATGTGTCAGACCCCAATGCTCGAGATTAATTCGAATTATAC 582
Db 1203 AGTCAATCTCTTTTGGACATGTGTCAGACCCCAATGCTCGAGATTAATTCGAATTATAC 1262
QY 583 TCCTCTCCATGAAGCTCAATTTAAAGGAAGATGATGTTTGGCTGCTGTTGTACAGCA 642
Db 1263 TCCTCTCCATGAAGCTCAATTTAAAGGAAGATGATGTTTGGCTGCTGTTGTACAGCA 1322
QY 643 TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 702
Db 1323 TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 1382
QY 703 ATCTGCCAAGCAGTGTCTTACTGTTGATATTAAGAAAGATGAACTCTTAGAAAGTCCAG 762
Db 1383 ATCTGCCAAGCAGTGTCTTACTGTTGATATTAAGAAAGATGAACTCTTAGAAAGTCCAG 1442
QY 763 GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACCATTAATGTCAACTGTCACGC 822

2983	QY	AATTAAGGAGTCGAGAGCTTATCTCCGGAACAAGGTCCTTAAACCCATATTTTAACTTT	3042
3663	Db	AATTAAGGAGTCGAGAGCTTATCTCCGGAACAAGGTCCTTAAACCCATATTTTAACTTT	3722
3043	QY	GAACACCTCTGGTAGTGGAAACAATCTTATAGATCTGTCTCCTGATGATATAAGAGTTTCA	3102
3723	Db	GAACACCTCTGGTAGTGGAAACAATCTTATAGATCTGTCTCCTGATGATATAAGAGTTTCA	3782
3103	QY	GTCTGTGGAGGAAGAGATGCAAAAGTAGTACAGTTCGAGAGCACAGAGATGGAGGTCATGCAGG	3162
3783	Db	GTCTGTGGAGGAAGAGATGCAAAAGTAGTACAGTTCGAGAGCACAGAGATGGAGGTCATGCAGG	3842
3163	QY	TGGAATCTTCAACAGATACATATTTCTCAAGATTCAAGAGTTTGTAAACAAGAAACTATG	3222
3843	Db	TGGAATCTTCAACAGATACATATTTCTCAAGATTCAAGAGTTTGTAAACAAGAAACTATG	3902
3223	QY	GGAAAGATACACTCACCGGAGAAAGAAGTTTCTGAAGAAACACACAACCATGCCAATGA	3282
3903	Db	GGAAAGATACACTCACCGGAGAAAGAAGTTTCTGAAGAAACACACAACCATGCCAATGA	3962
3283	QY	ACGAATGCTATTTTCATGGGTCTCCTTTGTGAATGCAATTTATCCACAAGGCTTTTGATGA	3342
3963	Db	ACGAATGCTATTTTCATGGGTCTCCTTTGTGAATGCAATTTATCCACAAGGCTTTTGATGA	4022
3343	QY	AGGCAATGGTACATAGGTGGTATGTTTGGAGCTGCAATTTATTTTGTCTGAAACCTCTTC	3402
4023	Db	AGGCAATGGTACATAGGTGGTATGTTTGGAGCTGCAATTTATTTTGTCTGAAACCTCTTC	4082
3403	QY	CAAAAGCAATCAATATGTATATGGAATTGGAGAGGTACTGGGTGTCCAGTTTCACAAAGA	3462
4083	Db	CAAAAGCAATCAATATGTATATGGAATTGGAGAGGTACTGGGTGTCCAGTTTCACAAAGA	4142
3463	QY	CAGATCTTGTTACATTTGCCACAGGACGTGCTCTTTTGGCCGGGTAAACCTTGGGAAAGTC	3522
4143	Db	CAGATCTTGTTACATTTGCCACAGGACGTGCTCTTTTGGCCGGGTAAACCTTGGGAAAGTC	4202
3523	QY	TTTCTCTGCAGTTCAGTGCATGAAATGGCACATCTCTCTCCAGGTCATCACCTCAGTTCAC	3582
4203	Db	TTTCTCTGCAGTTCAGTGCATGAAATGGCACATCTCTCTCCAGGTCATCACCTCAGTTCAC	4262
3583	QY	TGTTAGGCCCCAGTGTAAATGGCCCTAGCATTTAGCTGAATATGTTTATTTACAGAGGAGAAC	3642
4263	Db	TGTTAGGCCCCAGTGTAAATGGCCCTAGCATTTAGCTGAATATGTTTATTTACAGAGGAGAAC	4322
3643	QY	GGCTTATCTGAGTATTTAATTACTTACCAGATTATGAGGCCCTGAAGGTTATGTCGATGG	3702
4323	Db	GGCTTATCTGAGTATTTAATTACTTACCAGATTATGAGGCCCTGAAGGTTATGTCGATGG	4382
3703	QY	ATAAATAGTTTATTTTAAGAAACTTAAATCCACTGAACTTAAATCATCAAGCAGCAGTGG	3762
4383	Db	ATAAATAGTTTATTTTAAGAAACTTAAATCCACTGAACTTAAATCATCAAGCAGCAGTGG	4442
3763	QY	CTCTACTGTTTTTACTCCTTTGTGAAAAAAA	3794
4443	Db	CTCTACTGTTTTTACTCCTTTGTGAAAAAAA	4474

RESULT 15

RESOLUTION
ABZ11674

ABZ11674
ID ABZ11674 standard: cDNA: 5075 BP.

XX
XX

AC ABZ11674;

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XXXXXX

DT 20-JAN-2003 (first entry)

XX
XX

DE Human polynucleotide SEQ ID NO 556.

1. **Introduction**
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KW Human; genome mapping; gene therapy; food supplement; virus; fungus;

cell-proliferative disorder; neurodegenerative disease; bacterial; KW

KW Parkinson's disease; Alzheimer's disease; autoimmune disease;

haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide; antiarthritic; gene; ss.

Homo sapiens.

WO200270539-A2.

12-SEP-2002.

05-MAR-2002: 2002WO-US005095.

05-MAP-2001: 2001IS-00799451

(UYCE-) UYCEO TNC

Peng YF Zhou B Goodrich PW Asundi V Zhang J Zhao OA Ren F.

Tang Y.T., Zhou P., Goodrich R.W., Asundi V., Zhang J., Zhao Q.A.,
Yue H.T., Yang Y., Ma Y., Yamazaki Y., Chen P., Wang Z., Chosh M.

Xue AJ, Tang I, Ma I, Yamazaki V, Chen
Wehrman T, Wang J, Wang D, Drmanac RT:

WDT: 2002-759812/82

WPI: 2002-759812/
P-PSCDB: ABP69457

New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders.

Claim 1: SEO ID NO 556: 1012pp + Sequence Listing; English.

The invention relates to an isolated polynucleotide (1) comprising a nucleotide sequence selected from any of 948 sequences (AB211119-AB212066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP69802-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from Wipo at <http://wipo.int/pub/int/pub/abstracted/sequences>

Sequence 5075 BP: 1487 A: 1055 C: 1166 G: 1367 T: 0 U: 0 Other:

every Match

Very Match	at Local Similarity	Pred No. 0:	score 3387.2
		99.9%	85.2%

BC Local Similarity	99.9%	Fixed: NO: 0;	
Matches 3389:	Conservative	0: Mismatches	3: Indels
		0: Gaps	0: Gaps

403 AGGTTTGGGCGGAAAGACGTAGTTGAAATTTGCTTCAGAAATGGTGCAAGTGTCACAGC 462

[illegible]

450 AGGTTTGGGCCGGAAAGACGTAGTAGAATTCCTCATTGTCATTGCAATGATGTCATAATGTCATGC

463 ACGTGATGATGGGGGCCCTTATTCCCTCTTCATAATGCATGCTCTTTTGGTCATGCTGAAGT 522

510 CCTGATGATGGGGCCCTTATTCCCTCTTCA"TAATGCATGCTCTTTGGTCATGCTGAAGT 569

310 ACGTGAAGGAGGGCCCTATTCCTCCTCAATAAGCAAGCTCTTTTGATCATGCCTGAAAT

523 AGTCAAATCTCCCTTTTGGGACATGGTGGCAGACCCCAATGCTCGAGATAAATGGGAAATATATAC

570 AGTCAATCTCCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAATTGGAATTATAC 629

593 TGCCTCCATGAGCATGCAATTAAAGGAAAGATTGATGTTGCAATTGTGCTGTACAGCA 642

583 TCC TCT CCA TGA AGC TGC AAT ATA AGG AAG AAT TGA TGT TGG CAT TGT GTCT GTT A C A A C A C A 64

630 TCC^TCTCCATGAAGCTGCAATTAAGGAAGATTTGCAITGTGCTGTTACAGCA 882

Db 750 ATCTGCCAAGCAGTGTCTTACTGGTGAATATTAAGAAAGATGAATCTTTAGAAAGTGCCAG 809
Qy 763 GAGTGGCAATGAAGAAAATGATGGCTCTACTACACCAATTAATGTCAACTGCCAGC 822
Db 810 GAGTGGCAATGAAGAAAATGATGGCTCTACTACACCAATTAATGTCAACTGCCAGC 869
Qy 823 AAGTGATGCGACAAAAGTCAATCCCAATTAATTTGGCAGCAGGATATAACAGAGTAAAGAT 882
Db 870 AAGTGATGCGCAAGATCAATCCCAATTAATTTGGCAGCAGGATATAACAGAGTAAAGAT 929
Qy 883 TGTAAGCTGTTTACGCAACATGAGAGTGATGCTCAATGCTTAAAGATAAGGTGATCTGGT 942
Db 930 TGTAAGCTGTTTACGCAACATGAGAGTGATGCTCAATGCTTAAAGATAAGGTGATCTGGT 989
Qy 943 ACCAATACCAATGCTGTTCTTATGTCATTAATGATTAAGTAACTGATTTGGTCAAGCA 1002
Db 990 ACCAATACCAATGCTGTTCTTATGTCATTAATGATTAAGTAACTGATTTGGTCAAGCA 1049
Qy 1003 TGGTGCCTGTGTAATGCAATGCACTTGTGGCAATTTCACTCTCTCATGAGGCACTTC 1062
Db 1050 TGGTGCCTGTGTAATGCAATGCACTTGTGGCAATTTCACTCTCTCATGAGGCACTTC 1109
Qy 1063 TAAGAACAGGGTGAAGTATGTTCTTCTTAAAGTTATGGTGAGACCCCAACTGCT 1122
Db 1110 TAAGAACAGGGTGAAGTATGTTCTTCTTAAAGTTATGGTGAGACCCCAACTGCT 1169
Qy 1123 CAATTTGTCAATTAAGTGTATAGACTTGGCTCCACACCAAGTTAAAGAAAGATT 1182
Db 1170 CAATTTGTCAATTAAGTGTATAGACTTGGCTCCACACCAAGTTAAAGAAAGATT 1229
Qy 1183 AGCATATGAATTTAAAGGCCACTGTTGTCGAAGCTGCAGAGAGCTGATTTACTCG 1242
Db 1230 AGCATATGAATTTAAAGGCCACTGTTGTCGAAGCTGCAGAGAGCTGATTTACTCG 1289
Qy 1243 AATCAAAAAACATCTCTCTGGAATGTTGTAATTTCAAGCATCTCTCAACACATGAAC 1302
Db 1290 AATCAAAAAACATCTCTCTGGAATGTTGTAATTTCAAGCATCTCTCAACACATGAAC 1349
Qy 1303 AGCATATGATTTGCTGTCATCTCCATATCCCAAGAAAGCAATATGTGAATCTGT 1362
Db 1350 AGCATATGATTTGCTGTCATCTCCATATCCCAAGAAAGCAATATGTGAATCTGT 1409
Qy 1363 GCTAAGAAAAGGAGCAACATCAATGAAGAACTAAAGAAATTTCTGACTCTCTGCAAGT 1422
Db 1410 GCTAAGAAAAGGAGCAACATCAATGAAGAACTAAAGAAATTTCTGACTCTCTGCAAGT 1469
Qy 1423 GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT 1482
Db 1470 GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGT 1529
Qy 1483 TAATGCTCTGGATAATCTTGGTGAGACTTCTACACAGAGCTGATATTTGGTCACT 1542
Db 1530 TAATGCTCTGGATAATCTTGGTGAGACTTCTACACAGAGCTGATATTTGGTCACT 1589
Qy 1543 ACAAACTGCGCCCTACTCTGAGCTATGGGTGATCTCAACATTAATCCCTTCAGGG 1602
Db 1590 ACAAACTGCGCCCTACTCTGAGCTATGGGTGATCTCAACATTAATCCCTTCAGGG 1649
Qy 1603 CTTTACTGCTTTACAGATGGGAAATGAATAATGACGAACCTCTCCAAAGGGGTATCTC 1662
Db 1650 CTTTACTGCTTTACAGATGGGAAATGAATAATGACGAACCTCTCCAAAGGGGTATCTC 1709
Qy 1663 ATTAGGTAATTCAGAGGCGACAGACAAATGCTGGAAGCTGCAAAAGGCTGGAGATGTGA 1722
Db 1710 ATTAGGTAATTCAGAGGCGACAGACAAATGCTGGAAGCTGCAAAAGGCTGGAGATGTGA 1769
Qy 1723 AACTGTAAAAAATCTGTACTGTTTCAAGTGTCAACTGCAGACATTTGAAGGCGTCA 1782
Db 1770 AACTGTAAAAAATCTGTACTGTTTCAAGTGTCAACTGCAGACATTTGAAGGCGTCA 1829
Qy 1783 GTCTACACCACTTCAATTTTGCAGCTGGGTATTAACAGAGTGTCCGTGGGAAATATCTGCT 1842

Db 1830 GTCTACACCACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT 1889
Qy 1843 ACAGCATGGAGCTCATGTGCATGTAAAGATAAAGGAGGCTTGTACCTTTGCACAAATGC 1902
Db 1890 ACAGCATGGAGCTCATGTGCATGTAAAGATAAAGGAGGCTTGTACCTTTGCACAAATGC 1949
Qy 1903 ATGTTCTTATGGACATTTATGAAGTTTGCAGAACTTCTTCTTAAACATGAGCAGTAGTTAA 1962
Db 1950 ATGTTCTTATGGACATTTATGAAGTTTGCAGAACTTCTTCTTAAACATGAGCAGTAGTTAA 2009
Qy 1963 TGTAGCTGATTTATGGAATTTTACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
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Db 2070 AATTTGCAAACTTCTGCTCCAGCATGTTGTCAGACCTTACCAAAAAACACGGGATGAAA 2129
Qy 2083 TACTCCTTTGGATCTTGTAAAGATGGAGATPACAGATATTTCAAGATCTGCTTAGGGGAGA 2142
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Db 2430 TGTAGCAGCTCTACTTAATAAGTATTAATGTCATGTGTCATGCCACGGACAAATGGGCTTT 2489
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Db 2490 CACACCTTTGCAAGAGCAGCCCAAGAGGACGAAACACAGCTTTTGTGCTTTGCTGCTAGC 2549
Qy 2503 CCATGGAGCTCAACCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTTAGATTTAGTTTC 2562
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Db 2730 TTCAGGTCATCTAGCCCATCAAGCCTTTTGCAGCCAGCAGTCTTGACAACTTATCTGG 2789
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Db 2790 GAGTTTTTCAGAACTGCTTTCAGTAGTTAGTTCAAGTGGAAACAGAGGCTTCCAGTTT 2849
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Db 2910 ACTTGAGCACCTAATGGATATATTGTAGAGAGAAACAGATCACTTTGGATGATTTAGTTGA 2969

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QY 2923 GATGGGCAAAAGAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCACAAACT 2982
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 2983 AATTAAAGGAGCTCGAGAGACTTATCTCCGGACAACAGGCTCTTAACCCATATTTAACTTTT 3042
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 3030 AATTAAAGGAGCTCGAGAGACTTATCTCCGGACAACAGGCTCTTAACCCATATTTAACTTTT 3089
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QY 3090 GAACACCTCTGGTAGTGGAAACAATTTCTTTATAGATCTGTCTCCTGATGATAAGAGTTTCA 3149
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QY 3103 GTCTGTGGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTCAATGAGG 3162
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QY 3150 GTCTGTGGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGTCAATGAGG 3209
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QY 3163 TGGAAATCTTCAACAGATACAATATTTCTCAAGATTTCAGAGGTTTGTAAACAAGAAACTATG 3222
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QY 3210 TGGAAATCTTCAACAGATACAATATTTCTCAAGATTTCAGAGGTTTGTAAACAAGAAACTATG 3269
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QY 3223 GGAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCAATGCCAATGA 3282
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QY 3270 GGAAGATACACTCACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCAATGCCAATGA 3329
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QY 3283 ACGAATGCTATTTCAATGGGTCTCTTTTGTGAATGCAATTTATCCACAAGGCTTTGATGA 3342
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QY 3390 AAGCATGCGTACATAGGTGTGTATGTTTGGAGCTGGCAATTTATTTGCTGAAAACCTCTTC 3449
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 3450 CAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTGGGTGTCCAGTTCAAAAGA 3509
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QY 3463 CAGATCTTTGTACATTTGCCACAGCAGCTGCTCTTTTGGCGGGTAACCTTGGGAAAAGTC 3522
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QY 3510 CAGATCTTTGTACATTTGCCACAGCAGCTGCTCTTTTGGCGGGTAACCTTGGGAAAAGTC 3569
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QY 3523 TTTCTCGAGTTTCAGTGAATGAAAATGGCACATTTCTCTCCAGGTCACTCAGTCAC 3582
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 3570 TTTCTCGAGTTTCAGTGAATGAAAATGGCACATTTCTCTCCAGGTCACTCAGTCAC 3629
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 3583 TGGTAGGCCCAAGTGTAAATGGCCTAGCATTAAGCTGAATATGTTATTTACAGAGAGAACA 3642
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 3643 GGCTTATCCTGAGTATTTAATTTACTTACCAGATTTATGAGGCTGAAGGTATGGTTCGATGG 3702
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QY 3690 GGCTTATCCTGAGTATTTAATTTACTTACCAGATTTATGAGGCTGAAGGTATGGTTCGATGG 3749
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 3703 ATAAATAGTTATTTTAAGAACTAATTCCTCACTGAACTTAAATCATCAAGCAGCAGTGG 3762
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 3750 ATAAATAGTTATTTTAAGAACTAATTCCTCACTGAACTTAAATCATCAAGCAGCAGTGG 3809
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 3763 CCTCTACGTTTTTACTCTCTTTGCTGAAAAAAA 3794
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QY 3810 CCTCTACGTTTTTACTCTCTTTGCTGAAAAAAA 3841
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Search completed: December 18, 2006, 13:14:52
Job time : 2059.86 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2006, 13:00:27 ; Search time 16793.5 Seconds
(without alignments)
12643.339 Million cell updates/sec

Title: US-10-616-101-1

Perfect score: 3797

Sequence: 1 ctttgaagacactgatttc.....cctttgctgaaaaaaaaa 3797

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gse1:*
12: gb_gse2:*
13: gb_gse3:*
14: gb_gse4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1609.8	42.4	3417	6	AK048860 Mus muscu
2	1481.8	39.0	2226	6	AK149368 Mus muscu
3	1369.8	36.1	1967	6	AK047094 Mus muscu
4	1360.4	35.8	3194	6	AK080913 Mus muscu
5	1221.6	32.2	3612	14	DQ034114 Homo sapi
6	892.2	23.5	3107	14	DQ034115
7	884.4	23.3	888	8	CR983155 CR983155
8	859.6	22.6	926	8	CR987822 CR987822
9	784.2	20.7	838	1	AU140145 AU140145
10	770.6	20.3	898	10	DF808067 DF808067
11	766.8	20.2	834	5	CR947047 CR947047
12	709	18.7	848	9	DN536421 DN536421
13	692.8	18.2	819	9	DAY33094 DAY33094
14	687.8	18.1	955	4	CB183123 CB183123
15	672.4	17.7	675	4	CB128566 K-EST0178
16	672.2	17.7	1128	2	BM457025 BM457025
17	665.2	17.5	754	4	CB170279 CB170279
18	661.4	17.4	663	9	DA326495 DA326495
19	652	17.2	661	8	CR767085 DKF2p469A

c	20	652	17.2	923	5	CF407574
	21	649.2	17.1	659	10	R64714
	22	648.2	17.1	781	8	CN525726
	23	644.2	17.0	753	8	CV558255
	24	643.8	17.0	691	2	BG391376
c	25	643	16.9	750	9	DN537809
	26	642.8	16.9	759	1	AL601027
	27	637	16.8	709	4	BX925031
	28	636.6	16.8	756	5	CN459472
	29	635.4	16.7	759	5	CK635046
	30	634.4	16.7	950	3	BQ885764
	31	632.6	16.7	743	5	CF539235
	32	629.2	16.6	642	8	CR550014
	33	628.8	16.6	730	9	DN268735
	34	623	16.4	729	8	CN527536
	35	622.8	16.4	638	4	BX474686
	36	620.4	16.3	728	8	CN529262
	37	618.2	16.3	682	9	DA733093
	38	617.6	16.3	740	8	CO433927
	39	617.2	16.3	776	8	CO434293
	40	616.4	16.2	724	5	CF533694
	41	615.4	16.2	732	8	CO429777
	42	614.2	16.2	747	5	CF727485
	43	612	16.1	733	8	CN534125
	44	610.6	16.1	746	8	CN455195
	45	605	15.9	648	2	BG875327

ALIGNMENTS

RESULT 1	AK048860	3417 bp	mRNA	linear	HTC 02-SEP-2005
LOCUS	AK048860				
DEFINITION	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone: C230076L23 product: tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase, full insert sequence.				
ACCESSION	AK048860				
VERSION	AK048860.1	GI:26339607			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	10349636				
REFERENCE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
PUBMED	11076861				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				

- 2.4.2.30) (TANK2) (Tankyrase II) (TNKS-2) (TRF1- interacting ankryrin-related ADP-ribose polymerase 2) (tankyrase-like protein) (tankyrase-related protein) homolog [Homo sapiens], full insert sequence.
- AK149368 1 GI:74143548
 HRC; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
- 1 Carninci,P. and Hayashizaki,Y.
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- 2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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- 3 Shibata,K., Itoh,M., Aizawa,K., Nagasaka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,M., Matsumura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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 FANTOM Consortium
 The transcriptional landscape of the mammalian genome
 Science 309 (5740), 1559-1563 (2005)
 16141072
- 7 Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yaguchi,C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.
 RIKEN Genome Exploration Research Group
 Antisense transcription in the mammalian transcriptome


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ACCESSION AK047094
VERSION    AK047094.1 GI:26338577
KEYWORDS   HTC; CAP trapper.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

REFERENCE  1
AUTHORS    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
TITLE      High-efficiency full-length cDNA cloning
JOURNAL    Meth. Enzymol. 303, 19-44 (1999)
PUBMED    10349636
REFERENCE  2
AUTHORS    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
TITLE      Normalization and subtraction of cap-trapper-selected cDNAs to
JOURNAL    Genome Res. 10 (10), 1617-1630 (2000)
PUBMED    11042159
REFERENCE  3
AUTHORS    Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
            Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
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            Yoneda, Y., Teshikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
            Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE      RIKEN integrated sequence analysis (RISA) system--384-format
JOURNAL    sequencing pipeline with 384 multicapillary sequencer
PUBMED    Genome Res. 10 (11), 1757-1771 (2000)
PUBMED    11076861
REFERENCE  4
AUTHORS    The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
TITLE      Functional annotation of a full-length mouse cDNA collection

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JOURNAL REFERENCE
AUTHORS
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AUTHORS
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JOURNAL REFERENCE
AUTHORS
TITLE
JOURNAL REFERENCE
AUTHORS
FEATURES
source
CDS

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Phase I and II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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(Genome Network Core Team) and the FANTOM Consortium.
Antisense Transcription in the Mammalian Transcriptome
Science 309, 1564-1566 (2005)
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The FANTOM Consortium, Riken Genome Exploration Research Group and
Genome Science Group (Genome Network Project Core Group).
The Transcriptional Landscape of the Mammalian Genome
Science 309, 1559-1563 (2005)
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
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Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Iehii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
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ORIGIN

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Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length
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AK080913
AK080913.1 GI:26099551
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Mus musculus
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Iehikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6
AUTHORS RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.
TITLE Antisense Transcription in the Mammalian Transcriptome
JOURNAL Science 309, 1564-1566 (2005)
REFERENCE 7
AUTHORS The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
TITLE The transcriptional landscape of the Mammalian Genome
JOURNAL Science 309, 1559-1563 (2005)
REFERENCE 8
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Atakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanganaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayateu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saibach, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
FEATURES
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403 AGGTTTGGCGGAAGACGCTAGTTGAATTTGCTTCAGAAATGCTCAAGTGTCCAAAGC 462
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678 AGGTTTGGGAAGAGAGATGTTGTACAACTTGTCTGCAGATGGTGTCTATGTCCAGC 737
Qy A-CGTGATGATGGGGGCTTATTCCTCTTCATTAATCATGCTCTTTTGGTCATGCTGAAG 521
Db |||||
738 CCCGTGATGACGGGGTCTCATCCACTTCATAATGCTGCTCTTTTCGGCATGCTGAGG 797
Qy 522 TAGTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAAATATA 581
Db |||||
798 TTGTGAGTCTGTTACTGTGTCAAGGAGCAGATCCGAATGCCAGAGATAACTGGAACTATA 857
Qy 582 CTCTCTCCATGAAGCTGCAATTTAAAGGAAAGATTGATGTTTGCATTGTGCTGTTCAGC 641
Db |||||
858 CACACTGCAATGAAGCTGCCATTTAAAGGAAATTTGATGCTGTATTTGCTGCTGCAGC 917
Qy 642 ATGGAGCTGAGCCCAACCATCCGAAATA CAGATGGAAGGACAGCATTCGATTTAGCAGATC 701
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918 ACGAGCCGATCCAAACATCCGGAACACCGATGGAAATCAGCTCTGGACCTGGCAGATC 977
Qy 702 CATCTGCGAAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCA 761
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978 CTTTCAGCAAAAGCTGCTCTCAGAGTGAATACAAAAAGACGAACTCTCTAGAAAGCTGTA 1037
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Qy 822 CAAGTGTGCGAGAAAGTCAACTCCATTA CATTATGGCAGCAGGATATAACAGAGATAAGA 881
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Qy 882 TTGTACAGCTGTTACTGCAACATGGAGCTGATGCTCCATGCTTAAGATAAAGGTGATCTGG 941
Db |||||
1158 TAGTTTCAGCTGCTTCTACAGCATGGTGTGATGCTCCAGCGAAAGACAAAGGTGGACTTG 1217
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Db |||||
1218 TACCTCTTCAATATGATGCTCATACGACACTATGAGGTCA CAGAACTGCTGCTTAAGC 1277
Qy 1002 ATGGTGCCTGTGTAATGCAATGGACTTTGGGCAATTCACCTCTTTCATGAGGAGGAGTT 1061
Db |||||
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Db |||||
1338 CAAAGAACCGGGTAGAAGTCTGTTCTCTGTACTTAGTACGGT GCGGATCCAACTTGG 1397
Qy 1122 TCAATTGTCAATATAAAGTGTATAGACTTTGGCTCCCA CACACAGTTAAAGAAAGAT 1181
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Db		
1638	TACTGAGGAAGGAGCCAAACGCTCAACGAAAGAACAGGATTTTCATGACCCCTCTGCATG	1697
Qy		
Db		
1422	TGGCAATCTGAGAAAGCTCATTAATGATGTGTTGAAGTAGTGGTGAAACATGAAGCAAAAGG	1481
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Db		
1698	TTGCAGCTGAAAGAGCTCATTAATGATGTCTATGGAAGTTCTGCATAAGCAACGGAGCAAAGA	1757
Qy		
Db		
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1758	TGAATGCACTGGATAGTCTTGGTCAGACTGCTTTTGCACAGAGCTGCGCTTAGCGGGCCACC	1817
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1878	GCTTCAGCGCACGCGAGATGGGAATGAAGCAGTGCAACAGATTTCTGAGCGAGAGTACTC	1937
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1662	CATTAGGTAAATTCAGAGCGACAGACAAATGCTGGAAGTGCACAGCAATCTCTCTCCAAAGAGGGTATCT	1721
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Db		
1938	CTATGCGCACTTCGGAGCTGAGACTATCGTCTCTTAGAGGCATCGAAAGCTGGTGACTTGG	1997
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1722	AAACTGTAAAAAAACTGTGTACTGTTACAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTC	1781
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Db		
1998	AAACTGTGAGCACTCTGCAGCCGCGAGATGTGAACTGCGAGACCTGGAGGGCGCGC	2057
Qy		
Db		
1782	AGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGC	1841
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1902	CATGTTCTTATGGACATTTATGAAGTGTGCAGAACTTCTTTGTTAAACATGGAGCAGTAGTTA	1961
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1962	ATGTAGCTGATTTATGGAAATTTTACCTTTTACATGAAGCAGCAGCAAAAAGGAAATATG	2021
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2238	ATGTGGCGGACCTGTGGAAATTCACCCCTCTCCATGAAGCGGCAGCAACGGGAAATATAG	2297
Qy		
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2022	AAATTTGCAAACTTCTGCTCAGCATGGTGCAGACCCCTACCAAAAAAACAAGGGATGGAA	2081
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2298	AAATCTGCAAACTCCTTTCTAAACATGGAGCAGATCCAACTTAAGAGAAACAGAGATGGAA	2357
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Db		
2082	ATACTCTTTTGGATCTTGTTTAAAGATCGAGATACAGATATTCAAGATCTCTTAGGGGAG	2141
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2358	ATACACCCCTAGATCTGGTCTAAAGAAAGAGACACGGATATTTTAGAGCTCTCTGAGGGGCG	2417
Qy		
Db		
2142	ATGCAGCTTTTCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAAGTTGTCTT	2201
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Qy		
Db		
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Db		
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2478	CTCCAGAGAATATCAACTGCCGCGAGACCCCAAGGGCAGAAAATTCACCCCTCTCTCCACCTGG	2537
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Db		
2262	CAGCTGGTTATAAATTTAGAAGTTCAGAGTATTTGTTTACAACACGGAGCTGATGTGA	2321
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Db		
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Db		
2598	ATGCCCAGGACAAAGGAGGGCTATCCCACTTCAACAGCTGCGTCTTATGGGCAATGTTG	2657
Qy		
Db		
2382	ATGTAGCAGCTCTACTAATAAAGTATTAATGCATGTGTCAATGCGCACGGAACAAATGGGCTT	2441
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Db		
2658	ACATAGCAGCGTTACTGTATATAATACAAACAGTGTGTAAACGCAACGGAATAGTGGGCTT	2717

QY	2442	TCACACCTTTGCAGAAAGCAGCCCAAAAGGACGAAACACACGCTTTGTGCTTTGTGCTAG	2501
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QY	2502	CCCATGGAGGTGACCCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTTAGATTAGTTTT	2561
DB	2778	CACATGGCGCAGACCCCAACCATGAAGAACAGGAAGGTCAGACACCTTTAGATCTGGCGA	2837
QY	2562	CAGCGGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTCTGCGCCTCTT	2621
DB	2838	CGGCTGATGATCATCCGGGCTCTGCTGATAGATGCCATGCCCCCTGAGGCGCTTACCTACCT	2897
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QY	2682	CTTCAGGTCCATCTAGGCCCATCAAGCCTTTCTGCAGCCAGGAGTCTTGTGACAACTATCTG	2741
DB	2937	TCTCACCAGCGTCCACCCCTCTCTGCTGTCAGCAGCATAGATAAACCTCACTG	2996
QY	2742	GGAGTTTTTCAGAACTGCTCTTCACTAGTTAGTTCAAGTGGAAACAGAGGTGCTTCCAGTT	2801
DB	2997	GCCCGTTAA CGGATCTGGCTGTAGGAGGGGCCCTCCATGCAGGGATGCGCTCGGGTG	3056
QY	2802	TGGAGAAAAAG-----GAGGTTCCAGGAGTAGATTTTTCAGCAATCTCAATAGGA	2855
DB	3057	CAGAAAGGAAGGAGGAGAAGTTGCGGGTCTTGACATGAACATCAGGCCAGTTCTGTTAAGA	3116
QY	2856	ATCTTGCACCTTGAGCACCTAATGGATATATTTGAGAGAGAACAGATCACTTTTGGATGTAT	2915
DB	3117	GCCTTGGCCTTGAGCACCTGAGGACATTTTGNAAACAGAGCAGATTACGCTAGATGTGT	3176
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DB	3177	TGGCTGATATGGGTCA	3192

RESULT 5	
DQ034114	
LOCUS	
DEFINITION	3612 bp DNA linear GSS 02-JUN-2005 Homo sapiens TNKS gene, VIRTUAL TRANSCRIPT, partial sequence, genomic, survey sequence.
ACCESSION	DQ034114
VERSION	DQ034114.1 GI:66885323
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 3612) Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civallo, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE	A scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees (ar) PLOS Biol. 3 (6), E170 (2005)
JOURNAL	15869325
PUBMED	2 (bases 1 to 3612)
REFERENCES	Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civallo, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE	Direct Submission
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES	Location/Qualifiers
source	1. 3612 /organisms="Homo sapiens" /mol types="genomic DNA"

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	Query Match	32.2%; Score 1221.6; DB 14; Length 3612;		
	Best Local Similarity	63.2%; Pred. No. 0;		
	Matches 1872; Conservative	0; Mismatches 1020; Indels 69; Gaps 6;		
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Db	644	GGAAGTCTTCCTCCCTGCCACTCGCTGCAGGTTTTGGAAGGAAGGATGTTGTAGAACA	703	
Qy	633	TGTTACAGCATGAGCTGAGCACCACCATCCGAATACAGATGGAAGGACACATTGGATT	692	
Db	704	TACTACAGATGGGTGCTTAATGTCACGCTCGTGATGATGGAGGCTCATCCCGCTCATTA	763	
Qy	693	TAGCAGATCCATCTGCCAAGCAGTCTTACTTGGTGAATATAAGAAAAGATGAACTCTTAG	752	
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Qy	753	AAGTGCCAGGAGTGGCAATGAAGAAAAAATGATGGCTTACTCACCATTAATATGTCA	812	
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Qy	813	ACTGCCACGAGTGTGCGAGNAAGTCACTCCATTACATTGTCACAGGATATAACA	872	
Db	881	AGATCGATGTGTCATTGGAAATGACTTACTACCTTTTATAGGAGTGGTAAATGAAGAA	940	
Qy	873	GAGTAAAGATTGTACAGCTGTTACTGCAACATGGAGCTGATGCTCCATCTAAAGATAAG	932	
Db	941	AACNATGGCTTTACTG--ACTCCTCTAATGTGAATGGCCATGCAAGTATGGCGAAA	998	
Qy	933	GTGATCTGGTACCATTACACAATGCCCTGTTCTTATGGTCAATPATGAAGTAACTGA	992	
Db	999	GGGA-CTTGTGCTCTTCATATGATGCTTTCATATGGACATTTATGAACTCACAGACTG	1057	
Qy	993	TGGTCAAGCATGCTGCTGTGTAATGCAATGGAGCTTGTGGCAATTCACTCCTCTCATG	1052	
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Qy	1053	AGGCAGCTCTTAAGAACAGGTTGAAGTATGTTCTCTCTTAAGTTATGCTGCAGACC	1112	
Db	1118	AGGCTGCTTCCAAGAACGGTGTAGAAGTCTGCTCTTTGTTACTTAGCCATGGCGCTG	1177	
Qy	1113	CACACCTGCTCAATTGTTCACAAATAAAGTGCTATAGACTTGGCTCCCACACACAGTTAA	1172	
Db	1178	CTAGTTAGTCACTGCCATGGCCAAAGTGCTGTGGATATGGCTCCAACCTCGGAGCTTA	1237	
Qy	1173	AAGAAAGATTAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAGCTG	1232	
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Qy	1233	ATGTTACTCGAATCAAAAACATCTCTCTCGAATGTTGAATTTCAAGCATCCTCAAA	1292	
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Qy	1293	CACATGAAACAGCATTTGCTGCTGCTGCTATCTCCATATCCCCAAAAAGAACAAATAT	1352	
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Qy	1353	GTGAATCTGTTGCTAAGAAAGGAGCAACATCAATGAAAGACTAAAGAAATTTCTTGACTC	1412	
Db	1418	CAGAAATGTTTACTTTAGAAAGGAGCAAAATGTTTAATGAAAAAATAAAGATTTTCATG	1477	
Qy	1413	CTCTGCACGTGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTACTGCTGAAACATG	1472	
Db	1478	CCCTGCAATGTTGCAGCGCAAGAGCCCAATGATGTCAATGGAAGTCTTGCAATAGCATG	1537	
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QY	2577	GGGCTCTTCTGACAGCAGCCATGCCCATCTGCTGCTGCTCTTGTGTACAGCCTCAAG	2636
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QY	2637	TGCTCAATGGTGTGAAGCCGAGAGCCAGAGCCAGCTGCTCTCTTCAGGTCCATCTA	2696
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QY	2697	GCCATCAAGCCTTCTGAGCCAGCAGCTTTCGAACTTATCTCGGAGTTTTTCAGAAC	2756
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QY	2757	TGCTCTTCACTAGTGTAGTTCAGAGTGAACAGAGGGTCTTCCAGTTTGGAGAAAG--	2812
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QY	2991	GAGTCGAGAGACTTATCTCCGACACAAAGGCTTTAAACCCATATTTAACTTTGAACACT	3050
Db	3077	GAGTGAAGAGCTCTTAGGTGACAAAGGACCAATCTTTATTTGACTTTTCACTGTG	3136
QY	3051	CTGGTAGTGAACAATCTTATAGATCTGTCTCTGATGATTAAGAGTTTCACTGTGG	3110
Db	3137	TTAATCAGGGAACGATTTTGTGCTTGTCTCCAGAGATAAAGAAATATCACTAGTGG	3196
QY	3111	AGGAAGAGATGCAAGTAGTACAGTTTCAGAGCACAGAGATGGAGTCTATGAGGTGGAATCT	3170
Db	3197	AGAAGAGATGCAAGTAGTATTTTCGAAACACAGAGATGGTGGTAAATGCTGGCGCACT	3256
QY	3171	TCACAGATACAAATATTCAGAGATTTCAGAGGTTTGTAAACAGAAACTATGGGAAAGAT	3230
Db	3257	TCACAGATACAAATGCTTCGAAATTCGAAATTTGTCGAAAGTTGTCGAAAGTTGAGGAGCGT	3316
QY	3231	ACACTACCGGAGAAAGAGTTTCTGAAGAAACACAGACCATGCCAATGACGAATGC	3290
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Db	3377	TGTTTCATGGTCTCTCTTTCAATTAATGCCATTTATCATTAAGGGTTTGTATGAGCAATG	3436
QY	3351	CGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTGAAAACTCTTCCAAAGCA	3410
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QY	3411	ATCAATATGTATGAAATTTGAGGAGGTACTGGGTGTCAGTTCCAGTTCAAGAGACAGATCTT	3470
Db	3497	ACCAATATGTTTATGAAATTTGGAGGAGGAACAGGCTGCTTACACAGGAGCAGGTCTAT	3556
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Db	3557	GCTATATATGTACACAGCGC	3577

RESULT 6
LOCUS DQ034115
DEFINITION Pan troglodytes TNKS gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ034115
VERSION DQ034115.1 GI:66885324

KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE	1 (bases 1 to 3107)
AUTHORS	Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL	(Proc Natl Acad Sci USA) 102(10):1178-1182 (2005)
PUBMED	15869325
REFERENCE	2 (bases 1 to 3107)
AUTHORS	Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES	Location/Qualifiers
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Best Local Similarity	49.2%; Pred. No. 2.8e-226;
Matches 1275; Conservative	0; Mismatches 1255; Indels 63; Gaps 3;
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QY	1001 CATGTCCTGCTGTAAATGCAATGGACTTGTGGCAATTCACCTCTTCATGAGGACGT 1060
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QY	1061 TCTAAGAACAGGTTGAAGTATGTTCTTCTCTTAAGTATGTCGACACCACTG 1120
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Db	801 NNN 860
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Db	861 NNN 920
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mRNA sequence.
CR983155
CR983155.1 GI:68221489
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 888)
AUTHORS Heil O., Ebert, L., Hennig, S., Henze, S., Radelof, U., Schneider, D.
and Korn, B.
TITLE Human T-Lymphocytes library
JOURNAL Unpublished (2005)
COMMENT Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
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Email: www.rzpd.de
RZPD; RZPDp9017K2313.
RZPDLIB; (Human T-Lymphocytes) RZPD LIB No. 9017
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9017 Contact:
Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
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Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPDp9017K2313
contact RZPD (product- support@rzpd.de) for further information.
Primer name: qe3_4, Primer sequence: CGGTAAACAATTACACAG.
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human T-Lymphocytes with a NotI - oligo(dT) primer [5'
GACTAGTCTTAGATCGGAGCGCGCCCTTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to SalI adaptors,
digested with NotI and cloned into the NotI and SalI sites
of the pQE80LSN_cloned vector"

ORIGIN
Query Match 23.3%; Score 884.4; DB 8; Length 888;
Best Local Similarity 99.7%; Pred. No. 2.2e-224;
Matches 885; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2558 GTTTTCAGCGATGATGTGAGCGCTCTTCTGACAGCGCCATGCCCCCATCTGCTCTGCC 2617
DB 1 GTTTCAGCAGATGATGTGAGCGCTCTTCTGACAGCGCCATGCCCCCATCTGCTCTGCC 60
QY 2618 TCTTGTTCACAGCCTCAAGTCTCAATGGTGTGAGAGCCAGAGCCACTGCAGATGCT 2677
DB 61 TCTTGTTCACAGCCTCAAGTCTCAATGGTGTGAGAGCCAGAGCCACTGCAGATGCT 120
QY 2678 CTCTCTTCAGGTTCATCTAGCCCATCAAGCCTTTCTGAGCCAGCAGTCTTGACAATT 2737
DB 121 CTCTCTTCAGGTTCATCTAGCCCATCAAGCCTTTCTGAGCCAGCAGTCTTGACAATT 180
QY 2738 TCTGGGAGTTTTTTCAGAACTCTCTTTCAGTAGTCTTCAAGTGAAACAGAGGGTGCTTCC 2797
DB 181 TCTGGGAGTTTTTTCAGAACTCTCTTTCAGTAGTCTTCAAGTGAAACAGAGGGTGCTTCC 240
QY 2798 AGTTTGAGAGAAAAGGAGGGTTCCAGGAGTAGATTTTTCAGTAACTCAATTCGTAAGGAAT 2857

```

Fax: +49 30 32639 111

www.rzpd.de

This clone is available from RZPD;
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp901611435
contact RZPD (product- support@rzpd.de) for further information.
Primer name: qe3 4 - Primer sequence: CGGATAACAATTCACACAG.

FEATURES

Location/Qualifiers
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/clone_lib="RZPD no.9016"
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http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml
; ist strand cDNA was prepared from mRNA obtained from
human T-Lymphocytes with a NotI - oligo(dT) primer [5'
GACTAGTCTAGATCGGAGCGGCCCTTTTCTTTTCTTTT 3']
Double-stranded cDNA was ligated to SalI adaptors,
digested with NotI and cloned into the NotI and SalI sites
of the pQE80LSN_cloned vector"

ORIGIN

Query Match 22.6%; Score 859.6; DB 8; Length 926;
Best Local Similarity 98.6%; Pred. No. 9.3e-218;
Matches 917; Conservative 0; Mismatches 8; Indels 5; Gaps 5;
Qy 1628 GAAATGTACAGCACTCTCTCAAGAGGGTATCTCATTAGGTAATTCAGAGGCGACAGAGA 1687
Db 1 GAAATGTACAGCACTCTCTCAAGAGGGTATCTCATTAGGTAATTCAGAGGCGACAGAGA 60
Qy 1688 CAATGTCTGGAAGCTGCAGAGGCTGGAGATGTCGAAACTGTAAACAACTGTGACCTGTT 1747
Db 61 CAATGTCTGGAAGCTGCAGAGGCTGGAGATGTCGAAACTGTG-AAAAAAGCTGTGACTGTT 119
Qy 1748 CAGAGTGTCAACTGCAGAGACATTTGAAGGGGCTCAGTCTACACCACTTCATTTTGCAGCT 1807
Db 120 CAGAGTGTCAACTGCAGAGACATTTGAAGGGGCTCAGTCTACACCACTTCATTTTGCAGCT 179
Qy 1808 GGGTATACAGAGTGTCTGGTGGGAATATCTGCTACAGATGAGCTGATGTCATGCT 1867
Db 180 GGGTATAACAGAGTGTCTGGTGGGAATATCTGCTACAGATGAGCTGATGTCATGCT 239
Qy 1868 AAAGATAAGAGGCTTGTACCTTTGCACATGCATGTTCTTATGGACATTAATGAAGTT 1927
Db 240 AAAGATAAGAGGCTTGTACCTTTGCACATGCATGTTCTTATGGACATTAATGAAGTT 299
Qy 1928 GCAGAACTCTTGTAAACATGAGCAGTAGTAAATGTAGCTGATTTATGGAAATTTTACA 1987
Db 300 GCAGAACTCTTGTAAACATGAGCAGTAGTAAATGTAGCTGATTTATGGAAATTTTACA 359
Qy 1988 CTTTATCATGAAGCAGAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCCAGCAT 2047
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Qy 2048 GGTCCAGACCTTACAAAAAAGAGGATGGAATATCTCTTTGGATCTTGTGTTAAAGAT 2107
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Qy 2108 GGAGATACAGATATTCAGATCTGCTTAGGGGAGATGAGCTTTTGTAGATGCTGCCAAG 2167
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Db 540 AAGGGTGTGTTAGCCAGAGTGAAGAAGTTGTCTCTCTCTGATATATGTAATGTCGCGGAT 599
Qy 2228 ACCCAAGGCACATTCACACCTTTACATTTAGCAGCTGGTATATTAATTTTAGAAGTT 2287
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Qy 2408 AATGCGATGTCTCAATGCCAGGCAAAATGGGCTTTTCACACCTTTGCGACGAGCCCAA 2467
Db 780 AATGCGATGTCTCAATGCCAGGCAAAATGGGCTTTTCACACCTTTGCGACGAA-CAGCCCAA 838
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DEFINITION AUI40145 PLACE2 Homo sapiens cDNA clone PLACE2000021 5', mRNA
sequence.
ACCESSION AUI40145
VERSION AUI40145.1 GI:11001666
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 838)
Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
Ihii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Oeuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isegai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isegai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source
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Query Match 20.7%; Score 784.2; DB 1; Length 838;
Best Local Similarity 98.0%; Pred. No. 1.3e-197;
Matches 823; Conservative 0; Mismatches 13; Indels 4; Gaps 3;

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 Db 121 GCATTAACCAATCGTAAGCACTTGGACTTGGACCTGAGCACCCTATGATATATTTGGAGAG 180
 2895 AACAGATCACTTTGGATGATTTAGTTGAGATGGGCAAGGAGCTGAGGAGATTTGAA 2954
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 3015 AACAGGCTTAAACCATATTTAACTTTGAAACCTCTGCTGAGTGGAACTTCTTATAG 3074
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 3075 ATCTGTCTCTGATGATAAGAGTTTTCAGTCTGTGGAGGAAGAGATGCAAGTACAGTTTC 3134
 Db 361 ATCTGTCTCTGATGATAAGAGTTTTCAGTCTGTGGAGGAAGAGATGCAAGTACAGTTTC 420
 3135 GAGAGCACAGATGAGGTCATGAGGTGGAATCTTCAACAGATACAAATTTCTCAAGA 3194
 Db 421 GAGAGCACAGATGAGGTCATGAGGTGGAATCTTCAACAGATACAAATTTCTCAAGA 480
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 DEFINITION mRNA sequence.
 ACCESSION DT808067
 VERSION DT808067.1 GI:75739943
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 SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 898)
 REFERENCE Moore,S., Alexander,L., Brownstein,M., Guan,L., Lobo,S., Meng,Y.,
 AUTHORS

Tanaguchi,M., Wang,Z., Yu,J., Prange,C., Schreiber K., Shenmen,C.,
 Wagner,L., Bala,M., Barbazuk,S., Barber,S., Babakaiff,R.,
 Beland,J., Chun,E., Del Rio,L., Gibson,S., Hanson,R.,
 Kirkpatrick,R., Liu,J., Matsuo,C., Mayo,M., Santos,R.R., Stott,J.,
 Tsai,M., Wong,D., Siddiqui,A., Holt,R., Jones,S.J. and Marra,M.A.
 Bovine Genome Sequencing Program: Full-length cDNA sequencing
 Unpublished (2005)
 CONTACT: Robert Kirkpatrick
 Canada's Michael Smith Genome Sciences Centre
 BC Cancer Agency
 Suite 100, 570 West 7th Avenue, Vancouver, British Columbia,
 Canada, V5Z 4S6
 Tel: 1-604-707-5900 x5406
 Fax: 1-604-876-3561
 Email: robertk@bcgsc.ca
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 High quality sequence stop: 898.
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 Best Local Similarity 92.1%; Pred. No. 5.8e-194;
 Matches 824; Conservative 0; Mismatches 69; Indels 2; Gaps 1;
 QY 2901 TCACCTTGGATGTATTAGTTGAGATGGGGCAACAGGAGCTGAAGAGATTGGAATCAATG 2960
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 QY 3021 GTCCTAACCCATATTTAATTTGAACCTCTGGTAGTGGAGCAATTTCTTATAGATCTGT 3080
 Db 121 GTCCTAACCCATATTTAATTTGAACCTCTGGTAGTGGAGCAATTTCTTATAGATCTGT 180
 QY 3081 CTCCTGTATGATAAGAGTTTCAGTCTGTGGAGGAAGAGATGCAAGTACAGTTCCGAGAGC 3140
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 QY 3201 AGGTTTGTAAACAGAACTATGGGAAAGATACACTCATAGGAGAAAGAGTTTCTGAAG 3260
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 QY 3261 AAAACCAACCACTGCCAATGAACCAATGCTATTTTCATGGGTCTCTCTTTTGGTAATGCAA 3320
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 QY 3321 TTATCCAAAGGCTTTGATGAAAGGATGCGGTACATAGGTGGTATGTTTGGAGCTGGCA 3380
 Db 421 TTATCCAAAGGCTTTGATGAAAGGATGCGGTACATAGGTGGTATGTTTGGAGCTGGCA 480
 QY 3381 TTTATTTTGTGAAACTCTTCCAAAGCAATCAATATGATATGTAATTTGGAGGAGGTA 3440
 Db 481 TCTATTTTGTGAAACTCTTCCAAAGCAATCAATATGATATGTAATTTGGAGGAGGTA 540

TITLE
 JOURNAL
 COMMENT

FEATURES
 source

Qy 3441 CTGGGTGTCAGTTTCAAAAGACAGATCTTGTGTTACATTTGGCCACAGCAGCTGCTCTTTT 3500
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RESULT 11
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 LOCUS
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 KEYWORDS EST.
 SOURCE Bos taurus (cattle)

ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 834)
 Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
 Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
 Chitko-McKown,C.G., Pettea,G., Holt,I., Karamycheva,S., Liang,P.,
 Quackenbush,J. and Keefe,J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 Genome Res. 11 (4), 626-630 (2001)

TITLE 11282978
 JOURNAL
 COMMENT
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: 98 row: I column: 7
 Seq primer: GTAATACGACTCACTATAGGG.
 Location/Qualifiers

FEATURES
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 /lab_host="DH10B"
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 embryos."
 ORIGIN

Query Match 20.2%; Score 766.8; DB 5; Length 834;
 . Best Local Similarity 95.0%; Pred. No. 5.8e-193;

Matches 792; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
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 Qy 1528 ATATTGTGGTCATCTACAAACCTGCGCCCTACTCTCGAGCTATCGGTGTGATCCTAAACAT 1587
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 LOCUS
 DEFINITION 1372517 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION DN536421
 VERSION DN536421.1 GI:60988240
 KEYWORDS EST.
 SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 848)
 Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,

Wray, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: RLK8064 row: G column: 17
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Location/Qualifiers
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Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN

Query Match 18.7%; Score 709; DB 9; Length 848;
Best Local Similarity 91.5%; Pred. No. 1.7e-177;
Matches 762; Conservative 0; Mismatches 70; Indels 1; Gaps 1;

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DB 75 CAAGAGGGTATCCCATAGTAAATTCAGAGGAGAGAGCAATGTCTGGAAGCTGCAAG 134

QY 1709 GCTGAGAGTGTCCAACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAGAGAC 1768
DB 135 GCTGAGAGTGTAGAAACCGTAAAAAAATGTGTACTGTTCAGAGTGTCAACTGCAGAGAC 194

QY 1769 ATTGAAGGGCTCAGTCTACACCACTTCAATTTGACGTGGGTATACAGAGTGTCCGTG 1828
DB 195 ATTGAAGGACGTCACTACACCGCTCCATTTTGCAGCTGGCTATAATCGGGTGTCTGTG 254

QY 1829 GTGGAATATCTGTACAGCATGGAGCTGATGTGCATGCTTAAAGATAAGAGGCGCTTGTGA 1888
DB 255 GTGGAATATCTGTCAACACGAGCTGACGTGCATGCGAAGACAAAGAGGCGCTTGTGA 314

QY 1889 CTTTGGCAATGCATGTCTTTATGGACATTAATGAAGTTGCAGAACTTCTTGTAAACAT 1948
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QY 1949 GGAGCAGTAGTAAATGTAGTCAATTTATGGAATTTACACCTTTACATGAACAGCAGCA 2008
DB 375 GGAGCAGTAGTAAATGTAGTCAATTTATGGAATTTACACCTTTACATGAAGCTGACGC 434

QY 2009 AAAGGAAAATATGAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTCAACCAAAAAA 2068
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QY 2069 AACAGGATGGAATATCTCTTTGGATCTTGTAAAGATGGAGATACAGATATCAAGAT 2128
DB 495 AACAGGATGGAATATCAACCCCTTTGGATCTTGTAAAGATGGAGATACAGATATCAAGAT 554

QY 2129 CTGCTTAGGGAGATGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTTTAGCCAGATG 2188
DB 555 CTGCTTAGGGAGATGCAGCTTTATTTGGATGCTGCCAAGAGGGTGTTTAGCCAGATG 614

QY 2189 AAGAAGTTGTCTCTCTCTGATAATGTAAATTCGCGGATACCAAGGAGACATTCACCA 2248

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QY 2309 GGAGCTGATGTGAATGCCCAAGACAAAGAGGAGCTATTTCCTTTACATAATCAGCATCT 2368
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QY 2369 TACGGCATGTAGATGTAGCAGCTCTACTATAATAAGTATAATGCAATGTGTCAA 2421
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RESULT 13
DA733094
LOCUS
DEFINITION DA733094 NT2RP2 Homo sapiens cDNA clone NT2RP2002155 5', mRNA
sequence.
ACCESSION DA733094
VERSION DA733094.1 GI:81281747
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 819)
AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakahagi, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kishida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isoigai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
JOURNAL PUBMED 16344560
COMMENT Contact: Takao Isoigai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisearazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute (HRI); cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
HRI.
Location/Qualifiers
1..819
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cells after 2-weeks retinoic acid (RA) induction"

FEATURES
source

ORIGIN

Query Match 18.2%; Score 692.8; DB 9; Length 819;
Best Local Similarity 93.0%; Pred. No. 3.5e-173;
Matches 763; Conservative 0; Mismatches 52; Indels 5; Gaps 4;

QY 1525 TGCATATTTGGTCACTACAAACCTGGCGCTACTCTCTGAGCTATGGTGTGATCTTAA 1584
DB 1 TGCATATTTGGTCACTACAAACCTGGCGCTACTCTCTGAGCTATGGTGTGATCTTAA 60

Qy 1585 CATTATATCCCTTCAGGGCTTTACTGCTTTACAGATGGGAAATGAAAAATGTACAGCAACT 1644
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Qy 1645 CCTCCAGAGGGTATCTCATTAGGTAAATTCAGAGGCAGACAGCAATTTGCTGGGAAGCTGC 1704
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Db 181 AAAGGCTGGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGCAG 240
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Db 241 AGACATTGAAGGGCGTCAGTCTACACACTTCATTTTGCAGCTGGGTATTAACAGAGTGT 300
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Db 301 CGTGGTGGATATCTGCTACAGCATGAGCTGATGTCATGCTCAAGTAAAGTAAAGGAGCCT 360
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Db 361 TGTACCTTTGCACAAATGATGCTTCTTATGGACATTAATGAAGTTCAGAACTTCTTTGTTAA 420
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Db 481 AGCAAAAGGAAATATGAAATTTGCAAACTTCTCTCCAGCATGTCAGACCTTACCAA 540
Qy 2065 AAAAAACAGGATGGAATATCTCTTTGGATCTTTGTTAAAGAT--GGAGATACAGATATTC 2123
Db 541 AAAAAACAGGATGGAATATCTCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTC 600
Qy 2124 AAGATCTGCTTAGGGAGATGACGCTTTGCTAGATGTCGCAAG--AAGGTTGTTTAGC 2181
Db 601 CANATCTGCTTAGGGAAATGCA--CTTTGCTTAAATGCTGCCAANAAAGGCTTTAAAC 659
Qy 2182 CAGATGGAAGATGTTGCTCTCTGTAATGTAATTTGCCGCGATACCCAGGCGACACA 2241
Db 660 ANAATGAAGAAATGTCCTTCTACTGATATGTTAATGCGCGATACCCAGGCGAAG 719
Qy 2242 TTCAACACCTTTACATTT--AGCAGCTGGTTATAATAATTTAGAAAGTTGCGAGATTTGT 2300
Db 720 TTCCACACCTTTACATTTAANCANCTGGTTATAATAATTTAAAAAATTGCAAAATATTGT 779
Qy 2301 TACAACACGGAGCTGATGTAATGCCAGCAAGAGGAGG 2340
Db 780 TACACCCNGAACTAATTTTAAATGCCCCANAAACAAAGGAAG 819

RESULT 14
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LOCUS AGENCOURT 11385409 NIH MGC 164 Mus musculus cDNA clone
DEFINITION IMAGE:30244272 5', mRNA sequence.
CB183123
ACCESSION CB183123.1 GI:28181571
VERSION EST.
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 955)
NIH-MGC <http://mgi.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina

CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM0316 row: o column: 01
High quality sequence stop: 779.
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Non-normalized full-length enriched library from Pooled
mouse embryonic limb, maxilla and mandible, day 10.5 and
11.5 (size selected for the 0.5-1 kb fragments) Cloned
directionally, priming method: Oligo-dT. cDNA enrichment:
>1k bp. Average insert size 1.8k bp. Priming sequence:
5'GACTAGTCTTAGATCGGAGCGGCCCT(T) 3'. Tissue contributed
by David Rowe. Library constructed by ResGen, Invitrogen
Corp."

ORIGIN

Query Match 18.1%; Score 687.8; DB 4; Length 955;
Best Local Similarity 88.5%; Pred. No. 8.1e-172;
Matches 768; Conservative 0; Mismatches 98; Indels 2; Gaps 2;
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Db 61 ATGATATATTTGAGAGAGAACAGATTAACCTTAGATGTCCTAGTTGAATGGGCCACAAAG 120
Qy 2936 GAGTGAAGGAGATTTGGAATCAATGCTTATGGACATAGGCACAAACTAAATTAAGGAGTC 2995
Db 121 GACTGAAGAGAGATTGGAATCAATGCTTATGGACATCGACACAAAGCTGATTAAGGAGTT 180
Qy 2996 GAGAGACTTATCTCCGACAAACAGGCTTTAAACCCATATTTAACTTTGAAACACCTCTGCT 3055
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Qy 3056 AGTGGAAACAATTTCTATAGATCTGCTCTGATATAAGAGATTTTCAGTCTGTGGAGGAA 3115
Db 241 AGTGGAAACAATTTCTATAGATCTGCTCTGATATAAGAGATTTTCAGTCTGTGGAGGAA 300
Qy 3116 GAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGGTCAATGAGTGGGAATCTTCAAC 3175
Db 301 GAGATGCAAGATGACTGTGCGGAGCACAGAGATGGTGTACGACGAGCGCGGCTCTTCAAC 360
Qy 3176 AGATACAAATTTCTCAAGATTCAGAAAGTTTGTAAACAGAACTATGCGGAAGATACACT 3235
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Qy 3236 CACCGGAGAAAGAAAGTTTCTGAAGAAACACCAACCATGCAATGAACGAATGCTATTT 3295
Db 421 CACCGGAGAAAGAAAGTTTCTGAAGAAACACCAACCATGCAACGAAGGATGTTATTT 480
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Db 481 CATGGGCTCTCTTTTGTGAATGCGATTTATCCATAAGGCTTTTATGAAGGATCGCATAC 540
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Db 601 TATGTGTATNGGAATGGAGGTGGCCAGCGATGTCCAAATTCACAAGACAGATCGTGTGA 660
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 Db 661 CATTTGTCAAGCAGCTGCTGTTTGTGAGTAACCTTTGGGAAAGTCTTTCTCGAGTT 720
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 Db 840 TATCTATATACATGAGCTGANGATG 867

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 VERSION CB128566.1 GI:28091690
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 675)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel.: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 7 Row: A column: 10
 High quality sequence stop: 675.
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 /note="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including
 EcoRI site by treatment of T4 RNA ligase and the first
 strand cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transfection of
 competent cells E. coli Top10f by electroporation method.

FEATURES

source
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 /note="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including
 EcoRI site by treatment of T4 RNA ligase and the first
 strand cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transfection of
 competent cells E. coli Top10f by electroporation method.

The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN	Query Match	17.7%	Score 672.4	DB 4	Length 675
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QY	2477	ACACAGCTTTTGTGCTTTTGTGCTAGCCCATGGAGCTGACCCGACTCTTAAATAATCAGGAA	2536		
Db	61	ACACAGCTTTTGTGCTTTTGTGCTAGCCCATGGAGCTGACCCGACTCTTAAATAATCAGGAA	120		
QY	2537	GGACAAAACACCTTTAGATTTAGTTTTCAGGGAGATGTCAGCGCTCTTCTGACAGCAGCC	2596		
Db	121	GGACAAAACACCTTTAGATTTAGTTTTCAGGGAGATGTCAGCGCTCTTCTGACAGCAGCC	180		
QY	2597	ATGCCCCCATCTGCTCTGCTCTTGTTCAGAGCTCAAGTCTCAATGGTCTGAGAGC	2656		
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QY	2657	CCAGGAGCCACTGCAGATGCTCTCTCTTCAGGTCCATCTAGCCCATCAAGCCCTTTCTGCA	2716		
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QY	2777	AGTGAACAGAGGGTGTCTCCAGTTTTCAGAAAGAGGTTCCAGGAGTAGATTTTACG	2836		
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QY	3017	CAAGGTCCTTAACCCATATTTAACTTTGAACACCTCTCGTAGTGGAACTTCTTATAGAT	3076		
Db	601	CAAGGTCCTTAACCCATATTTAACTTTGAACACCTCTCGTAGTGGAACTTCTTATAGAT	660		
QY	3077	CTGTCTCTCTGATGAT 3091			
Db	661	CTGTCTCTCTGATGAT 675			

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model
Run on: December 18, 2006, 13:00:26 ; Search time 652.368 Seconds
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Perfect score: 3797
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	3797	100.0	3797	3	US-09-843-159B-1
3	3393.4	89.4	3816	3	US-09-696-668-2
4	3393.4	89.4	3816	3	US-09-843-159B-2
5	3388.8	89.2	4275	3	US-09-972-115A-5
6	3387.2	89.2	5075	3	US-09-799-451-556
7	3387.2	89.2	6018	3	US-09-849-602-11
8	3386	89.2	3394	3	US-09-427-154-1
9	3382.8	89.1	4512	3	US-09-350-982C-3
10	3291.8	86.7	3498	3	US-09-350-982C-4
11	2969.6	78.2	4493	3	US-09-972-115A-1
12	2968.2	78.2	4297	3	US-09-972-115A-3
13	1813.4	47.8	4134	3	US-09-196-387-1
14	1813.4	47.8	4134	3	US-09-841-835-1
15	1813.4	47.8	4134	3	US-09-972-115A-7
16	1449.6	38.2	4491	3	US-09-196-387-7
17	1449.6	38.2	4491	3	US-09-841-835-7
18	1297.8	34.2	4657	3	US-09-196-387-9
19	1297.8	34.2	4657	3	US-09-841-835-9
20	994	26.2	2409	3	US-09-964-899-40
21	518.4	13.7	520	3	US-09-972-115A-10
22	380.4	10.0	384	3	US-09-972-115A-9
23	249.4	6.6	770	3	US-09-270-767-13625

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25	121.2	3.2	523	3	US-09-841-835-12	Sequence 12, Appl
26	97.4	2.6	14770	3	US-09-220-132-30	Sequence 30, Appl
27	97.4	2.6	14770	3	US-09-949-016-1107	Sequence 1107, Ap
28	93	2.4	5235	2	US-09-031-485-35	Sequence 35, Appl
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c 31	93	2.4	5235	2	US-08-847-429A-36	Sequence 35, Appl
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c 33	93	2.4	5235	3	US-09-065-474-36	Sequence 35, Appl
34	93	2.4	5235	3	US-09-557-034-35	Sequence 35, Appl
c 35	93	2.4	5235	3	US-09-557-034-36	Sequence 35, Appl
36	93	2.4	5503	2	US-09-031-485-32	Sequence 32, Appl
c 37	93	2.4	5503	2	US-09-031-485-34	Sequence 34, Appl
38	93	2.4	5503	2	US-08-847-429A-32	Sequence 34, Appl
c 39	93	2.4	5503	2	US-08-847-429A-34	Sequence 34, Appl
40	93	2.4	5503	3	US-09-065-474-32	Sequence 32, Appl
c 41	93	2.4	5503	3	US-09-065-474-34	Sequence 32, Appl
42	93	2.4	5503	3	US-09-557-034-32	Sequence 32, Appl
c 43	93	2.4	5503	3	US-09-557-034-34	Sequence 34, Appl
44	90.8	2.4	8560	3	US-09-949-016-1788	Sequence 1788, Ap
45	90.8	2.4	8560	3	US-09-949-016-1789	Sequence 1789, Ap

ALIGNMENTS

RESULT 1
US-09-696-668-1
; Sequence 1, Application US/09696668
; Patent No. 6617102
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossovskaya, Valeria
; TITLE OF INVENTION: TANKYRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS C
; FILE REFERENCE: A-68292-1/RMS/DIR
; CURRENT APPLICATION NUMBER: US/09/696,668
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-696-668-1

Query Match 100.0%; Score 3797; DB 3; Length 3797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTGAAGACACTGGATTTCATCTTTTGGCTGGGGTTATCTCTGTGTCTCACTACAT 60
DB 1 CTTTGAAGACACTGGATTTCATCTTTTGGCTGGGGTTATCTCTGTGTCTCACTACAT 60
QY 61 AGACAAATATTAGCTGTGAGCAGATCTTTTGTGTGTCTTTGTAGTCCCGAGTTTAA 120
DB 61 AGACAAATATTAGCTGTGAGCAGATCTTTTGTGTGTCTTTTGTAGTCCCGAGTTTAA 120
QY 121 CAGAAACATCTGTGAGATAGATGGAAGGAATCTTAGCAGAGTTTGTCTACTGTA 180
DB 121 CAGAAACATCTGTGAGATAGATGGAAGGAATCTTAGCAGAGTTTGTCTACTGTA 180
QY 181 TCATAAGGTGTGATTTTACATATTTAAGTTTATATCTTTTGAACATCTGAAATGTATACA 240
DB 181 TCATAAGGTGTGATTTTACATATTTAAGTTTATATCTTTTGAACATCTGAAATGTATACA 240
QY 241 TACTAAATATGAGAACTCTATTGTAGAGTGAAGAACTTTGAACTTTGAGCTTCAGTFC 300
DB 241 TACTAAATATGAGAACTCTATTGTAGAGTGAAGAACTTTGAACTTTGAGCTTCAGTFC 300

Db	241	TACTAAATATGCAGAACTCTATTGTAGAGTCAGAAAACATTTGAACTTTGAGCTTTCAGTC	300
Qy	301	ACTTATTTTGPAATCTTTCTTTGAGGTTAGCAGTAGTACCAACCAAGCACTGCTTAGGT	360
Db	301	ACTTATTTTGPAATCTTTCTTTGAGGTTAGCAGTAGTACCAACCAAGCACTGCTTAGGT	360
Qy	361	ACCACTGCTGCTTAGTGGAGAGTCCCTCTGCTGCTTTATCATTTAAGGTTTGGCGGAAGA	420
Db	361	ACCACTGCTGCTTAGTGGAGAGTCCCTCTGCTGCTTTATCATTTAAGGTTTGGCGGAAGA	420
Qy	421	CGTAGTTGAATATTTGCTTTCAAGATGGTGCAGAGTGTCCAAGCAGCTGATGATGGGGCCT	480
Db	421	CGTAGTTGAATATTTGCTTTCAAGATGGTGCAGAGTGTCCAAGCAGCTGATGATGGGGCCT	480
Qy	481	TATTCCTCTTCATTAATGCATGCTCTTTTGGTGCATGCTGGAAGTAGTCAATCTCTTTTGGC	540
Db	481	TATTCCTCTTCATTAATGCATGCTCTTTTGGTGCATGCTGGAAGTAGTCAATCTCTTTTGGC	540
Qy	541	ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATATATCTCTCCATGAAGCTGC	600
Db	541	ACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATATATCTCTCCATGAAGCTGC	600
Qy	601	AATTTAAAGGAAAGATTGATGTTTGCATTTGCTGTATACAGATGGAGCTGAGCCAAACAT	660
Db	601	AATTTAAAGGAAAGATTGATGTTTGCATTTGCTGTATACAGATGGAGCTGAGCCAAACAT	660
Qy	661	CCGAAATACAGATGGAAGGACAGCATTTGGATTTTAGCAGATCCATCTGCCAAGCAGTGCT	720
Db	661	CCGAAATACAGATGGAAGGACAGCATTTGGATTTTAGCAGATCCATCTGCCAAGCAGTGCT	720
Qy	721	TACTGGTGAATATGAAGAGTAGAATCTTTAGAAAGTCCAGAGTGGCAATGAAGAAA	780
Db	721	TACTGGTGAATATGAAGAGTAGAATCTTTAGAAAGTCCAGAGTGGCAATGAAGAAA	780
Qy	781	AATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACCAAGTGAATGGCAGAAAGTC	840
Db	781	AATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACCAAGTGAATGGCAGAAAGTC	840
Qy	841	AACCTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTTTACTGCA	900
Db	841	AACCTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTTTACTGCA	900
Qy	901	ACATGGAGCTGATGTCATGCTTAAGATTAAGAGTGGTCAAGCATGCTGTTGTAATGC	960
Db	901	ACATGGAGCTGATGTCATGCTTAAGATTAAGAGTGGTCAAGCATGCTGTTGTAATGC	960
Qy	961	TTCTTTATGGTCATTTATGAAGTAACTGAACCTTTTGGTCAAGCATGCTGTTGTAATGC	1020
Db	961	TTCTTTATGGTCATTTATGAAGTAACTGAACCTTTTGGTCAAGCATGCTGTTGTAATGC	1020
Qy	1021	AATGGACTTTGGCAATTCACCTCTCTTCATGAGCGAGCTTCTAAGAACAGGGTTGAAGT	1080
Db	1021	AATGGACTTTGGCAATTCACCTCTCTTCATGAGCGAGCTTCTAAGAACAGGGTTGAAGT	1080
Qy	1081	ATGTTCTCTCTCTTTAGTTATGTGAGCCCAACACTGCTCAATTTGTCAATATAAAG	1140
Db	1081	ATGTTCTCTCTCTTTAGTTATGTGAGCCCAACACTGCTCAATTTGTCAATATAAAG	1140
Qy	1141	TGCTATAGACTTGGCTCCACACCAACAGTAAAAGAAAGATTAGCATATGAATTTAAAGG	1200
Db	1141	TGCTATAGACTTGGCTCCACACCAACAGTAAAAGAAAGATTAGCATATGAATTTAAAGG	1200
Qy	1201	CCACTCGTGTGCAAGCTGCAAGAGCTGTATCTCGAATCAAAAAACATCTCTC	1260
Db	1201	CCACTCGTGTGCAAGCTGCAAGAGCTGTATCTCGAATCAAAAAACATCTCTC	1260
Qy	1261	TCTGGAAATGGTGAATTTCAAGCATCTTCAACACATGAACACAGCATTTGCTGCTGC	1320
Db	1261	TCTGGAAATGGTGAATTTCAAGCATCTTCAACACATGAACACAGCATTTGCTGCTGC	1320
Qy	1321	TGCATCTCCATATCCCAAAAGAAAGCAAAATATGTGAACTGTTGCTTAAGAAAAGAGCAAA	1380
Db	1321	TGCATCTCCATATCCCAAAAGAAAGCAAAATATGTGAACTGTTGCTTAAGAAAAGAGCAAA	1380

Qy	1381	CATCAATGAAAGACTTAAGAAATCTTGACTCTCTGCAAGTGGCATCTGAGAAGCTCA	1440
Db	1381	CATCAATGAAAGACTTAAGAAATCTTGACTCTCTGCAAGTGGCATCTGAGAAGCTCA	1440
Qy	1441	TAATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAAAGTTAATGCTCTGGATTAATCT	1500
Db	1441	TAATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAAAGTTAATGCTCTGGATTAATCT	1500
Qy	1501	TGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTCACTTCAAAACCTGCCCTACT	1560
Db	1501	TGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTCACTTCAAAACCTGCCCTACT	1560
Qy	1561	CCTGAGCTATGGGTGATCCTTAACATTAATCCCTTCAGGGCTTTACTGCTTTACAGAT	1620
Db	1561	CCTGAGCTATGGGTGATCCTTAACATTAATCCCTTCAGGGCTTTACTGCTTTACAGAT	1620
Qy	1621	GGGAAATGAAATGTACAGCAACTCTTCAAGAGGGTATCTCATTAGTAAATTCAGAGGC	1680
Db	1621	GGGAAATGAAATGTACAGCAACTCTTCAAGAGGGTATCTCATTAGTAAATTCAGAGGC	1680
Qy	1681	AGACAGACAAATGCTGGAAGCTGCAAAAGCTGGAGATGTGCAAACTGTAAAAAATCTGTG	1740
Db	1681	AGACAGACAAATGCTGGAAGCTGCAAAAGCTGGAGATGTGCAAACTGTAAAAAATCTGTG	1740
Qy	1741	TACTGTTGAGAGTGTCACTGTCAGAGACATTTGAAGGGCTCAGTCTACACCACTTCATTT	1800
Db	1741	TACTGTTGAGAGTGTCACTGTCAGAGACATTTGAAGGGCTCAGTCTACACCACTTCATTT	1800
Qy	1801	TGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGTCACAGCATGAGCTGATGT	1860
Db	1801	TGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGTCACAGCATGAGCTGATGT	1860
Qy	1861	GCATGCTTAAAGATAAAGAGGCTTTGTACCTTTTGCACAATGTCATGTTCTTATGACATTA	1920
Db	1861	GCATGCTTAAAGATAAAGAGGCTTTGTACCTTTTGCACAATGTCATGTTCTTATGACATTA	1920
Qy	1921	TGAAGTTGCAAGACTTCTTGTAAACATGAGCAGTAGTTAAATGCTAGTGAATTTATGAA	1980
Db	1921	TGAAGTTGCAAGACTTCTTGTAAACATGAGCAGTAGTTAAATGCTAGTGAATTTATGAA	1980
Qy	1981	ATTTACACCTTTATCATGAAGCAGCAAGAAAGGAAATATGAAATTTGCAAACTTCTGCT	2040
Db	1981	ATTTACACCTTTATCATGAAGCAGCAAGAAAGGAAATATGAAATTTGCAAACTTCTGCT	2040
Qy	2041	CCAGCATGGTGCAGACCTTACCAAAAAAACAAGGATGGAATACTCCTTTGGATCTTGT	2100
Db	2041	CCAGCATGGTGCAGACCTTACCAAAAAAACAAGGATGGAATACTCCTTTGGATCTTGT	2100
Qy	2101	TAAAGATGGAGATACAGATATCAAGATCTGCTTAGGGAGATGCGCTTTGCTAGATGC	2160
Db	2101	TAAAGATGGAGATACAGATATCAAGATCTGCTTAGGGAGATGCGCTTTGCTAGATGC	2160
Qy	2161	TGCCAAGAAGGTTGTTTAGCCAGAGTGAAGAAAGTTGTTCTCTCTGATATGTAATTTG	2220
Db	2161	TGCCAAGAAGGTTGTTTAGCCAGAGTGAAGAAAGTTGTTCTCTCTGATATGTAATTTG	2220
Qy	2221	CCGCGATACCCCAAGGCGAGACATTTCAACACCTTTACATTTAGCAGCTGGTTATAATTT	2280
Db	2221	CCGCGATACCCCAAGGCGAGACATTTCAACACCTTTACATTTAGCAGCTGGTTATAATTT	2280
Qy	2281	AGAAATGCAAGTATTTGTTTACAAACCGGAGCTGATGTGAAATGCCAAGAAAGGAGG	2340
Db	2281	AGAAATGCAAGTATTTGTTTACAAACCGGAGCTGATGTGAAATGCCAAGAAAGGAGG	2340
Qy	2341	ACTTATTTCTTTTACATTAATGCAGCATCTTACGGGCACTGTAGATGTAGCAGCTCTAAT	2400
Db	2341	ACTTATTTCTTTTACATTAATGCAGCATCTTACGGGCACTGTAGATGTAGCAGCTCTAAT	2400
Qy	2401	AAAGTATAATGTCATGTCATTAATGCCAGCAAAATGGCTTTTACACCTTTGCGAGGAGC	2460
Db	2401	AAAGTATAATGTCATGTCATTAATGCCAGCAAAATGGCTTTTACACCTTTGCGAGGAGC	2460

Qy	2461	AGCCAAAAGGACGAAACA	CAGCTTTGTGCTTTGTGCTAGCTTGTGCTAGCCCATAGGAGCTGACCCGAC	2520
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Qy	2521	TCCTTAAAAATCAGGAAGGACAAAC	ACCTTTAGATTTAGTTTTCAGCGGATGATGTACGCGC	2580
Db	2521	TCCTTAAAAATCAGGAAGGACAAAC	CTTTAGATTTAGTTTTCAGCGGATGATGTACGCGC	2580
Qy	2581	TCCTTCTGACAGCAGCCATGCCCC	CCATCTGCTCTGCCCTCTTGTTTACAAGGCTTCAAGTGCT	2640
Db	2581	TCCTTCTGACAGCAGCCATGCCCC	CCATCTGCTCTGCCCTCTTGTTTACAAGGCTTCAAGTGCT	2640
Qy	2641	CAATGTGTGAGAAAGCCAGAGGAC	CACTGAGATGCTCTCTTTCAGTCCATCTAGCCC	2700
Db	2641	CAATGTGTGTGAGAAAGCCAGAGGAC	CACTGAGATGCTCTCTTTCAGTCCATCTAGCCC	2700
Qy	2701	ATCAAGCCTTTCTGACGCGAGCTT	GTGACAACTTATCTGGGAGTTTTTCAGAACTGTC	2760
Db	2701	ATCAAGCCTTTCTGACGCGAGCTT	GTGACAACTTATCTGGGAGTTTTTCAGAACTGTC	2760
Qy	2761	TTCAAGTAGTTAGTTCAAGTGGAA	CAGAGGGTGCTTCCAGTTTGGAGAAAAGGAGGTTC	2820
Db	2761	TTCAAGTAGTTAGTTCAAGTGGAA	CAGAGGGTGCTTCCAGTTTGGAGAAAAGGAGGTTC	2820
Qy	2821	AGGAGTAGATTTTAGCATAACT	CAATTCGTAAGGAATCTTGGACTTGAAGCTGGA	2880
Db	2821	AGGAGTAGATTTTAGCATAACT	CAATTCGTAAGGAATCTTGGACTTGAAGCTGGA	2880
Qy	2881	TATATTTGAGAGAGAACAGATCA	CTTTTGGATGTATTTAGTTGAGATGGGCGACAGAGCT	2940
Db	2881	TATATTTGAGAGAGAACAGATCA	CTTTTGGATGTATTTAGTTGAGATGGGCGACAGAGCT	2940
Qy	2941	GAAGGAGATTTGGAAATCAATG	CTTATGACATAGGCACAAACTAATTTAAAGGAGTCCGAG	3000
Db	2941	GAAGGAGATTTGGAAATCAATG	CTTATGACATAGGCACAAACTAATTTAAAGGAGTCCGAG	3000
Qy	3001	ACTTATCTCCGGACAAACAAGG	TCCTTAACCCATATTTAACTTTGAAACCTCTGGTAGTGG	3060
Db	3001	ACTTATCTCCGGACAAACAAGG	TCCTTAACCCATATTTAACTTTGAAACCTCTGGTAGTGG	3060
Qy	3061	AACAAATCTTATAGATCTGTCT	CTGTGATGATTAAGAGTTTCAGTCTGTGGAGGAAGAGAT	3120
Db	3061	AACAAATCTTATAGATCTGTCT	CTGTGATGATTAAGAGTTTCAGTCTGTGGAGGAAGAGAT	3120
Qy	3121	GCAAGATPACAGTTCCGAGGACA	CAGAGATGGAGTTCATGCGAGTGGAACTTTCAACAGATA	3180
Db	3121	GCAAGATPACAGTTCCGAGGACA	CAGAGATGGAGTTCATGCGAGTGGAACTTTCAACAGATA	3180
Qy	3181	CAATATTTCTCAAGATTCAGAA	GGTTTGTAAACAAGAACTATGGGAAAGATACACTCACCG	3240
Db	3181	CAATATTTCTCAAGATTCAGAA	GGTTTGTAAACAAGAACTATGGGAAAGATACACTCACCG	3240
Qy	3241	GAGAAAGAAGTTTCTGAAGAA	ACCAACCATGCCAATGAACGAATGCTATTTTCATGG	3300
Db	3241	GAGAAAGAAGTTTCTGAAGAA	ACCAACCATGCCAATGAACGAATGCTATTTTCATGG	3300
Qy	3301	GTCTCCTTTTGTGAATCAATTA	TCCACAAGGCTTTTGATGAAAGGATCGGTACATAGG	3360
Db	3301	GTCTCCTTTTGTGAATCAATTA	TCCACAAGGCTTTTGATGAAAGGATCGGTACATAGG	3360
Qy	3361	TGGTATGTTTGGAGCTGGCAT	TTATTTTTTGTGTAAGAACTCTTCCAAAAGCAATCAATATGT	3420
Db	3361	TGGTATGTTTGGAGCTGGCAT	TTATTTTTTGTGTAAGAACTCTTCCAAAAGCAATCAATATGT	3420
Qy	3421	ATATGGAATTTGGAGGAGGTAC	TGGGTGTCAGTTTCAAAAGACAGATCTTTGTACATTG	3480
Db	3421	ATATGGAATTTGGAGGAGGTAC	TGGGTGTCAGTTTCAAAAGACAGATCTTTGTACATTG	3480
Qy	3481	CCACAGGACGCTGCTCTTTT	TCGCGGGTAAACCTTGGGAAAGTCTTTCTCGAGTTTCAGTGC	3540
Db	3481	CCACAGGACGCTGCTCTTTT	TCGCGGGTAAACCTTGGGAAAGTCTTTCTCGAGTTTCAGTGC	3540
Qy	3541	AATGAAAATGGCAATTTCT	CTCCTCCAGGTCATCACTCAGTCACTGGTAGGCCAGGTGTAAA	3600

RESULT 2

US-09-843-159B-1

US-09-843-139B-1
: Sequence 1, Application US/098431159B

: Patent No. 6887675

; PATENT NO. 6887675
: GENERAL INFORMATION:

: APPLICANT: LINDA Y.

APPLICANT: Luo, Yin
APPLICANT: Chan, Evan

APPLICANT: Chan, Evan
APPLICANT: Xu, Yixiang

APPLICANT: Xu, Xiang

APPLICANT: Huang, Betty

; TITLE OF INVENTION: Tankyrase H,
 TITLE REFERENCE: A 59282-3/pmc/dhp

FILE REFERENCE: A-68292-2/RMS/DHR

; CURRENT APPLICATION NUMBER: US/00

; CURRENT FILING DATE: 2001-04-25

; PRIOR APPLICATION NUMBER: US 09/696,668

; PRIOR FILING DATE: 2000-10-25

; PRIOR APPLICATION NUMBER

;
PRIOR FILING DATE: 1999-10-25

NUMBER OF S

; SOFTWARE: Pat

; SEQ ID NO 1

LENGTH: 3797

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; TYPE: DNA

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Query Match

Query Match	100.0%	score 3797;
Best Local Similarity	100.0%	pred No 0:

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1797; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

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[illegible]

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QY 61 AGACAAATATAGCTGTGAGCAGATCTTTTGTGCTCTGTAGTCCCCAGTTAG 120

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QY
121 CAGAAACATTCTGTGAGATAGATGTGGGAAAGGAATTTCTAGCAAGAGTTTGTGCACGTGA 180

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QY 181 TCATAAGGTTGTGATTACATATTTAAGTTTATACCTTGAACATCTGAAAATGTATACA 240

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QY 241 TACTAAATATGCAGAACTCTATTGTAGAGTGAGAAACATTTGAACTTTGAGCTTTCAGTC 300

Abstract

QY 301 ACTATTGTATCTTTCTTTGAGGTAGCAGTAGTACCACCAAGGCAC TGCTTAGGT 360

QY 361 ACACCTGCTTGTAGTGGAGAGTCCCTCTGCTTTTATCATTAAGGTTTGGCGGAAAGA 420
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DB 421 CGTAGTTGAATATTTGCTTCAGAAATGCTGCAAGTGTCCAAGCAGCTCATGATGGGSCCT 480
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DB 481 TATTCTCTTCATTAATGCATGCTCTTTTGGTTCATGCTGAAGTAGTCAATCTCCTTTTGG 540
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DB 721 TACTGGTGAATATTAAGAAAGATGAATCTTTAGAAAGTGCAGAGTGGGCAATGAAGAAA 780
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DB 781 AATGATGGCTCTACTCACACCATTAATATGTCACCTGCCAGCAGTGCATGGCAGAAAGTC 840
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DB 1081 ATGTTCTCTTCTTTAAGTTATGCTGAGACCCCAACACTGCTCAATTTGTCAATATAAAG 1140
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DB 1141 TGCTATAGACTTGGCTCCCAACACACAGTAAAGAAAGATTAGCATATGAATTTAAGG 1200
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DB 1201 CCACTCGTTGTCGCAAGCTGCAAGAGCTGATGTTTACTCGAATCAAAAACATCTCTC 1260
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DB 1441 TAATGATGTTTGAAGTAGTGGTGAACATGAAGCAAAAGGTTAATGCTCTGGATAATCT 1500
QY 1501 TGCTCAGACTTCTCTACACAGAGCTGCATATTTGGTTCATCTCAAAACCTGCCCTACT 1560
DB 1501 TGCTCAGACTTCTCTACACAGAGCTGCATATTTGGTTCATCTCAAAACCTGCCCTACT 1560
QY 1561 CTTGAGCTATGGGTGTGATCTCTAACATTATATCCCTTCAGGGCTTTACTGCTTTACAGAT 1620
DB 1561 CTTGAGCTATGGGTGTGATCTCTAACATTATATCCCTTCAGGGCTTTACTGCTTTACAGAT 1620
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DB 1621 GGGAAATGAAATGTACAGCAATCTCTCCAAGAGGATCTCTATTAGTAAATTCAGAGGC 1680
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DB 1681 AGACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTGAAACTCTGAAAAAATGTG 1740
QY 1741 TACTGTTACAGATGTCAACTGTCAGAGACATTTGAAGGGCGTCAGTCTACACCACTTCATTT 1800
DB 1741 TACTGTTACAGATGTCAACTGTCAGAGACATTTGAAGGGCGTCAGTCTACACCACTTCATTT 1800
QY 1801 TGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCTACAGCATGGAGCTGATGT 1860
DB 1801 TGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCTACAGCATGGAGCTGATGT 1860
QY 1861 GCATGCTTAAAGATAAAGAGGCGCTTGTACCTTTGCACAATGCAATGCTTTATGACATTA 1920
DB 1861 GCATGCTTAAAGATAAAGAGGCGCTTGTACCTTTGCACAATGCAATGCTTTATGACATTA 1920
QY 1921 TGAAGTTGCAAACTTCTTGTAAACATGAGCAGTAGTAAATGCTAGTGAATTTATGGAA 1980
DB 1921 TGAAGTTGCAAACTTCTTGTAAACATGAGCAGTAGTAAATGCTAGTGAATTTATGGAA 1980
QY 1981 ATTTACACCTTTACATGAAGCAGCAGCAAGAAATATGAAATTTGCAAACTTCTGCT 2040
DB 1981 ATTTACACCTTTACATGAAGCAGCAGCAAGAAATATGAAATTTGCAAACTTCTGCT 2040
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DB 2041 CCAGCATGGTGCAGACCTTACCAAAAAAAGAGGATGGAATACTCTCTTTGGATCTGT 2100
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QY 2161 TGCCAAAGAGGTTGTTTAGCCAGAGTGAAGAAAGTGTCTTCTCTCATTAATGTAAATG 2220
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Db 2521 TCTTAAAAATCAGGAGGACAAACACCTTTAGATTAGTTTTCAGGGGATGATGTGTCAGCGC 2580
Qy 2581 TCCTCTGACAGCAGCATGCCCCATCTGCTCTGCCCTCTGTTTACAGCCCTCAAGTGCT 2640
Db 2581 TCTTCTGACAGCAGCATGCCCCATCTGCTCTGCCCTCTGTTTACAGCCCTCAAGTGCT 2640
Qy 2641 CAATGGTGTGAGAAGCCAGGAGCCATGTCAGATGCTCTCTCTGAGGTCCATCTAGGCC 2700
Db 2641 CAATGGTGTGAGAAGCCAGGAGCCATGTCAGATGCTCTCTCTGAGGTCCATCTAGGCC 2700
Qy 2701 ATCAAGCCCTTCTGACGACAGCAGTCTTGACAACTTATCTGGAGTGTTCAGAACTGTC 2760
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Qy 2821 AGGAGTGTAGTTCAGTAACTCAATTCGTAAGGAATCTTGACCTTGAGCACCCTAATGGA 2880
Db 2821 AGGAGTGTAGTTCAGTAACTCAATTCGTAAGGAATCTTGACCTTGAGCACCCTAATGGA 2880
Qy 2881 TATATTTGAGAGAAACAGATCACTTTGGATGTA TTAGTTGAGATGGGGCAACAAGAGCT 2940
Db 2881 TATATTTGAGAGAAACAGATCACTTTGGATGTA TTAGTTGAGATGGGGCAACAAGAGCT 2940
Qy 2941 GAAGAGATTGGAATCAATGCTTATGGACATAGGCACAACTAAATTAAGGATCGAGAG 3000
Db 2941 GAAGAGATTGGAATCAATGCTTATGGACATAGGCACAACTAAATTAAGGATCGAGAG 3000
Qy 3001 ACTTATCTCCGACAAACAGGTCTTAAACCATAATTTAACTTTGAACACCTCTGGTAGTGG 3060
Db 3001 ACTTATCTCCGACAAACAGGTCTTAAACCATAATTTAACTTTGAACACCTCTGGTAGTGG 3060
Qy 3061 AACAAATCTTATAGATCTGCTCTCTGATGATAAAGAGTTTCACTTTGAACACCTCTGGTAGTGG 3120
Db 3061 AACAAATCTTATAGATCTGCTCTCTGATGATAAAGAGTTTCACTTTGAACACCTCTGGTAGTGG 3120
Qy 3121 GCAAGTACAGTTCGAGACAGAGATGAGGTCACTGAGTGGAACTTCAACAGATA 3180
Db 3121 GCAAGTACAGTTCGAGACAGAGATGAGGTCACTGAGTGGAACTTCAACAGATA 3180
Qy 3181 CAATATTTCTCAAGATTCAGAAAGTTGTAAACAAGAACTTATGGGAAAGATACACTCACCG 3240
Db 3181 CAATATTTCTCAAGATTCAGAAAGTTGTAAACAAGAACTTATGGGAAAGATACACTCACCG 3240
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Qy 3301 GTCTCTTTTGTGAATGCAATTCACCAAGGCTTTGATGAAAGGATGCGTACATAGG 3360
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Qy 3361 TGGTATGTTTGGAGTGGCAATTTATTTGCTGAAAACTCTTCCAAAAGCAATCAATATGT 3420
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Db 3421 ATATGGAATTTGAGGAGGTACTGGGTGTCAGGTTCAAAAGACAGATCTTGTTCATTTG 3480
Qy 3481 CCACAGGACGTCTCTTTTGGGGTAACTTTGGGAAGTCTTCTTCCAGTTCAGTTC 3540
Db 3481 CCACAGGACGTCTCTTTTGGGGTAACTTTGGGAAGTCTTCTTCCAGTTCAGTTC 3540
Qy 3541 AATGAAATGGCACATCTCTCTCCAGGTCACTCAGTCACTGAGTGGAGGAGGAGTAA 3600
Db 3541 AATGAAATGGCACATCTCTCTCCAGGTCACTCAGTCACTGAGTGGAGGAGGAGTAA 3600
Qy 3601 TGGCCCTAGCATTTAGCTGAATATGTTATTTTACAGAGAGAACAGGCTTATCTGAGTATTT 3660
Db 3601 TGGCCCTAGCATTTAGCTGAATATGTTATTTTACAGAGAGAACAGGCTTATCTGAGTATTT 3660

Qy 3661 AATTACTTACCAGATTATGAGCCCTGAAGGTATGTCGATGATAAATAGTATTTTAAAG 3720
Db 3661 AATTACTTACCAGATTATGAGCCCTGAAGGTATGTCGATGATAAATAGTATTTTAAAG 3720
Qy 3721 AAACTAATTCACGAACTTAAATCATCAAGACAGAGTGGCCCTCTACGTTTACTCT 3780
Db 3721 AAACTAATTCACGAACTTAAATCATCAAGACAGAGTGGCCCTCTACGTTTACTCT 3780
Qy 3781 TTGCTGAAAAA 3797
Db 3781 TTGCTGAAAAA 3797

RESULT 3

US-09-696-668-2
; Sequence 2, Application US/09696668
; Patent No. 6617102
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ososovskaya, Valeria
; TITLE OF INVENTION: TANKYRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS C
; FILE REFERENCE: A-68292-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/696,668
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-696-668-2

Query Match 89.4%; Score 3393.4; DB 3; Length 3816;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 463 ACGTGATGATGGGGCCCTTATTCCTCTTCAATAATGTCATGCTCTTTTGGTCAATGCTGAAGT 522
Db 482 ACGTGATGATGGGGCCCTTATTCCTCTTCAATAATGTCATGCTCTTTTGGTCAATGCTGAAGT 541
Qy 523 AGTCAATCTCTTTTGGGACATGGTGACAGCCCAATGCTCGAGATAATTGGAATATATAC 582
Db 542 AGTCAATCTCTTTTGGGACATGGTGACAGCCCAATGCTCGAGATAATTGGAATATATAC 601
Qy 583 TCCTCTCCATGAAGTGCATTTAAAGGAAAGATGATGTTTGCATTTGCTGCTTACAGCA 642
Db 602 TCCTCTCCATGAAGTGCATTTAAAGGAAAGATGATGTTTGCATTTGCTGCTTACAGCA 661
Qy 643 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCAGATTTGGAATTAGCAGATCC 702
Db 662 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCAGATTTGGAATTAGCAGATCC 721
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Db 722 ATCTGCCAAAGCAGTCTTACTGGTGAATATAAGAAAGATGAACCTCTTAGAAAGTGCCAG 781
Qy 763 GAGTGGCAATGAAGAAAAAATGATGGCTCTTACTCACACCATTTAAATGTCAAATGTCGCAAGC 822
Db 782 GAGTGGCAATGAAGAAAAAATGATGGCTCTTACTCACACCATTTAAATGTCAAATGTCGCAAGC 841
Qy 823 AAGTATGGCAGAAAGTCAATTCATTTTGGCAGCAGGATATAACAGAGTAAAGAT 882
Db 842 AAGTATGGCAGAAAGTCAATTCATTTTGGCAGCAGGATATAACAGAGTAAAGAT 901

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Db	902	TGTACAGCTGT	TACTGCAACATGCAGCTGATGCCATGCTAAAAGATAAAGAGTGTATCTGGT	961	
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Db	962	ACCAT	TACACAATATGCCTGTGTTCTTATGTGTCATATTATGAAGTAACCTTTTGGTGTCAAGCA	1021	
Qy	1003	TGTG	CCCTGTGTAATCGCAATGGACCTTGCGCAATTCACCTCCTTTCATGAGCAGCAGCTTC	1062	
Db	1022	TGTG	CCCTGTGTAATCGCAATGGACCTTGTGGCAATTCACCTCCTTTCATGAGCAGCAGCTTC	1081	
Qy	1063	TAAGAA	CAGGGTTGAAGTATGTTCTCTTCTTTAAAGTTATGTTGTCGACGCCAACACCTGCT	1122	
Db	1082	TAAGNA	CAGGGTTGAAGTATGTTCTCTTCTTTAAAGTTATGTTGTCGACGCCAACACCTGCT	1141	
Qy	1123	CAATT	GTCACAATAAAGTAGTCTATPAGACTTTGGCTCCACACCACAGFTTAAAAAGAAAGATT	1182	
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Qy	1183	AGCAT	ATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAGCTGATCTTACTCG	1242	
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Qy	1303	AGCAT	TGCATTTGTCCTGCTGCTGCATCTCCATATCCAAAAGAACAAATATGTGAAC TGT	1362	
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Qy	1363	GCTAA	AAAAAGGAGCAACATCAATGAAAAGACTAAAGAAATTCCTGACTCCTCTGCACGT	1422	
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Qy	1423	GGCAT	CTGAGAAAGCTCATATGATGTGTTGTAAGTAGTGGTGAACATCAAGCAAGGT	1482	
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Qy	1543	ACAAA	CCCTGCGCCTACTCTCTGAGCTATGGGTGTGATCCTAAATATATATCCCTTCAGGG	1602	
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Qy	1603	CTTT	TACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCCTCCAAGAGGTATCTC	1662	
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Qy	1723	AAC	TGTAAAAAAACTGTGTACTGTTACAGATGTCAACTGCAGAGACATTTGAAGGGCGTCA	1782	
Db	1742	AAC	TGTAAAAAAACTGTGTACTGTTACAGATGTCAACTGCAGAGACATTTGAAGGGCGTCA	1801	
Qy	1783	GTCT	TACACCACTTCATTTTTCCAGCTGGGTATACAGAGTCCGTTGGTGGAAATATCTGCT	1842	
Db	1802	GTCT	TACACCACTTCATTTTTCCAGCTGGGTATACAGAGTCCGTTGGTGGAAATATCTGCT	1861	
Qy	1843	ACAG	CTGGAGCTGATGTGCATGCTAAAGATTAAGAGAGGCTTGTGACTTTTGACAAATGC	1902	
Db	1862	ACAG	CTGGAGCTGATGTGCATGCTAAAGATTAAGAGAGGCTTGTGACTTTTGACAAATGC	1921	
Qy	1903	ATG	TCTTATGGACATTTATGAAGTTGCAGAACTTCTTTGTTTAAACATGGAGCAGTAGTTAA	1962	
Db	1922	ATG	TCTTATGGACATTTATGAAGTTGCAGAACTTCTTTGTTTAAACATGGAGCAGTAGTTAA	1981	

Qy	1963	TGTAGCTGATTTATGGAATTTTACACTTTTACATGAAGCAGCGCAGCAAAAGGAAAATATGA	2022
Db	1982	TGTAGCTGATTTATGGAATTTTACACTTTTACATGAAGCAGCGCAGCAAAAGGAAAATATGA	2041
Qy	2023	AAATTCGAAACTTCCTGCTCCAGCATCGTCAGACCCCTACCAAAAAAACAAGGATCGAAA	2082
Db	2042	AAATTCGAAACTTCCTGCTCCAGCATCGTCAGACCCCTACCAAAAAAACAAGGATCGAAA	2101
Qy	2083	TACTCCTTTTGGATCTTGTTTAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA	2142
Db	2102	TACTCCTTTTGGATCTTGTTTAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA	2161
Qy	2143	TGCAGCTTTGCTAGATGCTGCCAAGAAGGGTGTGTAGCCAGAGTGAAGAAGTTGCTTTC	2202
Db	2162	TGCAGCTTTGCTAGATGCTGCCAAGAAGGGTGTGTAGCCAGAGTGAAGAAGTTGCTTTC	2221
Qy	2203	TCCTGATATGTTAAATTTGCCGCGATACCCAAGGCAGACATTCAACACCTTTTACATTTAGC	2262
Db	2222	TCCTGATATGTTAAATTTGCCGCGATACCCAAGGCAGACATTCAACACCTTTTACATTTAGC	2281
Qy	2263	AGCTGGTTTAAATAATTTAGAAAGTTTCAGAGTATTTGTTTACAACACGGAGCTGATGTGAA	2322
Db	2282	AGCTGGTTTAAATAATTTAGAAAGTTTCAGAGTATTTGTTTACAACACGGAGCTGATGTGAA	2341
Qy	2323	TGCCCAAGACAAAGGAGGACTTATTCCTTTACATAATAGCAGCATTTTACGGGCATGTAGA	2382
Db	2342	TGCCCAAGACAAAGGAGGACTTATTCCTTTACATAATAGCAGCATTTTACGGGCATGTAGA	2401
Qy	2383	TGTAGCAGCTCTACTAATTAAGTATTAATGCGATGTGTCAATGCCACGGACAAATGGGCTTT	2442
Db	2402	TGTAGCAGCTCTACTAATTAAGTATTAATGCGATGTGTCAATGCCACGGACAAATGGGCTTT	2461
Qy	2443	CACACCTTTTGACGAAGCAGCCCCAAAGGAGGAGAACACACAGCTTTGTGCTTTGTGCTAGC	2502
Db	2462	CACACCTTTTGACGAAGCAGCCCCAAAGGAGGAGAACACACAGCTTTGTGCTTTGTGCTAGC	2521
Qy	2503	CCATGGAGCTGACCCGACCTCTTAAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC	2562
Db	2522	CCATGGAGCTGACCCGACCTCTTAAAAATCAGGAAGGAGAACACACCTTTAGATTTAGTTTC	2581
Qy	2563	AGCGGATGATGTGAGGGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCTCTTG	2622
Db	2582	AGCGGATGATGTGAGGGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCTCTTG	2641
Qy	2623	TTACAGCCTCAAGTGTCTCAATGGTGTGAGAGCCCGCAGAGCCACCTGCAGATCTCTCTC	2682
Db	2642	TTACAGCCTCAAGTGTCTCAATGGTGTGAGAGCCCGCAGAGCCACCTGCAGATCTCTCTC	2701
Qy	2683	TTCAGGTCCATCTAGCCCATCAAGCCCTTTCTGCAGCCAGCAGCTCTTGACAACTTATCTGG	2742
Db	2702	TTCAGGTCCATCTAGCCCATCAAGCCCTTTCTGCAGCCAGCAGCTCTTGACAACTTATCTGG	2761
Qy	2743	GAGTTTTTCAGAACTGTCTTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGGTCTTCCAGTTT	2802
Db	2762	GAGTTTTTCAGAACTGTCTTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGGTCTTCCAGTTT	2821
Qy	2803	GGAGAAAAGGAGGTTCCAGGATGATTTTACGATAAATCTCAATTCGTAGGGAATCTTTGG	2862
Db	2822	GGAGAAAAGGAGGTTCCAGGATGATTTTACGATAAATCTCAATTCGTAGGGAATCTTTGG	2881
Qy	2863	ACTTTGACACTTAATGGATATATTTTGAGAGAGAACAGATCACTTTGGATGTATTAGTTGA	2922
Db	2882	ACTTTGACACTTAATGGATATATTTTGAGAGAGAACAGATCACTTTGGATGTATTAGTTGA	2941
Qy	2923	GATGGGGCAACAAGGACTGAGAGATTTGGAATCAATGCTTTATGGACATAGGCACAAACT	2982
Db	2942	GATGGGGCAACAAGGACTGAGAGATTTGGAATCAATGCTTTATGGACATAGGCACAAACT	3001
Qy	2983	AAHTAAGNGTCCAGAGACTTATCTCCGACAAACAAGGCTTTAAACCCATATTTAACTTT	3042
Db	3002	AAHTAAGNGTCCAGAGACTTATCTCCGACAAACAAGGCTTTAAACCCATATTTAACTTT	3061
Qy	3043	GAACACCTCTGGTAGTGGAAACAATTTCTTATAGATCTGTCTCTCTGATGATAAAGAGTTTCA	3102

Db 3062 GAACACCTCTGCTAGTGGAACTTCTTAGATCTGCTCTGATATAAGAGTTCA 3121
Qy 3103 GTCTGTGGAGGAGAGATCCAAAGTACAGTTTCAGAGGACACAGAGATGAGGTCAGG 3162
Db 3122 GTCTGTGGAGGAGAGATCCAAAGTACAGTTTCAGAGGACACAGAGATGAGGTCAGG 3181
Qy 3163 TGGAAATCTTCAACAGATACAAATATCTCAAGATTTCAGAGGTTTGTAAACAAGAACTATG 3222
Db 3182 TGGAAATCTTCAACAGATACAAATATCTCAAGATTTCAGAGGTTTGTAAACAAGAACTATG 3241
Qy 3223 GGAAGATACACTCACCGGAGAGAAAGAGTTTCTGAAGAAACCAACCAATGCCAATGA 3282
Db 3242 GGAAGATACACTCACCGGAGAGAAAGAGTTTCTGAAGAAACCAACCAATGCCAATGA 3301
Qy 3283 ACGAATGCTATTTCATGGGTCTCTTCTTGTGAATTCAGAAATTCACAAAGGCTTTGATGA 3342
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Qy 3343 AAGGATGCTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTGAAACTCTTC 3402
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Qy 3403 CAAAAGCAATCAATATGTATATGGAATTGGAGGAGTACTGGGTGTCCAGTTTCAAAAGA 3462
Db 3422 CAAAAGCAATCAATATGTATATGGAATTGGAGGAGTACTGGGTGTCCAGTTTCAAAAGA 3481
Qy 3463 CAGATCTGTTACATTTGGCCAGGAGCTGCTCTTTTCCGGGTAAACCTTGGGAAAGTC 3522
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Qy 3523 TTTCTCGAGTTTCAGTGCATGAATGCAATCTCTCCAGGTCACTCAGTCACT 3582
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Qy 3703 ATAAATAGTATTTTAAAGAACTAAATCCACGTGAACCTAAATATCAAGCAGCAGTGG 3762
Db 3722 ATAAATAGTATTTTAAAGAACTAAATCCACGTGAACCTAAATATCAAGCAGCAGTGG 3781
Qy 3763 CCTCTACGTTTCTCTCTTGTGTAAGAAAGAA 3797
Db 3782 CCTCTACGTTTCTCTCTTGTGTAAGAAAGAA 3816

RESULT 4
US-09-843-159B-2
; Sequence 2, Application US/09843159B
; Patent No. 6857675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; PRIORITY FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3816

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-843-159B-2
Query Match 89.4%; Score 3393.4; DB 3; Length 3816;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 403 AGGTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGATGCTGCAAGTGTCCAAGC 462
Db 422 AGGTTTGGGCGGAAAGACGTAGTTGAATATTTGCTTCAGATGCTGCAAGTGTCCAAGC 481
Qy 463 ACGTGATGATGGGGCCCTTATTCCTCTTCATAATGCATGCTCTTTTGGTGCATGCTGAAGT 522
Db 482 ACGTGATGATGGGGCCCTTATTCCTCTTCATAATGCATGCTCTTTTGGTGCATGCTGAAGT 541
Qy 523 AGTCAATCTCTTTTGGGACATGCTGAGACCCCAATGCTGAGATAATTTGAATTTATAC 582
Db 542 AGTCAATCTCTTTTGGGACATGCTGAGACCCCAATGCTGAGATAATTTGAATTTATAC 601
Qy 583 TCCTCTCCATGAAGTGCATTTAAAGGAAAGATTGATGTTTGCATGCTGCTGTACAGCA 642
Db 602 TCCTCTCCATGAAGTGCATTTAAAGGAAAGATTGATGTTTGCATGCTGCTGTACAGCA 661
Qy 643 TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 702
Db 662 TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 721
Qy 703 ATCTGCCAAAGCAGTGTCTTACTGTTGAATATAAGAAAGATGAACTCTTTAGAAAGTGCAG 762
Db 722 ATCTGCCAAAGCAGTGTCTTACTGTTGAATATAAGAAAGATGAACTCTTTAGAAAGTGCAG 781
Qy 763 GAGTGGCAATGAAGAAAGATGATGGCTCTACTCACACCATTTAATGTCACTGCCAGC 822
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Qy 883 TGTACAGCTGTTTACGCAACATGAGCTGATGCTCATGCTAAAGATAAAGGTGATCTGGT 942
Db 902 TGTACAGCTGTTTACGCAACATGAGCTGATGCTCATGCTAAAGATAAAGGTGATCTGGT 961
Qy 943 ACCATTACAAATGCTGCTTCTTATGCTCATTTAAGAGTAACTGAATTTTGGTCAAGCA 1002
Db 962 ACCATTACAAATGCTGCTTCTTATGCTCATTTAAGAGTAACTGAATTTTGGTCAAGCA 1021
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Db 1022 TGGTGCCTGTGTAATGCAATGGACTTGTGCAATTTCACTCTCTTCATGAGGAGCTTC 1081
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Db 1082 TAAGAACAGGGTGAAGTATGTTCTTCTTCTTAAGTTATGGTCAGACCCCAACACTGCT 1141
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Db 1142 CAATTTGTCACAAATAAAGTGTCTATAGACTTGGCTCCCAACACACAGTTTAAAGAAAGAT 1201
Qy 1183 AGCATATGAAATTTAAAGGCGCACTCGTTGCTGCAAGCTGCAAGAGCTGATGTTACTCG 1242
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Qy 1243 AATCAAAAAACATCTCTCTCTGGAAATGGTGAATTTTCAAGCATCTCAACACATGAAAC 1302
Db 1262 AATCAAAAAACATCTCTCTCTGGAAATGGTGAATTTTCAAGCATCTCAACACATGAAAC 1321
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Db 1382 GCTAAGAAAAGGAGCAACATCAATGAAAGACATAAGAAATTTCTTGACTCTCTGACGCT 1441
Qy 1423 GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAAGTAGTGTGAAACATGAAGCAAAAGGT 1482
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Qy 1603 CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCCAAAGAGGCTATCTC 1662
Db 1622 CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCCAAAGAGGCTATCTC 1681
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Qy 1783 GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT 1842
Db 1802 GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCT 1861
Qy 1843 ACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGGAGGCTTGTACTCTTTGCAACAATGC 1902
Db 1862 ACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGGAGGCTTGTACTCTTTGCAACAATGC 1921
Qy 1903 ATGTTCTTATGGACATTAATGAAGTTGACAGACTCTTGTGTTAAACATGGAGCAGTAGTTAA 1962
Db 1922 ATGTTCTTATGGACATTAATGAAGTTGACAGACTCTTGTGTTAAACATGGAGCAGTAGTTAA 1981
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Qy 2023 AATTGCAAACTTCTGCTCAGCATGTTGTCAGACCTTACCAAAAAAACAAGGATGGAAA 2082
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Qy 2083 TACTCCTTTGGATCTGTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA 2142
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Db 2162 TGCAGCTTTGCTAGATGCTGCAAGAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTCTTC 2221
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Qy 3043 GAACACCTCTGTTAGTGGAAACAATTTTATAGATCTCTCTCTGATGATAAAGAGTTTCA 3102
Db 3062 GAACACCTCTGTTAGTGGAAACAATTTTATAGATCTCTCTCTGATGATAAAGAGTTTCA 3121
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Db 3122 GTCTGTGGAGAGAGATGCAAAAGTACAGTTCGAGACACAGAGATGAGGTCATGCAGG 3181
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Qy 3403 CAAAAGCAATCAATATGATATGGAATTTGGAGAGGTAATGCGGCTGTCAGTTTCAAAAGA 3462
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RESULT 5
US-09-972-115A-5
; Sequence 5, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Moxin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Platyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4275
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(3781)
; OTHER INFORMATION:
US-09-972-115A-5

Query Match      89.2%; Score 3388.8; DB 3; Length 4275;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 403 AGGTTTGGCGGAAGACGTAGTTGAATATTTGCTTCAGATGGTGCAGAGTCCCAAGC 462
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QY 463 ACGTGATGATGGGGCCCTTATTCCTCTTCATAATGCATGCTCTTTGGTCAATGCTGAAGT 522
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QY 523 AGTCAATCTCTTTTGGACATGTTGTCAGACCCCAATGCTCGAGATAATTTGAATATPAC 582
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QY 1843 ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCCTGTACCTTTGCAATGC 1902
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DB 3481 CAAAAGCAATCAATATGATATGCAATTTGGAATTTGAGAGGAGTACTGGGTGTCACAAAGA 3540
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DB 3601 TTTCTCTCAGTTTCAAGTCAATGAAAATGGCAATTTCTCTCCAGGTCACTCAGTCAC 3660
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DB 3721 GGCTTATCTCAGTATTTTAAATTTACTTACCAGATTATGAGGCTCTGAAGTATGGTCGATGG 3780
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DB 3841 CCTCTAGTTTACTCTCTTCTGCTGAAAAAAA 3872

RESULT 6

US-09-799-451-556
; Sequence 556, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.

```
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yuning
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghoeh, Reena
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 556
; LENGTH: 5075
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(3750)
US-09-799-451-556

Query Match      89.2%; Score 3387.2; DB 3; Length 5075;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 403 AGCTTTTGGCGGAAGACGTAGTTGAATATTGCTTCAGAAATGGTGCAGAGTGTCCAGC 462
DB 450 AGCTTTTGGCGGAAGACGTAGTTGAATATTGCTTCAGAAATGGTGCAGAGTGTCCAGC 509
QY 463 AGCTGATGATGGGGCTTATTCCTTCATTAATGATGCTCTTTTGGTTCATGCTGAAGT 522
DB 510 AGCTGATGATGGGGCTTATTCCTTCATTAATGATGCTCTTTTGGTTCATGCTGAAGT 569
QY 523 AGTCAATCTCTTTTGGCAGATGGTGCAGACCCCAATGCTCAGATATTGGAATTTATAC 582
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DB 1230 AGCATATGAATTTAAAGGCCACTGTTGCTGCAAGCTGCAAGAGCTGATGTTACTCG 1289
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DB 1890 ACAGCATGGAGCTGATGTCATGCTTAAAGATAAAGAGGCGCTTTGACCTTTGCAAAATGC 1949
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RESULT 7

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US-09-849-602-11
; Sequence 11, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 6018
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-849-602-11
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Query Match      89.2%; Score 3387.2; DB 3; Length 6018;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 418 AGGTTTTTGGCGGAAACACGCTAGTTGAATATTTCTTCAGAAATGTCGCAAGTGTCCAAAGC 477
QY 463 ACCTGATGATGGGGCCCTTATTCCTCTTCAATATGTCATGCTCTTTTGGTCAATGCTGAAGT 522
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DB	658	TGGAGCTGAGCCCAACCATCCGAATACAGATGGAAGGACAGCATTTGGATTAGCAGATCC	717
QY	703	ATCTGCGCAAGCAGTCTTACTGGTGAATATAGAAAGATGAATCTTAGAAAGTGCCAG	762
DB	718	ATCTGCGCAAGCAGTCTTACTGGTGAATATAGAAAGATGAATCTTAGAAAGTGCCAG	777
QY	763	GAGTGGCAATGAAGAAAAAATGATGCTCTACTCACCAATTAATGTCAAATGCCACGC	822
DB	778	GAGTGGCAATGAAGAAAAAATGATGCTCTACTCACCAATTAATGTCAAATGCCACGC	837
QY	823	AGTGTATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAGAT	882
DB	838	AGTGTATGGCAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAGAT	897
QY	883	TGTACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTAAAGATAAAAGTGTCTGGT	942
DB	898	TGTACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTAAAGATAAAAGTGTCTGGT	957
QY	943	ACCATTTACAAATGCTGTTCTTATGCTCATTTATGAAGTAACTGAATTTGGTCAAGCA	1002
DB	958	ACCATTTACAAATGCTGTTCTTATGCTCATTTATGAAGTAACTGAATTTGGTCAAGCA	1017
QY	1003	TGGTGCCTGTGTAATGCAATGGACTGTGGCAATTTCACTCTCTCATGAGGCGACTTC	1062
DB	1018	TGGTGCCTGTGTAATGCAATGGACTGTGGCAATTTCACTCTCTCATGAGGCGACTTC	1077
QY	1063	TAAAGAACAGGGTGTGAAGTATGTTCTCTCTTAAAGTATGCTGAGACCCCAACTGCT	1122
DB	1078	TAAAGAACAGGGTGTGAAGTATGTTCTCTCTTAAAGTATGCTGAGACCCCAACTGCT	1137
QY	1123	CAATTGTCAATAAAGTGTATAGACTTGGCTCCACACACAGTTAAAGAAAGATT	1182
DB	1138	CAATTGTCAATAAAGTGTATAGACTTGGCTCCACACACAGTTAAAGAAAGATT	1197
QY	1183	AGCATATGAATTTAAAGGCCACTCGTGTGCAAGCTGCAAGAGCTGATGTTACTCG	1242
DB	1198	AGCATATGAATTTAAAGGCCACTCGTGTGCAAGCTGCAAGAGCTGATGTTACTCG	1257
QY	1243	AATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTCAAAACACATGAAC	1302
DB	1258	AATCAAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTCAAAACACATGAAC	1317
QY	1303	AGCATTTGCAATGCTGCTGCAATCTCCATATCCAAAAAGAAAGCAAAATATGAACTGTT	1362
DB	1318	AGCATTTGCAATGCTGCTGCAATCTCCATATCCAAAAAGAAAGCAAAATATGAACTGTT	1377
QY	1363	GCTAAGAAAAGGAGCAACATCAATGAAGAAAGCTAAAGAAATTTCTTGACTCTGCAAGT	1422
DB	1378	GCTAAGAAAAGGAGCAACATCAATGAAGAAAGCTAAAGAAATTTCTTGACTCTGCAAGT	1437
QY	1423	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTGTGGTGAACATGAAGCAAGGT	1482
DB	1438	GGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTGTGGTGAACATGAAGCAAGGT	1497
QY	1483	TAAATGCTCTGGATAATCTTTGGTGCAGACTTCTCTACACAGAGCTGCATATTGGTCACT	1542
DB	1498	TAAATGCTCTGGATAATCTTTGGTGCAGACTTCTCTACACAGAGCTGCATATTGGTCACT	1557
QY	1543	ACAAACCTGCCCGCTACTCTGAGCTATGGGTGTGATCCCTAATATATATCCCTTCAGGG	1602
DB	1558	ACAAACCTGCCCGCTACTCTGAGCTATGGGTGTGATCCCTAATATATATATATCCCTTCAGGG	1617

QY	1603	CTTTACTGCTTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCTCCAAAGAGGATCTC	1662
DB	1618	CTTTACTGCTTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCTCCAAAGAGGATCTC	1677
QY	1663	ATTAGGTAAATTCAGAGGCGACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTGCA	1722
DB	1678	ATTAGGTAAATTCAGAGGCGACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTGCA	1737
QY	1723	AACTGTAAAAAATCTGTACTGTTTACAGATGCTCAACTGTCAGAGACATTTGAAGGGCGTCA	1782
DB	1738	AACTGTAAAAAATCTGTACTGTTTACAGATGCTCAACTGTCAGAGACATTTGAAGGGCGTCA	1797
QY	1783	GTCTACACCACTTTCTATTTTGGACGTGGGTATAACAGAGTGTCCGCTGGTGAATATCTGCT	1842
DB	1798	GTCTACACCACTTTCTATTTTGGACGTGGGTATAACAGAGTGTCCGCTGGTGAATATCTGCT	1857
QY	1843	ACAGCATGGAGCTGATGTCATGCTTAAAGATAAAGAGGCGCTTGTACCTTTCACAAATGC	1902
DB	1858	ACAGCATGGAGCTGATGTCATGCTTAAAGATAAAGAGGCGCTTGTACCTTTCACAAATGC	1917
QY	1903	ATGTTCTTTATGAGACATTTAAGTTTGCAGAACTTCTTGTAAACATGGAGCAGTAGTTAA	1962
DB	1918	ATGTTCTTTATGAGACATTTAAGTTTGCAGAACTTCTTGTAAACATGGAGCAGTAGTTAA	1977
QY	1963	TGTAGCTGATTTATGAAAAATTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2022
DB	1978	TGTAGCTGATTTATGAAAAATTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA	2037
QY	2023	AATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCACCAAAAAAAGAGGATGAAA	2082
DB	2038	AATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCACCAAAAAAAGAGGATGAAA	2097
QY	2083	TACTCTTTTGGATCTGTTTAAAGATGGAGATACAGATATTTCAAGATCTCTTAGGGGAGA	2142
DB	2098	TACTCTTTTGGATCTGTTTAAAGATGGAGATACAGATATTTCAAGATCTCTTAGGGGAGA	2157
QY	2143	TGCAGCTTTGCTAGATGCTGCGCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTTTC	2202
DB	2158	TGCAGCTTTGCTAGATGCTGCGCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTTTC	2217
QY	2203	TCCTGATTAATGTAATTTGCGCGATACCCAGGCGAGACATTCAACACCTTTACATTTAGC	2262
DB	2218	TCCTGATTAATGTAATTTGCGCGATACCCAGGCGAGACATTCAACACCTTTACATTTAGC	2277
QY	2263	AGCTGGTTATTAATTTAGAGTTTGCAGAGTATTTGTTTACAAACAGGAGCTGATGAA	2322
DB	2278	AGCTGGTTATTAATTTAGAGTTTGCAGAGTATTTGTTTACAAACAGGAGCTGATGAA	2337
QY	2323	TGCCCCAGACAAAGGAGGACTTATTTCTTTTACATAATGCAGCATCTTACGGGCATGTAGA	2382
DB	2338	TGCCCCAGACAAAGGAGGACTTATTTCTTTTACATAATGCAGCATCTTACGGGCATGTAGA	2397
QY	2383	TGTAGCAGCTCTAATAATAAAGTATAATGTCATGTCATGTCATGTCACGGAATAATGGGCTTT	2442
DB	2398	TGTAGCAGCTCTAATAATAAAGTATAATGTCATGTCATGTCATGTCACGGAATAATGGGCTTT	2457
QY	2443	CACACCTTTGACGAAGCAGCCCAAAAGGAGGACACAGCTTTTCTGCTTCTGCTAGC	2502
DB	2458	CACACCTTTGACGAAGCAGCCCAAAAGGAGGACACAGCTTTTCTGCTTCTGCTAGC	2517
QY	2503	CCATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAAACACCTTTAGATTAGTTTC	2562
DB	2518	CCATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAAACACCTTTAGATTAGTTTC	2577
QY	2563	AGCGATGATGTACGCGCTCTTCTGACAGCAGCATGCCCCCATCTGCTGCCCCCTTTG	2622
DB	2578	AGCGATGATGTACGCGCTCTTCTGACAGCAGCATGCCCCCATCTGCTGCCCCCTTTG	2637
QY	2623	TTACAGGCTCAAGTGTCAATGTTGTCAGAGCCCGAGGCGCACTGCAGATGCTCTC	2682
DB	2638	TTACAGGCTCAAGTGTCAATGTTGTCAGAGCCCGAGGCGCACTGCAGATGCTCTC	2697
QY	2693	TTGAGTCCATCTAGCCCATCAAGCCTTTTCTGACGACGAGCTTTTGACAACTTATCTGG	2742

Db 2698 TTCAGGTCATCTAGCCCATCAAGCCCTTTCGACGACGAGTCTTGACAACTTATCTGG 2757
Qy 2743 GAGTTTTTCAGAACTGCTCTCAGTAGTTAGTTCAGGTGGAAACAGAGGCTCTCCAGTTT 2802
Db 2758 GAGTTTTTCAGAACTGCTCTCAGTAGTTAGTTCAGGTGGAAACAGAGGCTCTCCAGTTT 2817
Qy 2803 GGAGAAAAGAGGTTCCAGGAGTAGATTTTTCAGATAACTCAATTCGTAAGGAATCTTGG 2862
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Qy 2863 ACTTGAGCACCTAATGATATATTTTGAGAGAGACAGATCACTTTGGATGATTAGTTGA 2922
Db 2878 ACTTGAGCACCTAATGATATATTTTGAGAGAGACAGATCACTTTGGATGATTAGTTGA 2937
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Db 2938 GATGGGCGACAAAGAGCTGAAGGAGATTTGGAATCAATGCTTTATGACATAGGCAAACT 2997
Qy 2983 AATTAAAGGAGTCCAGAGACTTATCTCCGGACAAAGGCTTTAAACCCATATTTAACTTT 3042
Db 2998 AATTAAAGGAGTCCAGAGACTTATCTCCGGACAAAGGCTTTAAACCCATATTTAACTTT 3057
Qy 3043 GAACACCTCTGGTAGTGGAACTTCTTATAGATCTGCTCTCTGATGATTAAGAGTTTCA 3102
Db 3058 GAACACCTCTGGTAGTGGAACTTCTTATAGATCTGCTCTCTGATGATTAAGAGTTTCA 3117
Qy 3103 GTCTGTGGAGAAAGATGCAAACTACAGTTTCGAGAGACAGAGATGGAGTCAATGAGG 3162
Db 3118 GTCTGTGGAGAAAGATGCAAACTACAGTTTCGAGAGACAGAGATGGAGTCAATGAGG 3177
Qy 3163 TGGAACTCTTCAACAGATACAAATATCTCAAGATTGAGAGTTTGTAAACAGAAACTATG 3222
Db 3178 TGGAACTCTTCAACAGATACAAATATCTCAAGATTGAGAGTTTGTAAACAGAAACTATG 3237
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Db 3238 GGAAGATACACTCACCGGAGAAAGAGTTTCTGAAGNAACCAACACCATGCAATGA 3297
Qy 3283 ACGAATGCTATTTTCATGGGTCTCTTTTGTGAATGCAATATCAACAAAGCTTTGATGA 3342
Db 3298 ACGAATGCTATTTTCATGGGTCTCTTTTGTGAATGCAATATCAACAAAGCTTTGATGA 3357
Qy 3343 AAGCATCGCTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTGCTGAAAACCTCTTC 3402
Db 3358 AAGCATCGCTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTGCTGAAAACCTCTTC 3417
Qy 3403 CAAAGCAATCAATATGATATGAAATTTGGAGGAGTACTGGGTGCTCCAGTTCAACAAGA 3462
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Qy 3463 CAGATCTTTGATACATTTGCCACAGCAGCTGCTCTTTTGGCGGTAACTTTGGGAAAGTC 3522
Db 3478 CAGATCTTTGATACATTTGCCACAGCAGCTGCTCTTTTGGCGGTAACTTTGGGAAAGTC 3537
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Db 3598 TGGTAGCCCAAGTCTAAATGGCCCTAGCATAGCTGAAATATGTTATTTACAGAGGAGAACA 3657
Qy 3643 GGCCTTATCTCAGTATTTAATTTACTTACAGATATGAGGCTGAAGGTATGGTTCGATGG 3702
Db 3658 GGCCTTATCTCAGTATTTAATTTACTTACAGATATGAGGCTGAAGGTATGGTTCGATGG 3717
Qy 3703 ATAAATAGTTATTTTAAGAACTAATTTCCACTGAACCTTAAATCATCAAGCAGCAGTGG 3762
Db 3718 ATAAATAGTTATTTTAAGAACTAATTTCCACTGAACCTTAAATCATCAAGCAGCAGTGG 3777
Qy 3763 CCTCTAGTTTTTACTCTCTTTGCTGAAAAAAA 3794

Db 3778 CCTCTACGTTTTTACTCTCTTTGCTGAAAAAAA 3809
RESULT 8
US-09-427-154-1
; Sequence 1, Application US/09427154
; Patent No. 6589725
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: TANKYRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND
; FILE REFERENCE: A-68292-DJB/RMS/DAV
; CURRENT APPLICATION NUMBER: US/09/427,154
; CURRENT FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-427-154-1
Query Match 89.2%; Score 3386; DB 3; Length 3394;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 404 GGTTTTGGCGGAAAGACGTAGTTGAAATATTTGCTTCAGAAATGTCGAAGTGTCCAAGCA 463
Db 1 GGTTTTGGCGGAAAGACGTAGTTGAAATATTTGCTTCAGAAATGTCGAAGTGTCCAAGCA 60
Qy 464 CGTGATGATGGGGCCCTTATTCCTCTTCATAATGCATGCTCTTTTGGTCATGCTGAAGTA 523
Db 61 CGTGATGATGGGGCCCTTATTCCTCTTCATAATGCATGCTCTTTTGGTCATGCTGAAGTA 120
Qy 524 GTCAATCTCTTTTGGCAATGCTGAGAGACCCCAATGCTCGAGATAATTTGGAATTTACT 583
Db 121 GTCAATCTCTTTTGGCAATGCTGAGAGACCCCAATGCTCGAGATAATTTGGAATTTACT 180
Qy 584 CCTCTCCATCAAGCTGCAATTTAAAGGAAAGATTGATGTTTGCATTTGCTGTACAGCAT 643
Db 181 CCTCTCCATCAAGCTGCAATTTAAAGGAAAGATTGATGTTTGCATTTGCTGTACAGCAT 240
Qy 644 GGAGCTGAGCCAAACCATCCGAAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCCA 703
Db 241 GGAGCTGAGCCAAACCATCCGAAATACAGATGGAGGACAGCATTTGGATTTAGCAGATCCA 300
Qy 704 TCTGCCAAAGCAGTGTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTCCAGG 763
Db 301 TCTGCCAAAGCAGTGTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTCCAGG 360
Qy 764 AGTGGCAATGAAGAAAATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACGCA 823
Db 361 AGTGGCAATGAAGAAAATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACGCA 420
Qy 824 AGTGATGGCAAGAAAGTCAACTCCATTACATTTTGGCAGCAGGATATAACAGAGTAAAGATT 883
Db 421 AGTGATGGCAAGAAAGTCAACTCCATTACATTTTGGCAGCAGGATATAACAGAGTAAAGATT 480
Qy 884 GTACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTAAAGATAAGAGTGTCTGGTA 943
Db 481 GTACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTAAAGATAAGAGTGTCTGGTA 540
Qy 944 CCATTACACAATGCTCTCTTATGCTCATTTCAAGTAACTGAACCTTTTGGTCAAGCAT 1003
Db 541 CCATTACACAATGCTCTCTTATGCTCATTTCAAGTAACTGAACCTTTTGGTCAAGCAT 600
Qy 1004 GGTGCTGTGTAAATGCAATGGACTTGTGGCAATTTCACTCTCTTCATGAGGCAAGTCTCT 1063
Db 601 GGTGCTGTGTAAATGCAATGGACTTGTGGCAATTTCACTCTCTTCATGAGGCAAGTCTCT 660

Db 2821 GAAAGATACACTACCGGAGAAAGAGTTCTTGAAGAAACCAACCATGCCAATGAA 2880
Qy 3284 CGAATGCTATTTCATGGGTCTCTCTTTGTGAATCAATATTCACAAAGGCTTTGATGAA 3343
Db 2881 CGAATGCTATTTCATGGGTCTCTCTTTGTGAATCAATATTCACAAAGGCTTTGATGAA 2940
Qy 3344 AGGCATCGGTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTTGTGAAACCTCTCC 3403
Db 2941 AGGCATCGGTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTTGTGAAACCTCTCC 3000
Qy 3404 AAAAGCAATCAATGATGATATGAAATTTGGAGAGGTACTGGGTCTCCAGTTCACAAAGAC 3463
Db 3001 AAAAGCAATCAATGATGATATGAAATTTGGAGAGGTACTGGGTCTCCAGTTCACAAAGAC 3060
Qy 3464 AGATCTTGTATACATTTCCACAGGACGTCTCTTTTGGCGGTPAACCTTTGGGAAAGTCT 3523
Db 3061 AGATCTTGTATACATTTCCACAGGACGTCTCTTTTGGCGGTPAACCTTTGGGAAAGTCT 3120
Qy 3524 TTCTGTCAGTTCAAGTGAATGGAATGGCACATTTCTCTCCAGGTCACTCACTCACTCACT 3583
Db 3121 TTCTGTCAGTTCAAGTGAATGGAATGGCACATTTCTCTCCAGGTCACTCACTCACTCACT 3180
Qy 3584 GGTAGGCCAGTGAATGGCTAGCATTTAGCTGAATATGTTATTACAGAGGAGAACAG 3643
Db 3181 GGTAGGCCAGTGAATGGCTAGCATTTAGCTGAATATGTTATTACAGAGGAGAACAG 3240
Qy 3644 GCTTATCTCGTATTTAAATTTACTTACCAGATTTAGGCGCTGAAGGTATGGTTCGATGGA 3703
Db 3241 GCTTATCTCGTATTTAAATTTACTTACCAGATTTAGGCGCTGAAGGTATGGTTCGATGGA 3300
Qy 3704 TAAATAGTATTTAAGAACTAATTCACATGAACCTTAAATATCAATCAAGCAGAGTGGC 3763
Db 3301 TAAATAGTATTTAAGAACTAATTCACATGAACCTTAAATATCAATCAAGCAGAGTGGC 3360
Qy 3764 CTCTACGTTTACTCTCTTGTGTAAGAAAAA 3797
Db 3361 CTCTACGTTTACTCTCTTGTGTAAGAAAAA 3394

RESULT 9
US-09-350-982C-3
; Sequence 3, Application US/09350982C
; Patent No. 6455290
; GENERAL INFORMATION:
; APPLICANT: Berthelsen, Jens
; APPLICANT: Toma, Salvatore
; APPLICANT: Isacchi, Antonella
; TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, and Methods Rela
; TITLE OF INVENTION: Same
; FILE REFERENCE: PHRM-0043
; CURRENT APPLICATION NUMBER: US/09/350,982C
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4512
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PCR Primers
; NAME/KEY: misc_feature
; LOCATION: (1124)..(1124)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc_feature
; LOCATION: (2672)..(2672)
; OTHER INFORMATION: n is any nucleic acid
US-09-350-982C-3

Query Match 89.1%; Score 3382.8; DB 3; Length 4512;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3381; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 403 AGGTTTTGGCGGAGAACGATGTTGAATATTTGCTTCAGNATGGTGCAGATGTCGAAGC 462

Db 220 AGGTTTTGGCGGAGAACGATGTTGAATATTTGCTTCAGNATGGTGCAGATGTCGAAGC 279
Qy 463 ACGTGATGATGGGGCCCTTATTCCTCTTTCAATATGATGCTCTTTTGGTCAATGCTGAAGT 522
Db 280 ACGTATGATGGGGCCCTTATTCCTCTTTCAATATGATGCTCTTTTGGTCAATGCTGAAGT 339
Qy 523 AGTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAAATTTGGAATTTATAC 582
Db 340 AGTCAATCTCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAAATTTGGAATTTATAC 399
Qy 583 TCCTCTCCATGAAAGCTCAATTTAAAGGAAAGATTTGATGTTTGGCATTTGCTGTTTACAGCA 642
Db 400 TCCTCTCCATGAAAGCTCAATTTAAAGGAAAGATTTGATGTTTGGCATTTGCTGTTTACAGCA 459
Qy 643 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 702
Db 460 TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATCC 519
Qy 703 ATCTGCCAAAGCAGTGTCTTACTGTGTAATTAAGAAAGATGAACTCTTAGNAAAGTCCAG 762
Db 520 ATCTGCCAAAGCAGTGTCTTACTGTGTAATTAAGAAAGATGAACTCTTAGNAAAGTCCAG 579
Qy 763 GAGTGGCAATGAAAGAAAAATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACGC 822
Db 580 GAGTGGCAATGAAAGAAAAATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACGC 639
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Qy 943 ACCAATTACACAATGCCCTGTTCTTATGTCATTTAAGAGTAACTGAACTTTTGGTCAAGCA 1002
Db 760 ACCAATTACACAATGCCCTGTTCTTATGTCATTTAAGAGTAACTGAACTTTTGGTCAAGCA 819
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Db 1180 GCTAAGAAAAAGGAGCAACATCAATGAAAAAGACTTAAAGAAATTTTGTACTCTCTGCAAGT 1239
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Db 1420 CTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAATCTCTCCAAAGGGTATCTC 1479
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Db 1480 ATTAGGTAAATTCAGAGGACAGACAGCAATTTGCTGGAAGCTGCAAAAGGCTGAGATGTGGA 1539
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Qy 1843 ACAGCATGGAGCTGATGTGATGTCTAAAGATAAAGAGGCGCTTGATCTTTTGCACAATGC 1902
Db 1660 ACAGCATGGAGCTGATGTGATGTCTAAAGATAAAGAGGCGCTTGATCTTTTGCACAATGC 1719
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Qy 1963 TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
Db 1780 TGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 1839
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Db 1840 AATTTGCAAACTTTGCTCCAGCTGGTGCAGACCTTACCAAAAAAACAAGGATGGAAA 1899
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Db 1900 TACTCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGGAGA 1959
Qy 2143 TGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTCTTC 2202
Db 1960 TGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTCTTC 2019
Qy 2203 TCCTGATTAATGTAAATGTCGCGATACCCAGGCGAGACATTCACACCTTTTACATTTAGC 2262
Db 2020 TCCTGATTAATGTAAATGTCGCGATACCCAGGCGAGACATTCACACCTTTTACATTTAGC 2079
Qy 2263 AGCTGGTTTAAATTTAGAGTTGCAAGTATTTGTTTACACACGAGCTGATGTGAA 2322
Db 2080 AGCTGGTTTAAATTTAGAGTTGCAAGTATTTGTTTACACACGAGCTGATGTGAA 2139
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Db 2140 TGCCCAAGCAAAAGGAGACTTTATCTTTTACATAATGCAGCATCTTACGGCGATGTAGA 2199
Qy 2383 TGTAGCAGCTCTACTAATAAGTATAATGCAATGTCTCAATGCCAGCAAAATGGGCTTT 2442
Db 2200 TGTAGCAGCTCTACTAATAAGTATAATGCAATGTCTCAATGCCAGCAAAATGGGCTTT 2259
Qy 2443 CACACCTTTGACGAGAGCCCAAAAGGAGCAACAGCTTTGCTTTGTTGCTAGC 2502
Db 2260 CACACCTTTGACGAGAGCCCAAAAGGAGCAACAGCTTTGCTTTGTTGCTAGC 2319
Qy 2503 CCATGGAGCTGACCCGACTCTTTTAAATAATCAGGAAGCAAAACCTTTAGATTTT 2562
Db 2320 CCATGGAGCTGACCCGACTCTTTTAAATAATCAGGAAGCAAAACCTTTAGATTTT 2379
Qy 2563 AGCGGATGATGTACGCTCTTTCTGACAGCAGCCATGCCCCCATCTGCTGCCCTTTG 2622
Db 2380 AGCGGATGATGTACGCTCTTTCTGACAGCAGCCATGCCCCCATCTGCTGCCCTTTG 2439

Qy 2623 TTACAAGCCTCAAGTGTCTCAATGTGTGAGAGCCAGAGCCACTGCAGATGCTCTCTC 2682
Db 2440 TTACAAGCCTCAAGTGTCTCAATGTGTGAGAGCCAGAGCCACTGCAGATGCTCTCTC 2499
Qy 2683 TTTAGGTCCATCTAGCCCCATCAAGCCTTTTTCAGCCAGCAGTCTTGCAAACTTATCTGG 2742
Db 2500 TTTAGGTCCATCTAGCCCCATCAAGCCTTTTTCAGCCAGCAGTCTTGCAAACTTATCTGG 2559
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Qy 2803 GGAGAAAAGAGGAGTCTCCAGGAGTAGATTTTTCAGCATAACTCAATTCGTAAGCAATCTTGG 2862
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Qy 2863 ACTTGAGCACCTAATGTGATATATTTTGAGAGAGAAACAGATCACTTTTGGATGTATTAGTTGA 2922
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Db 3220 CAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTGGGTGTCCAGTTCAAAAGA 3279
Qy 3463 CAGATCTTTGTACATTTTGCACAGGAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3522
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Qy 3523 TTTCTCGCAGTTTCAAGTGAATGGAATGGCACTTCTCTCCAGGTCACTCACTCAGTCAC 3582
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Qy 3643 GGCTTATCTCGAGTATTTTATTTACTTACCAGATTTAGGGCTGAAGGTATGGTTCGATGG 3702
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Db 3580 CCTCTACGTTTACTCTCTTCTGCTGAAAAAAA 3611

RESULT 10
US-09-350-982C-4
; Sequence 4, Application US/09350982C
; Patent No. 6455290
; GENERAL INFORMATION:
; APPLICANT: Berthelsen, Jens
; APPLICANT: Toma, Salvatore
; APPLICANT: Isacchi, Antonella
; TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, and Methods Rel
; TITLE OF INVENTION: Same
; FILE REFERENCE: PHRM-0043
; CURRENT APPLICATION NUMBER: US/09/350,982C
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 3498
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PCR Primers
; NAME/KEY: CDS
; LOCATION: (1)..(3498)
; NAME/KEY: misc feature
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (1102)..(1102)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (2650)..(2650)
; OTHER INFORMATION: n is any nucleic acid
US-09-350-982C-4

Query Match 86.7%; Score 3291.8; DB 3; Length 3498;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3290; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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Qy 463 ACGTGATGATGGGGCCCTTATTCCTCTTCAATATGCAATGCTCTTTTGGTCAATGCTGAAGT 522
Db 258 ACGTGATGATGGGGCCCTTATTCCTCTTCAATATGCAATGCTCTTTTGGTCAATGCTGAAGT 317
Qy 523 AGTCAATCTCTTTTGGACATGTGACAGCCCAATGCTCGATATTAATGGAATTATAC 582
Db 318 AGTCAATCTCTTTTGGACATGTGACAGCCCAATGCTCGATATTAATGGAATTATAC 377
Qy 583 TCCTCTCCATGAAGCTGCAATTAAGGAAAGATTTGCTTTGCAATTTGCTGTGTACAGCA 642
Db 378 TCCTCTCCATGAAGCTGCAATTAAGGAAAGATTTGCTTTGCAATTTGCTGTGTACAGCA 437
Qy 643 TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTAGCAGATCC 702
Db 438 TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTAGCAGATCC 497
Qy 703 ATCTGCCAAAGCAGTGTCTTCTGCTGATTAAGAAAGATCAATCTTAGAAAGTGCAG 762
Db 498 ATCTGCCAAAGCAGTGTCTTCTGCTGATTAAGAAAGATCAATCTTAGAAAGTGCAG 557
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Qy 943 ACCATTACACAATGCCTGTTCTTATGGTCAATTAAGAAAGTAACTGAACTTTTGGTCAAGCA 1002
Db 738 ACCATTACACAATGCCTGTTCTTATGGTCAATTAAGAAAGTAACTGAACTTTTGGTCAAGCA 797
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Db 798 TGGTGCCCTGTGTAATGCAATGGCAATTCATGCGCAATTCACCTCTTTCATGAGGAGCTTC 857
Qy 1063 TAAGAACAGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGCAGACCCCAACACTGCT 1122
Db 858 TAAGAACAGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGCAGACCCCAACACTGCT 917
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Db 1458 ATTAGGTAATTCAGAGCAGACAGACAAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCGA 1517
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Db 1518 AACTGTAAAAAACTGTGTACTGTTTCAAGTGTCAACTGCAGAGACATTTGAAGGCGCTCA 1577
Qy 1783 GTCTACACCACTTCATTTTTCAGCTGGGTATTAACAGAGTGTCCGTGGTGAATATCTGCT 1842
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DB 1758 TGTAGCTGATTTATGGAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA 1817
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DB 1818 AATTTGCAAACTTCTGCTCCAGCATGTTGCAGACCTTACCAAAAAAACAAGGATGGAAA 1877
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DB 2058 AGCTGGTTATATAATTTAGAAAGTTGCAGAGTATTTGTTTACAACGAGGCTGATGAA 2117
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DB 2178 TGTAGCAGCTCTACTAATAAAGTAAATGTCATGTCTCAATGCCAGGACAAATGGCTTT 2237
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DB 2718 GATGGGCACAGGAGCTGAGGAGATGGAATCAATGCTTATGACATAGGCACAACT 2777
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DB 2778 AATTAAGGAGTCGAGAGACTTATCTCCGACAAACAGGCTTTAAACCATATTTAACTTT 2837
QY 3043 GAAACACCTCTGTTAGTGGACAAATTTCTATAGATCTGCTCTCTGATGAAGAGTTTCA 3102
DB 2838 GAAACACCTCTGTTAGTGGACAAATTTCTATAGATCTGCTCTCTGATGAAGAGTTTCA 2897
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DB 2958 TGGAAATCTTCAACAGATACAAATATTTCTCAAGATTCAGAAAGTTTGTAAACAAGAACTATG 3017
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QY 3703 A 3703
DB 3498 A 3498

RESULT 11
US-09-972-115A-1
; Sequence 1, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4493

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Qy 1963 TGATGCTGATTTATGGAAATTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
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Qy 2377 TGTAGATGTAGCAGCTCTACTATAAAGTATAATGTCATGTCATGTCACGACCAATG 2436
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Db 3252 CAATTAATTAAGAGGCTGAGAGACTTATCTCCGGACAAACAAAGTCTTAAACCCATATTT 3311
Qy 3037 AACTTTGAACACCTCTGGTAGTGAACAAATTTCTTATAGATCTGCTCTGATGATAAGA 3096
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RESULT 12
US-09-972-115A-3
; Sequence 3, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Platydzek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972.115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4297
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3801)
; OTHER INFORMATION:
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; OTHER INFORMATION: in to provide alignment.
; NAME/KEY: misc_feature
; LOCATION: (711)..(713)
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QY	DB	444	ATGGTCAAGTGTCCAAGCAGTCATGATGGGGCCCTATTTCCTTCATAATGCGATGCT	503	Unknown residue put
QY	DB	536	ATGGTCAAGTGTCCAAGCAGTCATGATGGGGCCCTATTTCCTTCATAATGCGATGCT	595	Unknown residue put
QY	DB	504	CTTTTGGTGCATGCTGAAGTAGTCAATCTCCTTTTGGCAGCATGGTGCAGACCCCAATGCTC	563	Unknown residue put
QY	DB	596	CTTTTGGTGCATGCTGAAGTAGTCAATCTCCTTTTGGCAGCATGGTGCAGACCCCAATGCTC	655	Unknown residue put
QY	DB	564	GAGATAATTGGAATTATATCTCTCTCCATGAAGTGCAGTTAAAGGAAAGATTGATGTTT	623	Unknown residue put
QY	DB	656	GAGATAATTGGAATTATATCTCTCCATGAAGTGCAGTTAAAGGAAAGATTGATGTTT	715	Unknown residue put
QY	DB	624	GCATTGGTGTTCACAGCATGGAGCTGAGCCCAACCATCCGAAATACAGATGGGAGGACAG	683	Unknown residue put
QY	DB	716	GCATTGGTGTTCACAGCATGGAGCTGAGCCCAACCATCCGAAATACAGATGGGAGGACAG	775	Unknown residue put
QY	DB	684	CATTGGATTATAGCAGATCCCATCTCCCAAGCAGTGTCTTACTGGTGAATATAAGAAAGATG	743	Unknown residue put

Db 1856 GAGACATTGAAGGGCTCAGTCTACACA CACTTCAATTTTTCAGCTGGGTATTAACAGAGTGT 1915
Qy 1824 CCGTGGTGAATATCTGCTACAGCATGGAGCTGATGTGCATGCTCTAAAGATAAAGAGGCC 1883
Db 1916 CCGTGGTGAATATCTGCTACAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGAGGCC 1975
Qy 1884 TTGTACCTTTGCACATGCATGTTCTTATGACATATTAAGAGTTGCAGAACTTCTTGTTA 1943
Db 1976 TTGTACCTTTGCACATGCATGTTTNTATGACATATTAAGAGTTGCAGAACTTCTTGTTA 2035
Qy 1944 AACATGGAGCAGTAGTTAATGTAGCTGATTTATGAAATTTTACACCTTTTACATGAAGCAG 2003
Db 2036 AACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAG 2095
Qy 2004 CAGCAAAAGGAAAATATGAAATTTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCA 2063
Db 2096 CAGCAAAAGGAAAATATGAAATTTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCA 2155
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Qy 2304 AACCGAGCTGATGTGAATGCCCAAGACAAGAGGACTTATTCTTTACATAATGCAG 2363
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Qy 2424 CCAGGACAAATGGCTTTTACACCTTTGCAGAGAGGCCCAAGAGGACGACAGC 2483
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Qy 2604 CATCTGCTCTGCCCTCTGTTTCAAGCCCTCAAGTGTCTCAATGGTGTGAGAGCCAGGAG 2663
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RESULT 13
US-09-196-387-1
; Sequence 1, Application US/09196387
; Patent No. 6277613
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

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; ADDRESSES: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,387
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,225
; FILING DATE: June 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4134 base pairs
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; STRANDEDNESS: double
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; US-09-196-387-1

Query Match 47.8%; Score 1813.4; DB 3; Length 4134;
Best Local Similarity 72.3%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 891; Indels 27; Gaps 2;

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1883 CTGTGTACCTTTGCACAATGCTGTTCTTATGACATTAATGAGTTGTCAGAACTTCTTGT 1942
2157 TTGTGTCCTTTTCAATATGCTGTTTATGACACTATGAGTGGCTGAGCTTTTAGTA 2216
1943 AAACATGAGCAGTAGTTAATGATGCTGATTTATGGAATTTTACACCTTTTACATGAAGCA 2002

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Db 2337 AAAAAAGAACAGAGATGGAAATACACCTTTGGATTTGGTAAAGGAGGAGACACAGATATT 2396
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RESULT 14

US-09-841-835-1
; Sequence 1, Application US/09841835
; Patent No. 6506587
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841.835
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2006, 17:00:29 ; Search time 3854.36 Seconds
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12104.784 Million cell updates/sec

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Perfect score: 3797

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3388.8	89.2	4275	6	US-10-163-587A-14
5	3387.2	89.2	4127	7	US-10-199-937-100
6	3387.2	89.2	4406	7	US-10-199-937-106
7	3387.2	89.2	4992	7	US-10-199-937-134
8	3387.2	89.2	5002	7	US-10-199-937-132
9	3387.2	89.2	5075	8	US-10-302-172-556
10	3387.2	89.2	6018	3	US-09-849-602-11
11	3387.2	89.2	6189	10	US-10-898-653-5
12	3297	85.8	3400	3	US-09-509-196A-1
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20	1813.4	47.8	4134	3	US-09-841-835-1
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ALIGNMENTS

RESULT 1

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; Sequence 1, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossovskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616.101
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-616-101-1

Query Match	100.0%	Score 3797;	DB 10;	Length 3797;
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Matches 3797;	Conservative	0;	Indels	0;
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RESULT 2

US-10-616-101-2

; Sequence 2, Application US/10616101

; Publication No. US20050074825A1

; GENERAL INFORMATION:

; APPLICANT: Luo, Ying

; APPLICANT: Chan, Eva

; APPLICANT: Xu, Xiang

; APPLICANT: Huang, Betty

; APPLICANT: Osovsakaya, Valeria

; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and

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; PRIOR FILING DATE: 2000-10-25

; PRIOR APPLICATION NUMBER: US 09/427,154

; PRIOR FILING DATE: 1999-10-25

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 3816

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-616-101-2

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US-09-972-115A-5
; Sequence 5, Application US/09972115A
; Publication No. US20030032769A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Platysek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4275
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(3781)
; OTHER INFORMATION:
US-09-972-115A-5

Query Match      89.2%; Score 3388.8; DB 3; Length 4275;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 403 AGCTTTTGGCGGAAAGACGTAGTTGAATATTGCTTCAGAAATGCTGCAAGTGTCCAAGC 462
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2281	TCCTGATAATGTTAAATTTGCCGCGATACCCAAGGCACACATTTCAACACCTTTTACATTTAGC	2340
2263	AGCTGGTTATAATAATTTAGAAGTTCAGAGTATTTGTTACAAACGGAGCTCATGTGAA	2322
2341	AGCTGGTTATAATAATTTAGAAGTTCAGAGTATTTGTTACAAACGGAGCTCATGTGAA	2400
2323	TGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGCAGCATCTTTACGGGCATGTAGA	2382
2401	TGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGCAGCATCTTTACGGGCATGTAGA	2460
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3103	GTCTGTGGAGGAAGATGCAAAAGTACAGTTTCGAGAGCAACAGAGATGGAGGTCATGCAGG	3162
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RESULT 4
US-10-163-587A-14
; Sequence 14, Application US/10163587A
; Publication No. US20030096263A1
; GENERAL INFORMATION:
; APPLICANT: Oliveira, Marcos
; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING
; FILE REFERENCE: 50229-306
; CURRENT APPLICATION NUMBER: US/10163,587A
; PRIORITY FILING DATE: 2003-01-10
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 5778
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3501)
; OTHER INFORMATION:
US-10-163-587A-14
Query Match 89.2%; Score 3388.8; DB 6; Length 5778;
Best Local Similarity 99.9%; Pred No. 0;
Matches 3390; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 403 AGGTTTTGGCGGAAAGAGTGTGTAATTTGCTTCAAGATGGTCAAGTGTCCAAGC 462
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Db 3558 CCTCTACGTTTTTACTCCTTTGCTGAAAAAAA 3589
RESULT 5
US-10-199-937-100
; Sequence 100, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 4127
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS (3508)
; LOCATION: (2)..(3508)
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (3509)..(4127)
US-10-199-937-100
Query Match 89.2%; Score 3387.2; DB 7; Length 4127;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 403 AGGTTTTGGCGGAAAGAGCTAGTTGAATATTTGCTTCAGAAATGGTCAAGTGTCCAAAGC 462
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RESULT 6
US-10-199-937-106
; Sequence 106, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKTRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; PRIOR FILING DATE: 2002-07-22
; PRIOR FILING DATE: 2000-06-28
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 4406

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3787)
US-10-199-937-106

Query Match      89.2%; Score 3387.2; DB 7; Length 4406;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 2213 ACAACCTGCGCCCTACTCTGAGCTATGAGTGTGATCTCTAATCAATATATCTCTTCAGGG 2272
QY 1603 CTCTTACTGCTTTTACAGATGGGAAATGAATAATGTAAGTGTGTTGAAGTGTGTTGAAGTGTGTT 1662
DB 2273 CTCTTACTGCTTTTACAGATGGGAAATGAATAATGTAAGTGTGTTGAAGTGTGTTGAAGTGTGTT 2332
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DB 2393 AACTGTAAAAAACHTGTGTACTGTTTCAAGTGTCAACTGCGAGACATTTGAAGGGCGTCA 2452
QY 1783 GTCTACACCACTTTCATTTTTCAGCTGGGTATATAACAGAGTGTCCGTTGGTGAATATCTGCT 1842

DB 2453 GTCTACACCACTTTCATTTTTCAGCTGGGTATATAACAGAGTGTCCGTTGGTGAATATCTGCT 2512
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QY 1903 ATGTTCTTATGGACATTAATGAAGTGTGCAAACTTCTTGTAAACATGAGCAGATGTTAA 1962
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3593	GATGGGSCACAAGGAGCTGAAGGAGATTGGAATCAATGCTTTATGGACATAGGCACAACT	3652
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3773	GTCTGTGGAGGAAGAGATGCAAAAGTAGCAGTTTCGAGAGCACAGAGATGGAGGTCATGCAGG	3832
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4253	TGGTAGCCCAAGTGAATGGCCTAGCATTTAGCTGAATATGTTATTTTACAGAGGAGAACAC	4312
3643	GGCTTATCTCTGAGTATTTAAATTAATCTTACCAGATTTATGAGGCTTGAAGGTTATGGTCGATGG	3702
4313	GGCTTATCTCTGAGTATTTAAATTAATCTTACCAGATTTATGAGGCTTGAAGGTTATGGTCGATGG	4372
3703	ATAAATAGTTATTTTAAAGAACTAATTTCCACTGAACTTAAATCATCAAAAGCAGCAGTGG	3762
4373	ATAAATAGTTATTTTAAAGAACTAATTTCCACTGAACTTAAATCATCAAAAGCAGCAGTGG	4432
3763	CCTCTAGCTTTTACTCTCTTTGCTGAAAAAAA	3794
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; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 132
; LENGTH: 5002
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (229)..(4383)
; US-10-199-937-132

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Query Match		89.2%	Score 3387.2	DB 7	Length 5002	
Best Local Similarity		99.9%	Pred. No. 0			
Matches 3389		Conservative 0	Mismatches 3	Indels 0	Gaps 0	
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Db	1083	AGGTTTGGCGCAAGACGTAGTGTGAATATTTGCTTCAGAAATGGTGCAAAATGTCCNAGC	1142			
Qy	463	ACGTGATGATGGGGGCGCTTATTCCTCTTCATAATGCATGCTCTTTTGGTCATGCTGAAGT	522			
Db	1143	ACGTGATGATGGGGGCGCTTATTCCTCTTCATAATGCATGCTCTTTTGGTCATGCTGAAGT	1202			
Qy	523	AGTCAATCTCTTTTGGGACATGGTGAGACCCCAATGCTCGAGATAATTTGGAATATATAC	582			
Db	1203	AGTCAATCTCTTTTGGGACATGGTGAGACCCCAATGCTCGAGATAATTTGGAATATATAC	1262			
Qy	583	TCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGCAATTGTGCTGTTCACAGCA	642			
Db	1263	TCCTCTCCATGAAGCTGCAATTAAAGGAAAGATTGATGTTTGCAATTGTGCTGTTCACAGCA	1322			
Qy	643	TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCAATGGATTTAGCAGATCC	702			
Db	1323	TGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCAATGGATTTAGCAGATCC	1382			
Qy	703	ATCTGCCAAAGCAGTGCTTACTGGTGAATATAGAAGAATGAATCTCTTAGAAGTGCCAG	762			
Db	1383	ATCTGCCAAAGCAGTGCTTACTGGTGAATATAGAAGAATGAATCTCTTAGAAGTGCCAG	1442			
Qy	763	GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACCAATAAATGTCAACTGCCACGC	822			
Db	1443	GAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACCAATAAATGTCAACTGCCACGC	1502			
Qy	823	AAGTGATGGCAGAAAGTCAACTCCAATTAATTTGGCAGCAGGATATAACAGATTAAGAT	882			
Db	1503	AAGTGATGGCAGAAAGTCAACTCCAATTAATTTGGCAGCAGGATATAACAGATTAAGAT	1562			
Qy	883	TGTACAGCTGTTACTGCCAATCGAGCTGATGCCATGCTTAAAGATAAAGTGATCTGCT	942			
Db	1563	TGTACAGCTGTTACTGCCAATCGAGCTGATGCCATGCTTAAAGATAAAGTGATCTGCT	1622			
Qy	943	ACCAATTACAATAGCCCTGTTCTTATGGTCAATTATGAAGTAACTGAACTTTTGGTCAAGCA	1002			
Db	1623	ACCAATTACAATAGCCCTGTTCTTATGGTCAATTATGAAGTAACTGAACTTTTGGTCAAGCA	1682			
Qy	1003	TGTTGCTGTGTAAATGCAATGGACTGTGGCAATTCACCTCTCTTCATGAGGACGCTTC	1062			
Db	1683	TGTTGCTGTGTAAATGCAATGGACTGTGGCAATTCACCTCTCTTCATGAGGACGCTTC	1742			
Qy	1063	TAAGACAGGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGCAGACCCCAACACTGCT	1122			
Db	1743	TAAGACAGGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGCAGACCCCAACACTGCT	1802			
Qy	1123	CAATTGTCAAAATAAAGTGCTATAGACTTTGGCTCCCAACCAACAGTTAAAGAAAGATT	1182			
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RESULT 8
US-10-199-937-132
; Sequence 132, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: Mceilligott, David L.
; TITLE OF INVENTION: TANKYBASE2 MATERIALS AND METHODS

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1983 AGCATGCAATGCTGCTGCAATCTCCATATCCCAAGAAAGCAATATGTTGAACTGTT 2042
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1603 CTTTACTGCTTTACAGATGGGAAATGAAATGATGATACAGCAACTCTCTCAAGAGGGTATCTC 1662
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2463 GTCTACACCACTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT 2522
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2523 ACAGCATGAGCTGATGCTCATGCTTAAGATAAAGAGAGCCCTTGTACCTTTGCACATGC 2582
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2583 ATGTTCTTATGACATTATGAAGTTGCAGAACTTCTTGTAAACATGGAGCAGTAGTTAA 2642
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2143 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTTGTAGCCAGAGTGAAGTGTCTTC 2202
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2203 TCCTGATTAATGTAATGTCGGGATACCCAGGCGACATTCACACCTTTTACATTTAGC 2262
2883 TCCTGATTAATGTAATGTCGGGATACCCAGGCGACATTCACACCTTTTACATTTAGC 2942

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3903 GGAAGATACACTCAACCGGAGAAAGAGTTTCTGAAGAAACCAACACCTATGCAATGA 3962
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3963 AGCAATGCTATTTCAATGGTCTCTTTTGTGAATCAATTTATCCCAAGAGGTTTATGA 4022
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Db 4443 CCTCTACGTTTACTCCTTTGCTGAAAAAAA 4474

RESULT 9

US-10-302-172-556
; Sequence 556, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids an
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803 ICNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 556
; LENGTH: 5075
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(3750)
US-10-302-172-556

Query Match 89.2%; Score 3387.2; DB 8; Length 5075;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 450 AGGTTTGGCGGAAAGACGTAGTGTGATATTTGCTTCAAAATGGTGAAATGTCCCAAGC 509
Qy 463 ACGTGATGATGGGGCCCTTATTCCTCTTCAATATGCTGCTCTTTTGGTCTATGCTGAAGT 522
Db 510 ACGTGATGATGGGGCCCTTATTCCTCTTCAATATGCTGCTCTTTTGGTCTATGCTGAAGT 569

Qy 523 AGTCAATCTCTTTTGGCAGCATGGTGCAGACCCCAATGCTCGAGATAAATTGGAATTATAC 582
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Db 990 ACCATTACAAATGCTGTTCTTTATGGTCAATATGAAAGTAACTGAACTTTTGGTCAAGCA 1049
Qy 1003 TGGTGCCTGTGTAATAATGCAATGGAATTTGTGGCAATTCACCTCTCTCATGAGGAGCTTC 1062
Db 1050 TGGTGCCTGTGTAATAATGCAATGGAATTTGTGGCAATTCACCTCTCATGAGGAGCTTC 1109
Qy 1063 TAAGAACAGGGTGAAGTATGTTCTCTCTTAAAGTATTTGGTGCAGACCCCAACACTGCT 1122
Db 1110 TAAGAACAGGGTGAAGTATGTTCTCTCTTAAAGTATTTGGTGCAGACCCCAACACTGCT 1169
Qy 1123 CAATTGTCACAATAAAGTGTCTATAGACTTTGGCTCCCAACACCAAGTATAAAGAAAGATT 1182
Db 1170 CAATTGTCACAATAAAGTGTCTATAGACTTTGGCTCCCAACACCAAGTATAAAGAAAGATT 1229
Qy 1183 AGCATATGAATTTAAAGGCACTGTTGCTGCAAGCTGCAAGAGCTGATGTTACTCG 1242
Db 1230 AGCATATGAATTTAAAGGCACTGTTGCTGCAAGCTGCAAGAGCTGATGTTACTCG 1289
Qy 1243 AATCAAAAACATCTCTCTCTGGAATTTGGAATTTCAAGCATCTCTCAAAACACATGAAC 1302
Db 1290 AATCAAAAACATCTCTCTCTGGAATTTGGAATTTCAAGCATCTCTCAAAACACATGAAC 1349
Qy 1303 AGCATTCATTTGCTGCTGCTGCTCATCTCCATATCCCAAAAGAAAGCAAAATATGTAACCTGT 1362
Db 1350 AGCATTCATTTGCTGCTGCTGCTCATCTCCATATCCCAAAAGAAAGCAAAATATGTAACCTGT 1409
Qy 1363 GCTAAGAAAAAGGCAAAACATCAATGAAAGAGACTAAAGAAATTTCTTGACTCTCTGACGT 1422
Db 1410 GCTAAGAAAAAGGCAAAACATCAATGAAAGAGACTAAAGAAATTTCTTGACTCTCTGACGT 1469
Qy 1423 GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAAAGGT 1482
Db 1470 GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAAGCAAAAGGT 1529
Qy 1483 TAATGCTCTGATTAATCTTGGTCAAGCTCTCTACACAGAGCTGCATATTTGGTCACTCT 1542
Db 1530 TAATGCTCTGATTAATCTTGGTCAAGCTCTCTACACAGAGCTGCATATTTGGTCACTCT 1589
Qy 1543 ACAAACCTGCGGCTACTCTGAGCTATGGGTGTGATCCTTAACATTTATATATCCCTTCAGGG 1602
Db 1590 ACAAACCTGCGGCTACTCTGAGCTATGGGTGTGATCCTTAACATTTATATATCCCTTCAGGG 1649

1603 QY CTTTACTGCTTTTACAGATGGGAAATGAAATGTCACAGCAATCTCTCCAGAGGGTATCTC 1662
1650 Db CTTTACTGCTTTTACAGATGGGAAATGAAATGTCACAGCAATCTCTCCAGAGGGTATCTC 1709
1663 QY ATTAGGTAAATTCAGAGGCGAGACAGACAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGTGGA 1722
1710 Db ATTAGGTAAATTCAGAGGCGAGACAGACAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGTGGA 1769
1723 QY TACTGTAAAAAATCTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCA 1782
1770 Db TACTGTAAAAAATCTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCA 1829
1783 QY GTCTACACCACTCTCAATTTTGCAGCTGGGTATTAACAGAGTGTCCGTGGTGGAAATATCTGCT 1842
1830 Db GTCTACACCACTCTCAATTTTGCAGCTGGGTATTAACAGAGTGTCCGTGGTGGAAATATCTGCT 1889
1843 QY ACAGATGGAGCTGATGTGTCATGCTTAAGATTAAGAGGAGGCTTTGACCTTTGCGACAATGC 1902
1890 Db ACAGATGGAGCTGATGTGTCATGCTTAAGATTAAGAGGAGGCTTTGACCTTTGCGACAATGC 1949
1903 QY ATGTTCTTATGACATTAATGAAGTTGCAGAACTCTTGTAAACATGAGGAGTGTAA 1962
1950 Db ATGTTCTTATGACATTAATGAAGTTGCAGAACTCTTGTAAACATGAGGAGTGTAA 2009
1963 QY TGTAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
2010 Db TGTAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2069
2023 QY AATTTGCAAACTTCTGCTCCAGCTGGTGACAGCCCTACCAAAAAAACAAGGATGGAAA 2082
2070 Db AATTTGCAAACTTCTGCTCCAGCTGGTGACAGCCCTACCAAAAAAACAAGGATGGAAA 2129
2083 QY TACTCCTTTGGATCTGTTTAAAGATGGAGATACAGATATTCAGATCTGCTTTAGGGGAGA 2142
2130 Db TACTCCTTTGGATCTGTTTAAAGATGGAGATACAGATATTCAGATCTGCTTTAGGGGAGA 2189
2143 QY TGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTGTAGCCAGGTGAAGAGTTGCTCTTC 2202
2190 Db TGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTGTAGCCAGGTGAAGAGTTGCTCTTC 2249
2203 QY TCCTGATTAATGTAATTTGCTCCGCTATCCCAAGGCGAGACATTCACACCTTTACATTTAGC 2262
2250 Db TCCTGATTAATGTAATTTGCTCCGCTATCCCAAGGCGAGACATTCACACCTTTACATTTAGC 2309
2263 QY AGCTGGTTATTAATTTAGAGTTGCGAGATTTGTTTACACCGGAGCTGATGTGAA 2322
2310 Db AGCTGGTTATTAATTTAGAGTTGCGAGATTTGTTTACACCGGAGCTGATGTGAA 2369
2323 QY TGCCCAAGACAAAGGAGGACTTTATTCCTTTTACATAATGCAGCATCTTACGGGCATGTAGA 2382
2370 Db TGCCCAAGACAAAGGAGGACTTTATTCCTTTTACATAATGCAGCATCTTACGGGCATGTAGA 2429
2383 QY TGTAGCAGCTCTACTAATAAGTATAATGTCATGTCTCAATGCCCGGACAAATGGGCTTT 2442
2430 Db TGTAGCAGCTCTACTAATAAGTATAATGTCATGTCTCAATGCCCGGACAAATGGGCTTT 2489
2443 QY CACACCTTTGCAAGAGCGCCCAAAAGGAGCAACACAGCTTTGCTGTTGCTAGC 2502
2490 Db CACACCTTTGCAAGAGCGCCCAAAAGGAGCAACACAGCTTTGCTGTTGCTAGC 2549
2503 QY CCATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTTAGATTAGTTTC 2562
2550 Db CCATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGACAAACACCTTTTAGATTAGTTTC 2609
2563 QY AGCGGATGATGTACGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTGCCCTCTTG 2622
2610 Db AGCGGATGATGTACGCGCTCTTCTGACAGCAGCCATGCCCCCATCTGCTGCCCTCTTG 2669
2623 QY TTACAGGCTCAAGTGTCTCAATGTTGTGAGAGCCGAGGAGCCACTGCAGATGCTCTCTC 2682
2670 Db TTACAGGCTCAAGTGTCTCAATGTTGTGAGAGCCGAGGAGCCACTGCAGATGCTCTCTC 2729
2683 QY TTCAGGTCATCTAGCCCATCAAGCCTTTCTGACGCCAGCAGTCTTGACAACTTATCTGG 2742

2730 Db TTCAGGTCATCTAGCCCATCAAGCCTTTCTGACGCCAGCAGTCTTGACAACTTATCTGG 2789
2743 QY GAGTTTTTCAAGACTGTCTTTCAGTAGTTAGTTCAAGTGAACAGAGGCTGCTTCCAGTTT 2802
2790 Db GAGTTTTTCAAGACTGTCTTTCAGTAGTTAGTTCAAGTGAACAGAGGCTGCTTCCAGTTT 2849
2803 QY GGAGAAAAGGAGGTTCCAGGAGTAGATTTTGTAGCATAACTCAATTCGTAAAGAACTTTGG 2862
2850 Db GGAGAAAAGGAGGTTCCAGGAGTAGATTTTGTAGCATAACTCAATTCGTAAAGAACTTTGG 2909
2863 QY ACTTGAGCACCTAATGAGATATTTTGTAGAGAGAAACAGATCACTTTTGGATGTAATTGTA 2922
2910 Db ACTTGAGCACCTAATGAGATATTTTGTAGAGAGAAACAGATCACTTTTGGATGTAATTGTA 2969
2923 QY GATGGGCGCAAGGAGCTGAAGGAGATTTGGAATCAATGCTTTATGGACATAGGCACAACT 2982
2970 Db GATGGGCGCAAGGAGCTGAAGGAGATTTGGAATCAATGCTTTATGGACATAGGCACAACT 3029
2983 QY AATTAAAGGAGCTCGAGAGACTTATCTCCGGAACAACAGGCTCTTAACCCATATTTAACTTT 3042
3030 Db AATTAAAGGAGCTCGAGAGACTTATCTCCGGAACAACAGGCTCTTAACCCATATTTAACTTT 3089
3043 QY GAACACCTCTCGTGTAGTGGAAACAATTTCTTTATAGATCTGTCTCTCGATGATAAAGAGTTTCA 3102
3090 Db GAACACCTCTCGTGTAGTGGAAACAATTTCTTTATAGATCTGTCTCTCGATGATAAAGAGTTTCA 3149
3103 QY GTCTGTGGAGAAAGATGCAAAAGTACAGTTTCGAGAGCACAGATGGAGTTCATGCAGG 3162
3150 Db GTCTGTGGAGAAAGATGCAAAAGTACAGTTTCGAGAGCACAGATGGAGTTCATGCAGG 3209
3163 QY TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAAAGTTTGTAAACAAGAACTATG 3222
3210 Db TGGAACTCTTCAACAGATACAAATTTCTCAAGATTCAGAAAGTTTGTAAACAAGAACTATG 3269
3223 QY GGAAGATACACTCAACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCACTATGCCAATGA 3282
3270 Db GGAAGATACACTCAACCGGAGAAAAGAGTTTCTGAAGAAAACCAACCACTATGCCAATGA 3329
3283 QY ACGAATGCTATTTTCAATGGGCTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATGA 3342
3330 Db ACGAATGCTATTTTCAATGGGCTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATGA 3389
3343 QY AAGCATGCGTACATAGGTGTATGTTTGGAGCTGGCAATTTATTTGCTGAAAACCTTTC 3402
3390 Db AAGCATGCGTACATAGGTGTATGTTTGGAGCTGGCAATTTATTTTGTGTAAGAACTTTC 3449
3403 QY CAAAAGCAATCAATATGTAATGGAATTTGGAGGAGTACTGGGTGTCCAGTTTCAAAAAGA 3462
3450 Db CAAAAGCAATCAATATGTAATGGAATTTGGAGGAGTACTGGGTGTCCAGTTTCAAAAAGA 3509
3463 QY CAGATCTTTGTACATTTGCGCACAGGAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3522
3510 Db CAGATCTTTGTACATTTTGGCACAGGAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3569
3523 QY TTTCTCGAGTTCAAGTGAATGAAAATGGCACATTTCTCTCCAGTCACTCACTCACTCACT 3582
3570 Db TTTCTCGAGTTCAAGTGAATGAAAATGGCACATTTCTCTCCAGTCACTCACTCACTCACT 3629
3583 QY TGGTAGGCCCAAGTGTAAATGGCCTTAGCATTAAGTGAATATGTTTATACAGAGGAGAAACA 3642
3630 Db TGGTAGGCCCAAGTGTAAATGGCCTTAGCATTAAGTGAATATGTTTATACAGAGGAGAAACA 3689
3643 QY GGCCTATCTCGAGTATTTTAAATTTACTTACAGATTTAGGGCTGAGGATGTTGCTGATGG 3702
3690 Db GGCCTATCTCGAGTATTTTAAATTTACTTACAGATTTAGGGCTGAGGATGTTGCTGATGG 3749
3703 QY ATAAATAGTATTTTAAAGAACTAATCCACTGAACCTTAAATCATCAAAACAGCAGTGG 3762
3750 Db ATAAATAGTATTTTAAAGAACTAATCCACTGAACCTTAAATCATCAAAACAGCAGTGG 3809
3763 QY CCTCTACGTTTACTCTCTTGTGAAAAAAA 3794

Db	3810	CCTCTACGTTTACTCCTTTGCTGAAAAAAA	3841	
RESULT 10				
US-09-849-602-11				
; Sequence 11, Application US/09849602				
; Publication No. US20030165834A1				
; GENERAL INFORMATION:				
; APPLICANT: Scanlan, Matthew J.				
; APPLICANT: Old, Lloyd J.				
; APPLICANT: Stockert, Elisabeth				
; APPLICANT: Chen, Yao-Tseng				
; TITLE OF INVENTION: Colon Cancer Antigen Panel				
; FILE REFERENCE: L0461/7105 (JRV)				
; CURRENT APPLICATION NUMBER: US/09/849,602				
; CURRENT FILING DATE: 2001-05-04				
; NUMBER OF SEQ ID NOS: 30				
; SOFTWARE: PatentIn version 3.0				
; SEQ ID NO 11				
; LENGTH: 6018				
; TYPE: DNA				
; ORGANISM: Homo sapien				
US-09-849-602-11				
Query Match 89.2%; Score 3387.2; DB 3; Length 6018;				
Best Local Similarity 99.9%; Pred. No. 0;				
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
Qy	403	AGGTTTTGGCGGAAAGACGTAGTGTGAATATTTGCTTCAGAAATGGTCAAGTGTCCAAAGC	462	
Db	418	AGGTTTTGGCGGAAAGACGTAGTGTGAATATTTGCTTCAGAAATGGTCAAGTGTCCAAAGC	477	
Qy	463	ACGTGATGATGGGGCCCTTATTCCTCTTCAATATGCAATGCTCTTTGGTCAATGCTGAAGT	522	
Db	478	ACGTGATGATGGGGCCCTTATTCCTCTTCAATATGCAATGCTCTTTGGTCAATGCTGAAGT	537	
Qy	523	AGTCNAATCTCTTTTGGACATGCTGCGACATCCCAATGCTCGAGATTAATGGAAATTATAC	582	
Db	538	AGTCNAATCTCTTTTGGACATGCTGCGACATCCCAATGCTCGAGATTAATGGAAATTATAC	597	
Qy	583	TCCTCTCCATCAAGCTGCAATTTAAAGGAAAGATTGATGTTTGGCATTTGCTGTGTACAGCA	642	
Db	598	TCCTCTCCATCAAGCTGCAATTTAAAGGAAAGATTGATGTTTGGCATTTGCTGTGTACAGCA	657	
Qy	643	TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGATAGAGATCC	702	
Db	658	TGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGATAGAGATCC	717	
Qy	703	ATCTGCCAAAGCAGTCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCCAG	762	
Db	718	ATCTGCCAAAGCAGTCTTACTGGTGAATATAAGAAAGATGAACTCTTAGAAAGTGCCAG	777	
Qy	763	GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACGC	822	
Db	778	GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTTAAATGTCAACTGCCACGC	837	
Qy	823	AAGTGATGGCAGAAAGTCAATCCCATTTACATTTGGCAGCAGGATATACAGAGTAAAGAT	882	
Db	838	AAGTGATGGCAGAAAGTCAATCCCATTTACATTTGGCAGCAGGATATACAGAGTAAAGAT	897	
Qy	883	TGTACAGCTGTACTGGCAACATGGAGCTGATGTCATGCTTAAGATAAGGTGATCTGGT	942	
Db	898	TGTACAGCTGTACTGGCAACATGGAGCTGATGTCATGCTTAAGATAAGGTGATCTGGT	957	
Qy	943	ACCATTAACAATGCTGCTTCTTATGGTCAATATGAAGTAACTGAATTTTGGTCAAGCA	1002	
Db	958	ACCATTAACAATGCTGCTTCTTATGGTCAATATGAAGTAACTGAATTTTGGTCAAGCA	1017	
Qy	1003	TGGTGCCTGTGTAATGCAATGGACTTGTGGCAATTCATCTCTCTTCATAGGAGGCTTC	1062	
Db	1018	TGGTGCCTGTGTAATGCAATGGACTTGTGGCAATTCATCTCTCTTCATAGGAGGCTTC	1077	
Qy	1063	TAAGNACAGGGTTGAAGTATGTTCTTCTTCTTAAGTTATGGTGCAGACCCACACTGCT	1122	

Db	1078	TAAGAACAGGGTTGAAGTATGTTCTTCTTCTTAAGTTATGGTGCAGACCCACACTGCT	1137	
Qy	1123	CAATTGTCACAATAAAAGTCTATAGACTTTGGTCCACACCAAGTAAAGAAAGATT	1182	
Db	1138	CAATTGTCACAATAAAAGTCTATAGACTTTGGTCCACACCAAGTAAAGAAAGATT	1197	
Qy	1183	AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAGAACTGATGTTACTCG	1242	
Db	1198	AGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAGAACTGATGTTACTCG	1257	
Qy	1243	AATCAAAAAACATCTCTCTGGAATATGGTGAATTTCAAGCATCTCAAAACACATGAAAC	1302	
Db	1258	AATCAAAAAACATCTCTCTGGAATATGGTGAATTTCAAGCATCTCAAAACACATGAAAC	1317	
Qy	1303	AGCATTCGATTTGCTGCTGCTCATCTCCATATCCCAAGAAAGCAAAATATGTAACATGTT	1362	
Db	1318	AGCATTCGATTTGCTGCTGCTCATCTCCATATCCCAAGAAAGCAAAATATGTAACATGTT	1377	
Qy	1363	GCTAAGAAAAAGGAGCAAAACATCAATGAAGAACTTAAAGAAATTTCTTGACTCCTCTGCAAGT	1422	
Db	1378	GCTAAGAAAAAGGAGCAAAACATCAATGAAGAAAGCTTAAAGAAATTTCTTGACTCCTCTGCAAGT	1437	
Qy	1423	GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAAAGGT	1482	
Db	1438	GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAAAGGT	1497	
Qy	1483	TAATGCTCTGGAATAATCTTGGTCAAGCTTCTCTACACAGAGCTGCATATTTGTTGTCATCT	1542	
Db	1498	TAATGCTCTGGAATAATCTTGGTCAAGCTTCTCTACACAGAGCTGCATATTTGTTGTCATCT	1557	
Qy	1543	ACAAACCTGCGGCTACTCCTGAGCTATGGTGTGATCCTTAACATTTATCCCTTCAGGG	1602	
Db	1558	ACAAACCTGCGGCTACTCCTGAGCTATGGTGTGATCCTTAACATTTATCCCTTCAGGG	1617	
Qy	1603	CTTTACTGCTTTACAGATGGAAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCTC	1662	
Db	1618	CTTTACTGCTTTACAGATGGAAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCTC	1677	
Qy	1663	ATTAGGTAATTTAGAGGCAGACAGACAAATTTGCTGGAAAGCTGCAAAAGCTGGAGATGCGA	1722	
Db	1678	ATTAGGTAATTTAGAGGCAGACAGACAAATTTGCTGGAAAGCTGCAAAAGCTGGAGATGCGA	1737	
Qy	1723	AACGTAAAAAATGTTGTTACTGTTACAGATGTTCACTGCAGAGACATTTGAAGGCGCTCA	1782	
Db	1738	AACGTAAAAAATGTTGTTACTGTTACAGATGTTCACTGCAGAGACATTTGAAGGCGCTCA	1797	
Qy	1783	GTCTACACCACTTCATTTTGCAGCTGGGTATAAACAGAGTGTCCGTGGTGAATATCTGCT	1842	
Db	1798	GTCTACACCACTTCATTTTGCAGCTGGGTATAAACAGAGTGTCCGTGGTGAATATCTGCT	1857	
Qy	1843	ACAGCATGGAGCTGATGTCATGCTAAAGATAAAGAGGGCCCTTGATCCTTTGGCAATATGC	1902	
Db	1858	ACAGCATGGAGCTGATGTCATGCTAAAGATAAAGAGGGCCCTTGATCCTTTGGCAATATGC	1917	
Qy	1903	ATGTTCTTATGGACATTTAAGTTGACAACTTCTTTTAAACATGGAGCAGTAGTTAA	1962	
Db	1918	ATGTTCTTATGGACATTTAAGTTGACAACTTCTTTTAAACATGGAGCAGTAGTTAA	1977	
Qy	1963	TGTAGCTGATTTATGGAAATTTTACACCTTTACATGAAGAGCAGCAGCAAAAGGAAATATGA	2022	
Db	1978	TGTAGCTGATTTATGGAAATTTTACACCTTTACATGAAGAGCAGCAGCAAAAGGAAATATGA	2037	
Qy	2023	AATTTGCAAACTTCTGCTCAGCATGTGTCAGACCCCTTACCAAAAAAAGAGGGATGGAAA	2082	
Db	2038	AATTTGCAAACTTCTGCTCAGCATGTGTCAGACCCCTTACCAAAAAAAGAGGGATGGAAA	2097	
Qy	2083	TACTCCTTTGGATCTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA	2142	
Db	2098	TACTCCTTTGGATCTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGA	2157	
Qy	2143	TGCAGCTTTGCTAGATGCTGCCAAGAAAGGGTGTGTTAGCCAGAGTGAAGAAAGTTGCTTTC	2202	

Db 2158 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTTGTTTAGCCAGAGTGAAGAGTGTCTTC 2217
Qy 2203 TCCTGATATGTAATTTGCGCGATACCCAGGCGAGACATTCACACCTTTACATTTAGC 2262
Db 2218 TCCTGATATGTAATTTGCGCGATACCCAGGCGAGACATTCACACCTTTACATTTAGC 2277
Qy 2263 AGCTGGTTATATAATTTAGAAAGTTGCGAGATATTTGTTTACAAACGAGCTGATGTGA 2322
Db 2278 AGCTGGTTATATAATTTAGAAAGTTGCGAGATATTTGTTTACAAACGAGCTGATGTGA 2337
Qy 2323 TGCCCAAGCAAAAGGAGGACTTATTCCTTTACATATGAGCATCTTACGGGCATGTAGA 2382
Db 2338 TGCCCAAGCAAAAGGAGGACTTATTCCTTTACATATGAGCATCTTACGGGCATGTAGA 2397
Qy 2383 TGATGAGCTCTACTAATAAGATTAATGATGTGTAATGTCATGTCGAGCAAAATGGGCTTT 2442
Db 2398 TGATGAGCTCTACTAATAAGATTAATGATGTGTAATGTCATGTCGAGCAAAATGGGCTTT 2457
Qy 2443 CACACCTTTTGCAAGAGCAGCCCAAAAGGAGCAACACAGCTTTTGTCTTTGCTTAC 2502
Db 2458 CACACCTTTTGCAAGAGCAGCCCAAAAGGAGCAACACAGCTTTTGTCTTTGCTTAC 2517
Qy 2503 CCATGGAGCTGACCCGACTCTTTTAAATAATCAGGAAGCAAAACACCTTTAGATTTAGTTTC 2562
Db 2518 CCATGGAGCTGACCCGACTCTTTTAAATAATCAGGAAGCAAAACACCTTTAGATTTAGTTTC 2577
Qy 2563 AGCGATGATGTGAGCGCTCTTCTGACAGCAGCCATGCCCATCTGCTCTGCCCTCTTG 2622
Db 2578 AGCGATGATGTGAGCGCTCTTCTGACAGCAGCCATGCCCATCTGCTCTGCCCTCTTG 2637
Qy 2623 TTACAAGCCTCAAGTGTCTCAATGGTGTGAGAAAGCCAGGAGCCACTGCGATGCTCTCTC 2682
Db 2638 TTACAAGCCTCAAGTGTCTCAATGGTGTGAGAAAGCCAGGAGCCACTGCGATGCTCTCTC 2697
Qy 2683 TTCAGGTCATCTAGCCCATCAAGCCTTTCTGACGAGCAGCTCTTGACAACCTTATCTGG 2742
Db 2698 TTCAGGTCATCTAGCCCATCAAGCCTTTCTGACGAGCAGCTCTTGACAACCTTATCTGG 2757
Qy 2743 GAGTTTTTTCAGAACTGTCTTCAAGTAGTGTAGTTCAAGTGGAACAGAGGCTTCCAGTTT 2802
Db 2758 GAGTTTTTTCAGAACTGTCTTCAAGTAGTGTAGTTCAAGTGGAACAGAGGCTTCCAGTTT 2817
Qy 2803 GGAGAAAAGAGGTTTCCAGGAGTAGATTTTACCATAACTCAATTCGTAAGGAATCTTGG 2862
Db 2818 GGAGAAAAGAGGTTTCCAGGAGTAGATTTTACCATAACTCAATTCGTAAGGAATCTTGG 2877
Qy 2863 ACTTGAGCACTTAATGGATATATTTAGAGAGAAACAGATCACTTTGGATGATTTAGTTGA 2922
Db 2878 ACTTGAGCACTTAATGGATATATTTAGAGAGAAACAGATCACTTTGGATGATTTAGTTGA 2937
Qy 2923 GATGGGCAACAGGAGCTGAAGGAGTTGGAATCAATGCTTATGACATAGGCACAACT 2982
Db 2938 GATGGGCAACAGGAGCTGAAGGAGTTGGAATCAATGCTTATGACATAGGCACAACT 2997
Qy 2983 AATTAAGGAGTTCGAGAGACTTATCTCCGCAACAAAGGCTTTAAACCCATATTTAACTTT 3042
Db 2998 AATTAAGGAGTTCGAGAGACTTATCTCCGCAACAAAGGCTTTAAACCCATATTTAACTTT 3057
Qy 3043 GAACACCTCTGATGAGAACTTTCTTATAGATCTGCTCTGATGATATAAGAGTTTCA 3102
Db 3058 GAACACCTCTGATGAGAACTTTCTTATAGATCTGCTCTGATGATATAAGAGTTTCA 3117
Qy 3103 GTCTGGAGGAGAGATCAAGTACAGTTGGAATCAATGCTTATGACATAGGCATGAGG 3162
Db 3118 GTCTGGAGGAGAGATCAAGTACAGTTGGAATCAATGCTTATGACATAGGCATGAGG 3177
Qy 3163 TGGAAATCTTCAACAGATACATATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTATG 3222
Db 3178 TGGAAATCTTCAACAGATACATATTTCTCAAGATTCAGAGGTTTGTAAACAGAACTATG 3237
Qy 3223 GGAAAGATACCTCAACCGAGAGAAAGAGTTTCTGAAGAAAAACCAACCATGCCAATGA 3282
Db 3238 GGAAAGATACCTCAACCGAGAGAAAGAGTTTCTGAAGAAAAACCAACCATGCCAATGA 3297

Qy 3283 ACGAATGCTATTTTCAATGGGTCTCCTTTTGTCAATGAATATCCAAAGGCTTTTGATGA 3342
Db 3298 ACGAATGCTATTTTCAATGGGTCTCCTTTTGTGAATGAATATCCAAAGGCTTTTGATGA 3357
Qy 3343 AAGCATCGGTACATAGGTGTATGTTTGGAGCTGGCAATTTATTTTGTGTAAGAACTCTTC 3402
Db 3358 AAGCATCGGTACATAGGTGTATGTTTGGAGCTGGCAATTTATTTTGTGTAAGAACTCTTC 3417
Qy 3403 CAAAGCAATCAATATGATATGGAATTTGGAGGAGGTACTGGGTGTCAGATTCACAAAGA 3462
Db 3418 CAAAGCAATCAATATGATATGGAATTTGGAGGAGGTACTGGGTGTCAGATTCACAAAGA 3477
Qy 3463 CAGATCTTTGTATCATTTGCCACAGCAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3522
Db 3478 CAGATCTTTGTATCATTTGCCACAGCAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGTC 3537
Qy 3523 TTTCTCGAGTTCAGTGTCAATGAAATGGCAATTCCTCTCAGGTCACTCAGTCAC 3582
Db 3538 TTTCTCGAGTTCAGTGTCAATGAAATGGCAATTCCTCTCAGGTCACTCAGTCAC 3597
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Qy 3703 ATAAATAGTTATTTTAAAGAACTAATTCCTCACTGAACCTTAAATATCAAAAGCAGCAGTGG 3762
Db 3718 ATAAATAGTTATTTTAAAGAACTAATTCCTCACTGAACCTTAAATATCAAAAGCAGCAGTGG 3777
Qy 3763 CCTCTACGTTTACTCTCTTCTGCTGAAAAAAA 3794
Db 3778 CCTCTACGTTTACTCTCTTCTGCTGAAAAAAA 3809

RESULT 11

US-10-898-653-5
; Sequence 5, Application US/10898653
; Publication No. US20050143370A1
; GENERAL INFORMATION:
; APPLICANT: Helleday et al
; TITLE OF INVENTION: Therapeutic Compounds
; FILE REFERENCE: J660-046
; CURRENT APPLICATION NUMBER: US/10/898,653
; CURRENT FILING DATE: 2004-07-23
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 5
; LENGTH: 6189
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-898-653-5

Query Match 89.2%; Score 3387.2; DB 10; Length 6189;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 403 AGGTTTTGGCGGAAAGACGTTAGTTGAATATTTGCTTCAGAAATGTCAGAGTGTCAAAGC 462
Db 577 AGGTTTTGGCGGAAAGACGTTAGTTGAATATTTGCTTCAGAAATGTCAGAAATGTCAAAGC 636
Qy 463 ACGTGATCATGGGGCCCTTATTCCTCTCAATAATGTCATGCTCTTTTGGTCAATGCTGAAAGT 522
Db 637 ACGTGATCATGGGGCCCTTATTCCTCTCAATAATGTCATGCTCTTTTGGTCAATGCTGAAAGT 696
Qy 523 AGTCAATCTCTTTTGGACATGGTGACAGCCCAATGCTCGAGATAATTTGGAATTTATAC 582
Db 697 AGTCAATCTCTTTTGGACATGGTGACAGCCCAATGCTCGAGATAATTTGGAATTTATAC 756
Qy 583 TCCTCTCAATGAAGCTGCAATTTAAAGGAAAGATGATGTTTGTGCTGTTTACAGCA 642

Db	757	TCCTCTCCATGAGCTGCATTAAGGAAGATTGATGTTTGCATTGCTGTGTACAGCA	816
Qy	643	TGGAGCTGAGCCAAACCATCCGAAATA CAGATGGAAGGACAGCATTTGATTTAGCAGATCC	702
Db	817	TGGAGCTGAGCCAAACCATCCGAAATA CAGATGGAAGGACAGCATTTGATTTAGCAGATCC	876
Qy	703	ATCTGCCAAGCAGTCTTACTGCTGTAATATAAGAAAGATGAATCTTAGAAGTGCAG	762
Db	877	ATCTGCCAAGCAGTCTTACTGCTGTAATATAAGAAAGATGAATCTTAGAAGTGCAG	936
Qy	763	GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTTAAATGCTCAACTGCCACGC	822
Db	937	GAGTGGCAATGAAGAAAAATGATGGCTCTACTCACACCATTTAAATGCTCAACTGCCACGC	996
Qy	823	AAGTGATGGCAGAAAGTCAACTCCATTAACAATTTGGCAGCAGGATATAACAGAGTAAAGAT	882
Db	997	AAGTGATGGCAGAAAGTCAACTCCATTAACAATTTGGCAGCAGGATATAACAGAGTAAAGAT	1056
Qy	883	TGTACAGCTGTTACTGCAACATGGAGCTGATGTCCTAAGATTAAGATTAAGGTGATCTGGT	942
Db	1057	TGTACAGCTGTTACTGCAACATGGAGCTGATGTCCTAAGATTAAGATTAAGGTGATCTGGT	1116
Qy	943	ACCATACACAATGCCCTGTTCTTATGCTCATTAATGAAGTAACTGAACTTTTGGTCAAGCA	1002
Db	1117	ACCATACACAATGCCCTGTTCTTATGCTCATTAATGAAGTAACTGAACTTTTGGTCAAGCA	1176
Qy	1003	TGGTGCCTGTGTAATGCAATGGAATTTGTGGCAATTCACCTCTTCATGAGGCGAGCTTC	1062
Db	1177	TGGTGCCTGTGTAATGCAATGGAATTTGTGGCAATTCACCTCTTCATGAGGCGAGCTTC	1236
Qy	1063	TAAGAACAGGGTGAAGTATGTTCTTCTCTTAAAGTAACTGAACTTTTGGTCAAGCA	1122
Db	1237	TAAGAACAGGGTGAAGTATGTTCTTCTCTTAAAGTAACTGAACTTTTGGTCAAGCA	1296
Qy	1123	CAATTTGCACAAATAAAGTGTCTATAGCTTGGCTCCACACCAAGTAAAGAAAGATT	1182
Db	1297	CAATTTGCACAAATAAAGTGTCTATAGCTTGGCTCCACACCAAGTAAAGAAAGATT	1356
Qy	1183	AGCATATGAATTTAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATTTACTCG	1242
Db	1357	AGCATATGAATTTAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATTTACTCG	1416
Qy	1243	AATCAAAAACATCTCTCTGGAATTTGGTGAATTTCAAGCATCCTCAACACATGAAC	1302
Db	1417	AATCAAAAACATCTCTCTGGAATTTGGTGAATTTCAAGCATCCTCAACACATGAAC	1476
Qy	1303	AGCATTTGATTTGCTGCTGATCTCCATATCCCAAAGAAAGCAATATGTGAATCTGT	1362
Db	1477	AGCATTTGATTTGCTGCTGATCTCCATATCCCAAAGAAAGCAATATGTGAATCTGT	1536
Qy	1363	GCTAAGAAAAGGAGCAACATCAATGAAGAAAGCTAAGAAATTTCTTGACTCTCTGCAAGT	1422
Db	1537	GCTAAGAAAAGGAGCAACATCAATGAAGAAAGCTAAGAAATTTCTTGACTCTCTGCAAGT	1596
Qy	1423	GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAGCAAGAGT	1482
Db	1597	GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGTGAAACATGAGCAAGAGT	1656
Qy	1483	TAATGCTCTGATTAATCTTTGGTCAAGCTTCTCTACACAGAGCTGCATATTGTGGTCACT	1542
Db	1657	TAATGCTCTGATTAATCTTTGGTCAAGCTTCTCTACACAGAGCTGCATATTGTGGTCACT	1716
Qy	1543	ACAAACCTGCCGCTACTCTGAGCTATGGGTGTGATCTTAACTATATATCCCTTCAGGG	1602
Db	1717	ACAAACCTGCCGCTACTCTGAGCTATGGGTGTGATCTTAACTATATATCCCTTCAGGG	1776
Qy	1603	CTTTACTGCTTTACAGATGGGAATGAATGTTACAGCACTCTCCAGAGGGTATCTC	1662
Db	1777	CTTTACTGCTTTACAGATGGGAATGAATGTTACAGCACTCTCCAGAGGGTATCTC	1836
Qy	1663	ATTAGGTAAATTACAGAGGAGACAGACAATTCCTGGAAGCTCAAGAGGCTGGAGATGTGGA	1722
Db	1837	ATTAGGTAAATTACAGAGGAGACAGACAATTCCTGGAAGCTCAAGAGGCTGGAGATGTGGA	1896

Qy	1723	AACGTGTAATAAAAACTGTGTACTGTTT CAGAGTGTCAACTGCAGAGACATTTGAAGGCGTCA	1782
Db	1897	AACGTGTAATAAAAACTGTGTACTGTTT CAGAGTGTCAACTGCAGAGACATTTGAAGGCGTCA	1956
Qy	1783	GTCTACACACATTTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT	1842
Db	1957	GTCTACACACATTTTCAATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT	2016
Qy	1843	ACAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGGAGGCTTTGTACCTTTTGCAACAATGC	1902
Db	2017	ACAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGGAGGCTTTGTACCTTTTGCAACAATGC	2076
Qy	1903	ATGTTCTTATGGACATTAATGAAGTTGCAGAACTTCTTGTTTAAACATGAGCAGTAGTTAA	1962
Db	2077	ATGTTCTTATGGACATTAATGAAGTTGCAGAACTTCTTGTTTAAACATGAGCAGTAGTTAA	2136
Qy	1963	TGTAGCTGATTTTATGGAATTTTACACCTTTTATGAAGCAGCAGCAAAAGGAAATATGA	2022
Db	2137	TGTAGCTGATTTTATGGAATTTTACACCTTTTATGAAGCAGCAGCAAAAGGAAATATGA	2196
Qy	2023	AATTTGCAAACTTTCTGCTCCAGCATGGTGCAGACCCCTTACCAAAAAAACAAGGGATGAAA	2082
Db	2197	AATTTGCAAACTTTCTGCTCCAGCATGGTGCAGACCCCTTACCAAAAAAACAAGGGATGAAA	2256
Qy	2083	TACTCCTTTGGATCTTGTTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGAGA	2142
Db	2257	TACTCCTTTGGATCTTGTTTAAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGGAGA	2316
Qy	2143	TGCAGCTTTTCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGATTTGCTTTC	2202
Db	2317	TGCAGCTTTTCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGATTTGCTTTC	2376
Qy	2203	TCCTGATAATGTAATTTAGAACTGCCCGGATACCCAAAGGAGACATTTCAACACCTTTTACATTTAGC	2262
Db	2377	TCCTGATAATGTAATTTAGAACTGCCCGGATACCCAAAGGAGACATTTCAACACCTTTTACATTTAGC	2436
Qy	2263	AGCTGGTTATTAATTTAGAACTGGCAGAGTATTTGTTTACAAACACGAGCTGATGTGAA	2322
Db	2437	AGCTGGTTATTAATTTAGAACTGGCAGAGTATTTGTTTACAAACACGAGCTGATGTGAA	2496
Qy	2323	TGCCAAGACAAAAGGAGGAGCTTATTTCTTTTACATAATGCAGCATCTTTACGGGCATGTAGA	2382
Db	2497	TGCCAAGACAAAAGGAGGAGCTTATTTCTTTTACATAATGCAGCATCTTTACGGGCATGTAGA	2556
Qy	2383	TGTAGCAGCTCTACTAATAAAGTATATATGATGTCTCAATGCCACGCAAAATGGGCTTT	2442
Db	2557	TGTAGCAGCTCTACTAATAAAGTATATATGATGTCTCAATGCCACGCAAAATGGGCTTT	2616
Qy	2443	CACACCTTTGCAAGAGCAGCCCAAAAGGAGCAACACACAGCTTTGTGCTTTGCTGTAGC	2502
Db	2617	CACACCTTTGCAAGAGCAGCCCAAAAGGAGCAACACACAGCTTTGTGCTTTGCTGTAGC	2676
Qy	2503	CCATGGAGCTGACCCGACTCTTAAATAATCAGGAAGGACAAACACCTTTTAGATTTAGTTTC	2562
Db	2677	CCATGGAGCTGACCCGACTCTTAAATAATCAGGAAGGACAAACACCTTTTAGATTTAGTTTC	2736
Qy	2563	AGCGGATGATGT CAGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCCCTTTG	2622
Db	2737	AGCAGATGATGT CAGCGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCTGCCCCCTTTG	2796
Qy	2623	TTACAAAGCTCAAGTGTCTCAATGGTGTGAGAACCCAGGAGCCACTGCAGATGCTCTCTC	2682
Db	2797	TTACAAAGCTCAAGTGTCTCAATGGTGTGAGAACCCAGGAGCCACTGCAGATGCTCTCTC	2856
Qy	2683	TTCAAGTCCATCTAGCCCATCAAGCCCTTTTTCAGCCAGCAGTCTTTCACAACTTATCTGG	2742
Db	2857	TTCAAGTCCATCTAGCCCATCAAGCCCTTTTTCAGCCAGCAGTCTTTCACAACTTATCTGG	2916
Qy	2743	GAGTTTTTCAGAACTGTCTTTCAGTGTAGTTTCAAGTGTGGAACAGAGGGTGTCTCCAGTTT	2802
Db	2917	GAGTTTTTCAGAACTGTCTTTCAGTGTAGTTTCAAGTGTGGAACAGAGGGTGTCTCCAGTTT	2976

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Qy 1262 CTGGAATGTTGGAATTTCAAGCATCTCTCAACACATGAACACAGCATTTGCAATTTGCTGCT 1321
Db 781 CTGGAATGTTGGAATTTCAAGCATCTCTCAACACATGAACACAGCATTTGCAATTTGCTGCT 840
Qy 1322 GCATCTCATATCCAAAAAGAAAGCAATATGTGAACTGTGTTGCTTAAGAAAAGGAGCAAAC 1381
Db 841 GCATCTCATATCCAAAAAGAAAGCAATATGTGAACTGTGTTGCTTAAGAAAAGGAGCAAAC 900
Qy 1382 ATCAATGAAGAAGCTAAGAAATTTGACCTCTCTGACGCTGCGATCTGAGAAAGCTCAT 1441
Db 901 ATCAATGAAGAAGCTAAGAAATTTGACCTCTCTGACGCTGCGATCTGAGAAAGCTCAT 960
Qy 1442 AATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGTTAATGCTCTGGATAATCTTT 1501
Db 961 AATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGTTAATGCTCTGGATAATCTTT 1020
Qy 1502 GGTGAGACTTCTCTACACAGAGCTGCAATATGTGGTCACTTACAAACCTGCGCGCTACTC 1561
Db 1021 GGTGAGACTTCTCTACACAGAGCTGCAATATGTGGTCACTTACAAACCTGCGCGCTACTC 1080
Qy 1562 CTGAGCTATGGGTGATCTCTAAACATTAATATCCCTTCAGGGCTTTAATGCTCTGGATAATCTTT 1621
Db 1081 CTGAGCTATGGGTGATCTCTAAACATTAATATCCCTTCAGGGCTTTAATGCTCTGGATAATCTTT 1140
Qy 1622 GGAATGAAGATGTACAGCAACTCTCTCAAGAGGGTATCTCATPAGGTAAATTCAGAGGCA 1681
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Qy 1682 GACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTGAAACTGTAAAAAAACTGTGT 1741
Db 1201 GACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTGAAACTGTAAAAAAACTGTGT 1260
Qy 1742 ACTGTTGAGAGTGTCACTGACAGAGCATTTGAAGGGGCTGAGTCTACACCACTTCATTTT 1801
Db 1261 ACTGTTGAGAGTGTCACTGACAGAGCATTTGAAGGGGCTGAGTCTACACCACTTCATTTT 1320
Qy 1802 GCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCTACAGCATGGAAGTGTG 1861
Db 1321 GCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCTACAGCATGGAAGTGTG 1380
Qy 1862 CATGCTAAAGATAAAGAGGCTTGTACCTTTTGCAAAATGATGCTTATPAGACATTAAT 1921
Db 1381 CATGCTAAAGATAAAGAGGCTTGTACCTTTTGCAAAATGATGCTTATPAGACATTAAT 1440
Qy 1922 GAAGTTGCAGAACTTCTGTTTAAACATGGAGCAGTGTAAATGATGCTTATPAGAA 1981
Db 1441 GAAGTTGCAGAACTTCTGTTTAAACATGGAGCAGTGTAAATGATGCTTATPAGAA 1500
Qy 1982 TTTACACCTTTACATGAAGCAGCAGCAAGAAATATGAAATTTGCAAACTTCTGCTC 2041
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Qy 2402 AAGTATATGTCATGTGTCAANTGCGACGACAAATGGGCTTTACACCTTTGCGACGAGGA 2461
Db 1921 AAGTATATGTCATGTGTCAANTGCGACGACAAATGGGCTTTACACCTTTGCGACGAGGA 1980
Qy 2462 GCCCAAAAGGAGCAACACAGCTTTTGTGCTTAGCCCATGGAGCTGACCCGACT 2521
Db 1981 GCCCAAAAGGAGCAACACAGCTTTTGTGCTTAGCCCATGGAGCTGACCCGACT 2040
Qy 2522 CTTAAAAATCAGGAAGCAAAACACCTTTTAGATTTTGTAGCGGATGTAGTGTGAGGCT 2581
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Qy 2762 TCAGTAGTTAGTTCAAGTGGAACAGAGGCTTCTTCCAGTTTGGAGAAAGAGGTTTCCA 2821
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Db 2401 ATATTTCAGAGAGAACAGATCACTTTTGGATGTATTAGTTGAGATGGGGCAACAGAGGCTG 2460
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Qy 3062 ACAATCTTTATAGATCTGTCTCTCTGATGATAAAGAGTTTCACTGTGTGGAGGAAGAGATG 3121
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QY 3722 AACTAAATCCAGTAACTTAAATCATCAAGCAGCAGTGGGCTCTAGCTTTTACTCCTT 3781
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RESULT 13
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; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
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; APPLICANT: McElligott, David L.
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(3508)

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Query Match 86.8%; Score 3296.2; DB 7; Length 3508;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3298; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 403 AGGTTTGGCGGGAAGACGTAGTTGAATATTGCTTCAGAAATGGTGCAGTGTCCAGC 462
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Qy 2503 CCATGGAGCTGACCCGACTCTTTAAAAATCAGGAAGGAACAAACACTTTTAGATTGTTTC 2562
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Qy 2563 AGCGGATGATGTACGCGCTCTTTTGAAGAGCCATGCCCCCATCTGCTCTGCCCTCTTG 2622
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Qy 2683 TTCAGGTCATCTAGCCCATCAAGCCTTTCTGCAAGCCAGGAGCTTTGCAACTTATCTGG 2742
Db 2488 TTCAGGTCATCTAGCCCATCAAGCCTTTCTGCAAGCCAGGAGCTTTGCAACTTATCTGG 2547
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Db 2608 GGAGAAAAAGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAAGAAATCTTGG 2667
Qy 2863 ACTTGAGCAGCTTAATGTGATATATTTTGAGAGAGAAACAGATCACTTTTGGATGTATTAGTTGA 2922
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Qy 2923 GATGGGGCACAAGGAGCTGAAGGAGTTGGAATCAATGCTTATGACATAGGCAAACT 2982
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; Publication No. US20030032769A1
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Db 1272 TGGTGCCTGTGTAATGCAATGGACTTGTGGCAATTCACCTCTCTCATGAGGAGCTTC 1331
Qy 1063 TAAGAACAGGGTTCGAAGTATGTTCTCTCTCTTAAGTTATGGTGCAGACCCCAACACTGCT 1122
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Db 2112 ACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCCCTTGTACCTTTGCAACAATGC 2171
Qy 1903 ATGTTCTTATGGACATTAATGAAGTTGCAAGACTTCTGTTAAACATGAGCAGTAGTTAA 1962
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Db 3312 AACTTTGAAACCTCTCGTGTAGTGAAACAAATTTTATATAGATCTGCTCTGATGATAAGA 3371

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1584	Qy	ACATTATATCCCTTCAGGGCTTTACTGCTTTTACAGATGGGAAATGAAAAATGTACAGCAAC	1643
1676	Db	ACATTATATCCCTTCAGGGCTTTACTGCTTTTACAGATGGGAAATGAAAAATGTACAGCAAC	1735
1644	Qy	TCCTCCAAGAGGGTATCTCATTTAGTGTAAATTCAGAGGCAGACAGACAAATTCCTCGAAGCTG	1703
1736	Db	TCCTCCAAGAGGGTATCTCATTTAGTGTAAATTCAGAGGCAGACAGACAAATTCCTCGAAGCTG	1795
1704	Qy	CAAAAGGCTGGAGATGTCGAAACTCTGTAATAAACTGTGTACTGTTTCAGAGTGTCAACTGCA	1763
1796	Db	CAAAAGGCTGGAGATGTCGAAACTCTGTAATAAACTGTGTACTGTTTCAGAGTGTCAACTGCA	1855
1764	Qy	GAGACATTGAAGGGCGTCAGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGT	1823
1856	Db	GAGACATTGAAGGGCGTCAGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGT	1915
1824	Qy	CCGTGGTGGAAATATCTCGTACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGAGAGGCC	1883
1916	Db	CCGTGGTGGAAATATCTCGTACAGCATGGAGCTGATGTGCATGTCTAAAGATAAAGAGAGGCC	1975
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1976	Db	TTGTACCTTTGCAAAATGCTATTTATGGACATTTATGAAGTTCAGACACTTCTTGTGTTA	2035
1944	Qy	AACATGAGCAGTAGTATTAATGTAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAG	2003
2036	Db	AACATGAGCAGTAGTATTAATGTAGCTGATTTATGGAATTTTACACCTTTACATGAAGCAG	2095
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2064	Qy	AAAAAACAGGGATGGAATACTCTTTGCTTAAAGATGGAGTACAGATATTC	2123
2156	Db	AAAAAACAGGGATGGAATACTCTTTGCTTAAAGATGGAGTACAGATATTC	2215
2124	Qy	AAGATCTGCTTAGGGAGATGACAGCTTGTCTAGATGCTGCAAGAGGGTGTGTTAGCCA	2183
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2336	Db	CAACACCTTTACATTTTAGCA--GGTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	2392
2304	Qy	AACAGCAGCTGATGTCAATGCCCAAGACAAAGGAGGACTTATTCTCTTTACATAATGCAG	2363
2393	Db	NN	2452
2364	Qy	CATCTTACGGGCATGTAGATGTAGCAGCTCTACTAATAAAGTATAATGTGTCATGTC	2423
2453	Db	NN	2512
2424	Qy	CCACGGACAAATGGGCTTTACACCTTTGCACGACGCCAAGAGGAGACACAGC	2483
2513	Db	NN	2572
2484	Qy	TTTGTGCTTTGCTAGCCCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGACAA	2543
2573	Db	NN	2632
2544	Qy	CACCTTTAGATTTAGTTCGCGGATGATGTCAGCGCTCTTCTGACAGCAGCCATGCCCC	2603
2633	Db	NN	2692
2604	Qy	CATCTGCTCTGCCCTCTTGTGTTAACAAGCCTCAAGTGTCAATGTGTGTGAGAGCCAGGAG	2663
2693	Db	CATCTGCTCTGCCCTCTTGTGTTAACAAGCCTCAAGTGTCAATGTGTGTGAGAGCCAGGAG	2752

2654	QY	CCACTGCAGATGCTCTCTCTTCAGGTCCTATCTAGCCCATCAAGCCTTCTTCGACGCCAGCA	2723
2753	Db	CCACTGCAGATGCTCTCTCTTCAGGTCCTATCTAGCCCATCAAGCCTTCTTCGACGCCAGCA	2812
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2813	Db	GTCCTTGACCACTTATCTGGGAGTTTTTCAGAACCTGTCTTCAGTAGTTAGTTCAAGTGGAA	2872
2784	QY	CAGAGGGTGCTTCCAGTTTTGAGAAAAAGAGGTTCCAGGAGTAGATTTTGTAGCATAACTC	2843
2873	Db	CAGAGGGTGCTTCCAGTTTTGAGAAAAAGAGGTTCCAGGAGTAGATTTTGTAGCATAACTC	2932
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2933	Db	AAITTCGTAAGGAATCTTGACCTTCAGCACCTAATATGGAATATTTTNAGAGAGAAACAGATCA	2992
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2993	Db	CTTTGGGATGTAATAGTTGAGATGGGCAACAGGAGCTGAAGGAGATTTGGAATCAATGCTTT	3052
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3053	Db	ATGGACATATGAGCAAAAACCTAATTTAAAGGTTTCGAGAGACTTATCTCCGGACAACAAGGTC	3112
3024	QY	TTAAACCCATATTTAACTTTGAACACCTCTGGTAGTGGAACAATTTCTTATATAGATCTGTCTC	3083
3113	Db	TTAAACCCATATTTAACTTTGAACACCTCTGGTAGTGGAACAATTTCTTATATAGATCTGTCTC	3172
3084	QY	CTGATGATAAGAGTTTCAGTCTGTGAGGAGAGATGCAAGTACAGTTTCGAGAGCACACA	3143
3173	Db	CTGATGATAAGAGTTTCAGTCTGTGAGGAGAGATGCAAGTACAGTTTCGAGAGCACACA	3232
3144	QY	GAGATGGAGGTCATGACAGGTGGAACTCTTCAACAGATACAATATTTCTCAAGATTCAGAAAG	3203
3233	Db	GAGATGGAGGTCATGACAGGTGGAACTCTTCAACAGATACAATATTTCTCAAGATTCAGAAAG	3292
3204	QY	TTTGTGAAC-----AAGAAACTATGGGAAGATACATCAACCGGAGAAAAAGAGTTT	3254
3293	Db	TTTGTGAACAGAGCCAAAGATTTCGGCACAGGAAAGATACATCAACCGGAGAAAAAGAGTTT	3352
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3353	Db	CTGAAGAAACCAACAATGCCAATGAAAGATGCTATTTTCATGGGTCTCCTTTTGTGA	3412
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3413	Db	ATGCAATTTATCCACAAAGGCTTTGATCAAAAGGATGCGTACATAGGTGGTATGTTTGGAG	3472
3375	QY	CTGGCATTTATTTTGTGTAACCTCTTCCAAAAGCAATCAATATGTATATGGAATTTGGAG	3434
3473	Db	CTGGCATTTATTTTGTGTAACCTCTTCCAAAAGCAATCAATATGTATATGGAATTTGGAG	3532
3435	QY	GAGGTACTGGGTGTCAGTTTCAAAAGACAGATCTTGTTCATTTTGGCCACAGGACGTGC	3494
3533	Db	GAGGTACTGGGTGTCAGTTTCAAAAGACAGATCTTGTTCATTTTGGCCACAGGACGTGC	3592
3495	QY	TCCTTTCCGGGTAAACCTTCGGAAAGTCTTTCTGCAAGTTTCAGTGCATCAAAATGSCAC	3554
3593	Db	TCCTTTCCGGGTAAACCTTCGGAAAGTCTTTCTGCAAGTTTCAGTGCATCAAAATGSCAC	3652
3555	QY	ATTCCTCTCCAGGTCACTCACTCAGTCACTGGTAGGCCAGGTGTAATATGGCCTTAGCATTTAG	3614
3653	Db	ATTCCTCTCCAGGTCACTCACTCAGTCACTGGTAGGCCAGGTGTAATATGGCCTTAGCATTTAG	3712
3615	QY	CTGAATATGTTATTTACAGAGGAAACAGGCTTATCTCTGAGTATTTTAAATTTACTTTACAGA	3674
3713	Db	CTGAATATGTTATTTACAGAGGAAACAGGCTTATCTCTGAGTATTTTAAATTTACTTTACAGA	3772
3675	QY	TTATGAGCCCTGAAGGTTATGGTCGATGATAAATAGTTATTTTAAAGAAACCTAATTTCCACT	3734
3773	Db	TTATGAGCCCTGAAGGTTATGGTCGATGATAAATAGTTATTTTAAAGAAACCTAATTTCCACT	3832

Qy	3735	GAACCTAAAAATCAATCAAGCAGCAGTGGCCTCTACGTTTATCTCCTTTGCTGAAAAAAA	3794
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Search completed: December 18, 2006, 21:41:00
Job time : 3863.36 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2006, 17:00:26 ; Search time 754.113 Seconds
(without alignments)
10686.273 Million cell updates/sec

Title: US-10-616-101-1

Perfect score: 3797

Sequence: 1 ctttgagacactgatttc.....cctttgctgaaaaa 3797

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3026960 seqs, 1061187768 residues

Total number of hits satisfying chosen parameters: 6053920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3387.2	89.2	3815	US-11-266-748A-23602	Sequence 23602, A
2	3387.2	89.2	6189	US-11-266-748A-23750	Sequence 23750, A
3	1813.4	47.8	4134	US-11-266-748A-29428	Sequence 29428, A
4	1794.8	47.3	8901	US-11-266-748A-22929	Sequence 22929, A
5	663.8	17.5	675	US-11-266-748A-251004	Sequence 251004, A
6	663.8	17.5	675	US-11-266-748A-311521	Sequence 311521, A
7	570	15.0	594	US-11-266-748A-39554	Sequence 39554, A
8	570	15.0	594	US-11-266-748A-152365	Sequence 152365, A
9	535.6	14.1	929	US-11-266-748A-189602	Sequence 189602, A
10	533.6	14.1	564	US-11-266-748A-55144	Sequence 55144, A
11	533.6	14.1	564	US-11-266-748A-217436	Sequence 217436, A
12	515.6	13.6	668	US-11-266-748A-165504	Sequence 165504, A
13	515.6	13.6	668	US-11-266-748A-244089	Sequence 244089, A
14	503.2	13.3	1000	US-11-266-748A-116071	Sequence 116071, A
15	503.2	13.3	1000	US-11-266-748A-158235	Sequence 158235, A
16	503.2	13.3	1000	US-11-266-748A-221377	Sequence 221377, A
17	503.2	13.3	1000	US-11-266-748A-286109	Sequence 286109, A
18	503.2	13.3	1000	US-11-266-748A-337538	Sequence 337538, A
19	503.2	13.3	1000	US-11-266-748A-396481	Sequence 396481, A
20	503.2	13.3	1000	US-11-266-748A-467527	Sequence 467527, A
21	336.8	8.9	566	US-11-266-748A-379999	Sequence 379999, A
22	336.8	8.9	566	US-11-266-748A-463378	Sequence 463378, A

ALIGNMENTS

RESULT 1

US-11-266-748A-23602
; Sequence 23602, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 23602
; LENGTH: 3815
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23602

Query Match 89.2%; Score 3387.2; DB 8; Length 3815;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 337 AGGTTTTGGCGGAAGACGCTAGTGTGATTTGCTTCAGAAATGTCGCAAGC 396

Sequence 8589, Ap
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Sequence 3160, Ap
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RESULT 2

US-11-266-748A-23750
; Sequence 23750, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
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; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23750
; LENGTH: 6189
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23750

Query Match 89.2%; Score 3387.2; DB 8; Length 6189;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3389; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 403 AGGTTTTGGCGGAAAGACGTTAGTTGAATTTGCTTCAGAAATGGTCAAGTGTCCAAGC 462
Db 577 AGGTTTTGGCGGAAAGACGTTAGTTGAATTTGCTTCAGAAATGGTCAAGTGTCCAAGC 636
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Qy 2143 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAGTTGTCTTC 2202
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Db 2377 TCCTGATAATGTAATTTGCGCGGATACCCCAAGGCAGACATTTCAACACCTTTTACATTTAGC 2436
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QY 3157 AATTAAGGAGTCGAGAGCTTATCTCCGACAAACAGGTCTTAACCCATATTTAACTTT 3216
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QY 3103 GTCTGTGGAGGAGATGCAAGTACAGTTCGAGAGCACAGAGATGAGGTCTGAGG 3162
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QY 3277 GTCTGTGGAGGAGATGCAAGTACAGTTCGAGAGCACAGAGATGAGGTCTGAGG 3336
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QY 3163 TGAATCTTCAACAGATCAATATCTCAAGATTCAGAAAGTTTCTAACAAGAACTATG 3222
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QY 3337 TGAATCTTCAACAGATCAATATCTCAAGATTCAGAAAGTTTCTAACAAGAACTATG 3396
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QY 3223 GGAAGATACACTCAACCGAGAGAAAGAGTTTCTGAAGAAACCAACCAACCATGCCAATGA 3282
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QY 3457 AGCAATGCTATTTCAATGGGTCTCTTTTGTGAATGCAATATCCCAAGGCTTTGATGA 3516
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QY 3343 AAGCATGCGTACATAGGTGATGTTTGGAGCTGGCATTTATTTGCTGAAACTCTTC 3402
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QY 3517 AAGCATGCGTACATAGGTGATGTTTGGAGCTGGCATTTATTTGCTGAAACTCTTC 3576
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QY 3637 CAGATCTTTGATATTTGCCACAGCAGCTGCTCTTTTGGCGGGTAACTTTGGGAAGTC 3696
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QY 3523 TTTCTCGAGTTTCACTGCAATGAAATGGCAATCTCTCTCCAGGTCTCACTCAGTCAAC 3582
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QY 3877 ATAAATAGTTATTTTAAAGAACTAATTTCCACTGAACCTAAATCATCAAAGCAGCAGTGG 3936
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Db |||||

RESULT 3
US-11-266-748A-29428
; Sequence 29428, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6

; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700, 293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29428
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-29428

Query Match 47.8%; Score 1813.4; DB 8; Length 4134;
Best Local Similarity 72.3%; Pred. No. 0;
Matches 2395; Conservative 0; Mismatches 891; Indels 27; Gaps 2;

QY 383 TCCCTCTGGCTTTATCATTAAGGTTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAG 442
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QY 657 TCTCCCTGCACTCGCTGCGAGGTTTTGGAAGGAAGATGTTGTAGAACACTTACTACAG 716
Db |||||
QY 443 AATGGTCAAGTGTCCAAGCAGTGAATGATGGGGCCCTTATTCCTCTTCAATAATCATGC 502
Db |||||
QY 717 ATGGGTCTAATGTCACGCTCGTGAATGATGGAGGTCTCATCCCGCTTTCATAATGCCGT 776
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QY 503 TCTTTTGTGATGCTGAAGTAGTCAATCTCTTTTGGACATGTTGGACAGACCCCATGCT 562
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QY 777 TCTTTTGGCCATGCTGAGGTTGTGAGTCTGTTTGTGCGCAAGGAGCTGTATCCAAATGCC 836
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QY 563 CGAGATAATTCGAATTTATCTCTCCATCAAGCTGCAATTTAAAGGAAAGATTGATGTT 622
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QY 837 AGGATATCTGGAATATACACTCTGATGAGAGTCTGATTTAAAGGGAAGATCGATGTG 896
Db |||||
QY 623 TGCATTTGCTGTTTACAGCATGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACA 682
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QY 897 TGCATTTGCTGCTGCGAGCAGGAGCTGACCCAAACATTCGGAACACATGATGGGAAATCA 956
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QY 683 GCATTTGATTTAGCAGATCCATCTGCCAAAGCAGTCTTACTGTTGAATATGAAGAAAT 742
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QY 957 GCCCTGGACCTGGCAGATCTCTTACGCAAAAAGCTGTCTTACAGGTGAATACAAAGAAAGAC 1016
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QY 743 GAATCTTTAGAAAGTCCAGGAGTGGCAATCAAGAAAAAATGATGGCTCTACTCACACCA 802
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QY 1017 GAATCTTAGAAGCTCTAGAGGTGTTAATGAGAAAAAATGATGGCTTACTGACTCT 1076
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QY 803 TTAATGTCAACTGCCACGCAAGTGAATGGCAGAAAGTCAACTCCATTTACATTTGGCAGCA 862
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QY 1077 CTAAATGTGAATTTGCATGCAAGTGAATGGCGAAAGTGCAGCTCTTTACATCTAGCAGG 1136
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QY 863 GGATATAACAGATTAAGATTTGACAGCTGTACTGCAACATGGAGCTGATGTCATGCT 922
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QY 1137 GGCTACAAACAGATTCGAATAGTTTCACTTCTTCTTACAGCATGGTGTGATGTTTATGCA 1196
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QY 1197 AAAGATAAGGTGATCTGGTACCATTACAAATGCTGCTTCTTATGTTGTCATTATGAGTGC 1256
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QY 983 ACTGAACCTTTTGGTCAAGCATGGTGCCTGTGTAAATGCAATGGAAGCTTGTGGCAATTCAT 1042
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QY 1257 ACAGAACTGCTACTAAAGCATGGAGCTTGTGTATGTCATGATGCTCTGCGCAGTTTACT 1316
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QY 1043 CCTTTTATGAGGAGCAGTCTTCAAGAACAGGTTTGAAGTATGTTCTTCTTCTTAAAGTTAT 1102
Db |||||
QY 1317 CCACTGCAAGGAGTCTTCCAAAGAACCGGTGTAAGAGTCTGCTCTTCTTCTTACTTAGCCAT 1376
Db |||||

Qy	1103	GGTG	CAGACCCAA	CACTGCTCA	ATGTGTCACAA	TAAAGT	GCTATAG	ACTTGG	CTCC	CACA	1162
Db	1377	GGCG	CTGATCCT	TAGTTC	CAACTG	CGCAATG	GCGAAAG	TGCTG	TGATAT	TGGCTCCA	1436
Qy	1163	CCAC	AGTTAA	AGAAAG	ATTAG	CATATGA	NTTTAA	AGGCC	ACACTCG	TGTGTC	1222
Db	1437	CCGG	AGCTTAG	GAGAG	ATTG	CACTTAT	GAAATTTAA	AGGT	CATTCTT	TACTAC	1496
Qy	1223	CGAA	AGCTG	ATGTT	ACTCG	AATCA	AAAAA	CACTCT	CTCG	AAATGG	1282
Db	1497	AGAG	AGCAG	ACTTAG	CTAA	AGTTTAA	AAAAA	CACTCG	CTCT	CGAAAT	1556
Qy	1283	CATC	CTCA	AAACAT	AGAA	CAG	CAATG	CTATG	CTG	TCAT	1342
Db	1557	CAAC	CGCAG	CTCAT	GA	AAACAG	CACTG	CACTG	CTG	TG	1616
Qy	1343	AAGC	AAAT	TGTG	AACTG	TTCTA	AGAAAG	GAGCA	AAACAT	CAATG	1402
Db	1617	AAAC	NAAG	TGAC	AAATTTG	TACTTAG	AAAAA	AGGAG	CAAA	TGTTAAT	1676
Qy	1403	TTCT	TG	ACTC	CTCG	ACG	TGGCAT	CTG	AGAA	AGCTCAT	1462
Db	1677	TTCA	TG	ACTC	CTCG	ATG	TTCAG	CGG	AAAG	CCCAT	1736
Qy	1463	GTGA	AA	CATGA	AGCA	AAAG	TTAATG	CT	TGG	TAATCT	1522
Db	1737	CATA	AG	CATG	CGCC	AAAGAT	GAATG	CACTG	GA	CACTG	1796
Qy	1523	GCTG	CA	TATTTG	TGGT	CA	TTAC	AAAC	CTG	CGGCT	1582
Db	1797	GC	CG	CCCTAG	CAG	CCCACT	G	CACTG	CA	CTG	1856
Qy	1583	AAC	ATTAT	TCCCTT	CA	CGGCTT	TACTG	CTT	TAC	AGATG	1642
Db	1857	TCC	AT	ATCTCT	TAC	AGGCTT	CA	CAG	AGCA	AGATG	1916
Qy	1643	CTC	CTCC	AG	AGG	GTATCT	CA	TAG	GTAA	TTAC	1702
Db	1917	ATT	CTG	AGT	GAG	AGTAC	CACTAT	ACG	TACTT	CTG	1976
Qy	1703	G	CA	AGGCTG	GAG	ATG	TCG	AAAC	CTG	TAA	1762
Db	1977	TCT	AAA	AGCTG	GAG	ACTT	G	GAAC	CACTT	TG	2036
Qy	1763	AG	AG	CA	ATTG	AAAG	CGGCTG	AGTCT	CA	CAC	1822
Db	2037	AG	AG	CA	CTTAG	GGGCGG	CACTT	CA	CGCC	CTT	2096
Qy	1823	TC	CGTGGT	GAATAT	CTG	CTAC	AGCAT	TGG	AGCTG	ATG	1882
Db	2097	TC	TGTTG	TAG	GTAC	CTG	CTAC	CA	CGGTC	CGATG	2156
Qy	1883	CTT	GTAC	TTTG	CA	AAATG	CA	TGTTCTT	ATG	GACAT	1942
Db	2157	TTG	GTG	CCCTT	CAT	AATG	CTGTT	CAT	ATG	GAC	2216
Qy	1943	AA	CA	TG	GAG	CACTAG	CTT	AT	TG	GAATTT	2002
Db	2217	AG	CA	CTT	GGG	CTTCT	G	TAATG	GA	AACTT	2276
Qy	2003	GC	AG	AAAA	AGG	AAATAT	G	AAATTTG	C	AAACTT	2062
Db	2277	GC	AG	CTTAA	AG	NAAGTAT	G	AAATCTG	CA	AGCTC	2336
Qy	2063	AAAA	AAAA	CAG	GATG	GAATA	ATCT	CTTT	TG	ATCTTT	2122
Db	2337	AAAA	AA	CA	GATG	GAATA	TAC	ACCTTT	TG	GATTTG	2396
Qy	2123	CA	AG	ATCT	CTG	TAG	GGG	AGATG	CAG	CTTCT	2182
Db	2397	CAG	CA	CTTACT	G	AAAGG	GGATG	CTG	CTTT	TG	2456
Qy	2183	AG	AGTGA	GAAG	TGTCTT	CTCT	G	ATAATG	T	TAATTTG	2242

[illegible]

Db	3516	GAGGAGAAATCAACAACCATCAAAATGAGCGCATGTTGTTTCATGGTCTCTCTTTCAATTAAT	3575
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Db	3576	GCCATTATTCTAAAGGGTTTGATGCGGACATGCATACATAGGAGAAATGTTTGGGGCC	3635
Qy	3377	GGCATTATTATTTGCTGAAAACTCTTCCAAAAGCCAATCAATATGTATATGGAATTTGGAGGA	3436
Db	3636	GGGATTATTATTTGCTGAAAACCTCTCAAAAAGCAACCAATATGTTTATGGAATTTGGAGGA	3695
Qy	3437	GGTACTGGGTGTCAGTTCTCAAAAGACAGATCTTTGTACATTTTGCCACAGCGAGCTGCTC	3496
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Qy	3497	TTTTGCCGGGTAACTCTTGGGAAAGTCCTTTCTGCGAGTTTCAGTGCAATGAAATGGCAAT	3556
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Qy	3557	TCTCCTCCAGGTCAATCACTCAGTCACCTGGTAGGCCCCAGTGAATGGCTTAGCAATAGCT	3616
Db	3816	CGCGCTCCAGGGCACCACTCAGTCATTTGGTAGACCGAGCGTCAATGGCTGGCATAATGCT	3875
Qy	3617	GAATATGTTATTATACAGAGGAGAACAGGCTTATCCTCGAGTATTTAAATTAATTACCAGATT	3676
Db	3876	GAATATGTCATCTACAGGAGGAACAGGCATACCCAGAGTATCTTATCACTTACCAGATC	3935
Qy	3677	ATGAGGCGCTGAAG	3689
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RESULT 4

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US-11-266-748A-22929
; Sequence 22929, Application US/11266748A
; Publication No. US20050134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22929
; LENGTH: 8901
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-22929

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Query Match 47.3%; Score 1794.8; DB 8; Length 8901;
Best Local Similarity 72.5%; Pred. NO. 0;
Matches 2365; Conservative 0; Mismatches 872; Indels 27;

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Db	62	ATAATGCTGTCTTTTGGCCATGCTGAGGTGTGAGTCTGTATTGTGCCAAGAGCTG	121
Qy	552	ACCCAAATGTCGAGATAATTTGGAATATTACTCTCTCCATGAAGCTGCAATTTAAAGAA	611
Db	122	ATCCAAATGCCAGGATAATGGAATCTATACACCTCTGCAATGAAGCTGCTATTAAAGGGA	181
Qy	612	AGATTGATGTTTGCATTTGCTGTTACAGCATGGAGCTGAGCCAAACCATCCGAATACAG	671
Db	182	AGATCGATGTGTGATTTGTCTGTCGAGCAGCGAGCTGACCCAAACATTCGGAACTG	241
Qy	672	ATGGAAGCAGACATTTGATTTAGCAGATCCATCTGCCAAAGCAGTCTTACTTGGTGAAT	731
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Qy	732	ATAAGAAGATGAATCTTTAGAAAGTCCAGGAGTGGCAATGAAGAAAAAATGATGGCTC	791
Db	302	ACRAAGAAGACGAATCTCTAGNAGCTCTAGGAGTGGTAATGAAGAAAAACTAATGGCTT	361
Qy	792	TACTCACACATTTAAATGTCAACTGCCACCGAAGTATGSCAGNAAAGTCAACTCCATTAC	851
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Qy	912	ATGTCCATGCTTAAAGATAAAGGTGATCTGGTACCATTTACAAATGTCCTGTTTATGCTC	971
Db	482	ATGTTTCATGCAAAAGACAAAGTGGACTTGTGCTCTTCTCATATGTCATGTTCATATGGAC	541
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Db 1502 AGCTTTTGTAGTAAAGCATGGGGCTTCTGTCATGTGGGGGACTTATGGAATTTTACCCCTC 1561
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Db 1622 CAGATCCNACTAAAGAGNACAGAGNTGGAATACACCTTTGGATTTGTTAAGAGAGAG 1681
Qy 2112 ATACAGATATTCAGATCTGCTTTAGGGAGATGAGCTTTGCTAGATGCTGCCAAGAGG 2171
Db 1682 ACACAGATATTCAGGACTTACTGAAAGGGGATGCTGCTTTGTTGGATGCTGCCAAGAGG 1741
Qy 2172 GTTGTAGCAGAGTGNAGAGTTGCTTCTCTGATATGTAATTTGCCGATACCC 2231
Db 1742 GCTCCCTGGCAAGAGTGCAGAGCTCTGTACCCAGAGAAATATCAACTGCAGACACCC 1801
Qy 2232 AAGCAGACATTCACACCTTTTACATTTAGCAGCTGGTTATATAATTTAGAAAGTTGCAG 2291
Db 1802 AGGCAGAAATTCACCCCTCTGCACCTGGCAGCAGGCTATAATAACCTGGAAAGTCTG 1861
Qy 2292 AGTATTTGTTACACACGGAGCTGATGTGAATGCCAAGACAAAGGAGGACTTATTCCTT 2351
Db 1862 AATATCTTCTAGAGCATGGAGCTGATGTTAATGCCACAGGAGGTTTAAATTCCTC 1921
Qy 2352 TACATAATGAGCATCTTACGGGATGATGATGATGAGCAGCTCTACTAATAAGTATATG 2411
Db 1922 TTTAATAATGGGCACTTATGGGCATGTTGATAGATAGCGGCTTATATGATAAATAACAACA 1981
Qy 2412 CATGTGTCATTCACCGACAAATATGGGCTTTTACACACCTTTGCAGAAAGCAGCCCAAGG 2471
Db 1982 CGTGTATAATGCAACAGATTAAGTGGGGTTTACTCCCTCCATGAAGCAGCCAGAAAG 2041
Qy 2472 GACGAAACACAGCTTTGTGTTGTGAGCCCATGGAGCTGACCCGACTTTTAAAAATC 2531
Db 2042 GAAGGAGCAGCTGTGGGCCCTCTCTCTAGGCGCATGTTGGCAGACCCCAACCATGAAGAAC 2101
Qy 2532 AGGAGGACAAACCTTTAGATTTTGTTCAGGGGATGATGTCAGGCTCTTCTGACAG 2591
Db 2102 AGGAAGGCCAGAGCCCTCTGGATCTGGCAACAGCTGACGATATCAGAGCTTTGCTGATAG 2161
Qy 2592 CAGCCATGCCCCCATCTGCTCTGCCCTCTTGTTTACAAAGCCCTCAAGTGTCTCAATGGTGA 2651
Db 2162 ATGCCATGCCCCCAGAGGCGCTTACCTACCTGTTTAAAGCTCAGG----- 2206

Qy 2652 GAAGCCAGAGAGCCACTGCGAGATGCTCTCTCTTCAGGTCCATCTAGCCCATCAAGCCTTT 2711
Db 2207 -----CTACTGTAGTGAGTGCCTCTCTGATCTCACCATGATCCACCCCTCTCGCCTCT 2260
Qy 2712 CTGAGCCACAGTCTTTGACAACTTATCTGGAGTTTTTTTCAGAACTGCTCTTCTCAGTAGTTA 2771
Db 2261 CGGCTGCCACAGCATAGACAACTCTACTGGCCCTTTAGCAGAGTTGGCCGTAGAGGAG 2320
Qy 2772 GTTCAAGTGGAAACAGAGGGTGTCTTCCAGTTTGGAGAAAAAG-----GAGGTTCCAGGAG 2825
Db 2321 CCTCCAAATGCAAGGATGCGCGCGGGAACAGAAAGGAAGGAGGAGTAGTTCTGCTC 2380
Qy 2826 TAGATTTTACATTAATCAATTCGTAGGAATCTTGGACCTTGGACCTTAATGATATAT 2885
Db 2381 TTGACATGAATATCAGCCAATTTCTAAAAAGCCCTGGCCCTTGAACACCTTCGGGATATCT 2440
Qy 2886 TTGAGAGAGAACAGATCACCTTTTGGATGATTAATAGTTGAGATGGGGCACAAGAGCTGAAGG 2945
Db 2441 TTGAAACAGAACAGATTACTAGATGTTTGGCTGATATGGGTCTAGNAGNAGTTGAAAG 2500
Qy 2946 AGATTGGAATCAATGCTTATGGACATAGGCACAAACTTAATTAAGAGAGTCGAGAGACTTA 3005
Db 2501 AAATAGGCATCAATGCATATGGGCACCGCCACAAATTAATCAAAAGGAGTAGAAAGACTCT 2560
Qy 3006 TCTCCGAGACAAAGGCTTTAAACCATATTTAACTTTGAACACCTCTGGTAGTGAACAA 3065
Db 2561 TAGGTGGACAAACAGGCACCAATCTCTTATTTGACTTTTCTACTGTGTTAAATCAGGGAACGA 2620
Qy 3066 TTCTTATAGATCTGTCTCTGATGATAAAGAGTTTCACTCTGTGGAGGAGAGATGCAAA 3125
Db 2621 TTTTGTGGATCTTGTCTCCAGAGATTAAGNATATCACTCAGTGGAGAGAGAGATGCAAA 2680
Qy 3126 GTACAGTTTCAGAGCAGACAGAGATGGAGGTCTGTCAGGTGGAATCTTCAACAGATACAATA 3185
Db 2681 GTACTATTTCAGAAACACAGAGATGGTGAATGCTGGCGGCATCTTCAACAGATACAATG 2740
Qy 3186 TTCTCAAGATTCAGAGGTTTGTAAACAAAGAACTATATGGGAAAGATACACTCACCGGAGAA 3245
Db 2741 TCAATCGAATTTCAAAAAGTTGTCAACAAAGAGTTTGGGGAGCGGTTCTGCCACCGACAGA 2800
Qy 3246 AAGAAGTTCTTGAAGAAAACCAACACCATGCCAATGAACGAATCTATTTTCACTGGGTCTC 3305
Db 2801 AGNAGTGTCTGAGGAGATCAACACCATCAATGAGCGCATGTGTTTTCATGTTCTC 2860
Qy 3306 CTTTGTGAATGCAATTTATCCAAAGGCTTTGATGAAAAGCATGCGTACATAGGTGGTA 3365
Db 2861 CTTTCATTAATGCCATTTATTCATAAAGGTTTGTATGAGCGACATGCATACATAGGAGGAA 2920
Qy 3366 TGTGAGCTGGCATTTTATTTGCTGAAAACCTTCCAAAAGCAATCAATATCTATATG 3425
Db 2921 TGTGCGGGCGGGATTTATTTTGTCTAAAACCTCTCAAAAAGCAACAAATATGTTATG 2980
Qy 3426 GAATTGAGAGAGTACTGCGGTGCCAGTTTCAAAAAGACAGATCTTTGTATATTTGCCACA 3485
Db 2981 GAATTGAGAGAGGAAACAGGCTGCCCTACACAAGGACAGGTCAATGCTATATATGTACAC 3040
Qy 3486 GGCAGCTGCTCTTTTGGCGGGTAACTTGGGAAAGTCTTTTCTGCGAGTTTCAAGTGAATGA 3545
Db 3041 GACAAATGCTCTTCTGTGAGAGTGACCCCTTGGGAAATCTTTCTGCAAGTTTAGCACCATGA 3100
Qy 3546 AAATGGACATTTCTCTCCAGGTCTCATCTCAGTCACTGCTAGGCCAGGTGAATGCCC 3605
Db 3101 AAATGGCCCAACCGCCCTCCAGGGCACCACTCAGTTCATTGGTAGACCGGCGTCAATGGGC 3160
Qy 3606 TAGCATTAGCTGAATATGTTTATTTACAGAGAGAAACAGGCTTATCTCAGTATTTAATTA 3665
Db 3161 TGGCATATGCTGAATATGTCATCTACAGAGAGNACAGGCATACCCAGAGTATCTTATCA 3220
Qy 3666 CTTTACCAGATTTAGGCGCTGAAG 3689
Db 3221 CTTTACCAGATCATGAAGCCAGAG 3244

Db 495 ATGCCCCCATCTGCTCTGCCCCCTTGTATTACAAAGCCTCAAGTGCTCAATGGTGTGAGAAGC 436
Qy 2657 CCAGAGGCCACTGCAGATGCTCTCTCTTTCAGGTGCATCTAGCCCATCAAGCCTTCTTGCA 2716
Db 435 CCAGAGGCCACTGCAGATGCTCTCTCTTTCAGGTGCATCTAGCCCATCAAGCCTTCTTGCA 376
Qy 2717 GCCAGAGCTTGCACAACTTATCTGGGAGTCTTTCAGAACTGTCTTCAGTAGTTAGTTCA 2776
Db 375 GCCACCAAGTCTTGACAACTTATCTGGGAGTGTCTTCAAACTGTCTTCAGTAGTTAGTTCA 316
Qy 2777 AGTGAACAGAGGGTCTTCCAGTTTGAGAAAAGAGAGGTTCCAGGAGTAGATTTTAGC 2836
Db 315 AGTGAACAGAGGGTCTTCCAGTTTGACAAAAGAGAGGTTCCAGGAGTAGATTTTAGC 256
Qy 2837 ATAACTCAATTCGTAAGGAATCTTGGACTTGAGCACTTAATGGAATATTTTGAGAGAGAA 2896
Db 255 ATAACTCAATTCGTAAGGAATCTTGGACTTGAGCACTTAATGGAATATTTTGAGAGAGAA 196
Qy 2897 CAGATCACTTTGGATGTATTAGTTGAGATGGGCACAGAGGCTGAAGGAGATTGGAATC 2956
Db 195 CAGATCACTTTGGATGTATTAGTTGAGATGGGCACAGAGGCTGAAGGAGATTGGAATC 136
Qy 2957 AATGCTTATGACATAGGCACAACTAATTAAGGAGTCGAGAGACTTATCTCCGGCAA 3016
Db 135 AATGCTTATGACATAGGCACAACTAATTAAGGAGTCGAGAGACTTATCTCCGGCAA 76
Qy 3017 CAAGGCTTAAACCCATATTTAACTTTGAACACCTCTGGTAGTGAACAAATTTCTTATAGAT 3076
Db 75 CAAGGCTTAAACCCATATTTAACTTTGAACACCTCTGGTAGTGAACAAATTTCTTATAGAT 16
Qy 3077 CTGCTCTCTGATGAT 3091
Db 15 CTGCTCTCTGATGAT 1

RESULT 7
US-11-266-748A-99554
; Sequence 99554, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99554
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-99554
; Query Match 15.0%; Score 570; DB 8; Length 594;

Best Local Similarity 99.7%; Pred. No. 3e-149;
Matches 592; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
Qy 3194 ATTGAGAGGTTTGTAAAG-AAAATATGGGAAAGATACACTCACCGG-AGAAAAAGAG 3251
Db 1 ATTGAGAGGTTTGTAAAGAAAACTATGGAAAGATACACTCACCGGAAAGAAAGAG 60
Qy 3252 TTTCTGAAGAAAACCAACCATGCCAATGAACGAATGCTATTTCATGGGTCTCTCTTTTG 3311
Db 61 TTTCTGAAGAAAACCAACCATGCCAATGAACGAATGCTATTTCATGGGTCTCTCTTTTG 120
Qy 3312 TGAATGCAATTTATCCAAAAGGCTTTTCATGAAAGGCATGGTACATAGGTGGTATGTTG 3371
Db 121 TGAATGCAATTTATCCAAAAGGCTTTTCATGAAAGGCATGGTACATAGGTGGTATGTTG 180
Qy 3372 GAGCTGGCATTTATTTTGTGAAAACTCTTCCAAAAGCAATCAATATGATATGTAATG 3431
Db 181 GAGCTGGCATTTATTTTGTGAAAACTCTTCCAAAAGCAATCAATATGATATGTAATG 240
Qy 3432 GAGGAGTACTGGGTGTCAGTTTCACAAAGCAGATCTTGTACATTTGCCACAGGCAGC 3491
Db 241 GAGGAGTACTGGGTGTCAGTTTCACAAAGCAGATCTTGTACATTTGCCACAGGCAGC 300
Qy 3492 TGCTCTTTTCCCGGTAACCTTGGGAAAGTCTTTCCTGCAGTTCAGTGCAATGAAATGG 3551
Db 301 TGCTCTTTTCCCGGTAACCTTGGGAAAGTCTTTCCTGCAGTTCAGTGCAATGAAATGG 360
Qy 3552 CACATCTCTCCAGGTCACTCACTAGTCACTGGTAGGCCAGGTGTAATAGGCCTTAGCAT 3611
Db 361 CACATCTCTCCAGGTCACTCACTAGTCACTGGTAGGCCAGGTGTAATAGGCCTTAGCAT 420
Qy 3612 TAGCTGAATATGTTATTTACAGAGGAGAAAGGCTTATCTGAGTATTTAAATTAATCTACC 3671
Db 421 TAGCTGAATATGTTATTTACAGAGGAGAAAGGCTTATCTGAGTATTTAAATTAATCTACC 480
Qy 3672 AGATTATGAGGCTTGAAGGTATGGTGCATGATAAATAGTATTTTAAAGAACTTAATCTACC 3731
Db 481 AGATTATGAGGCTTGAAGGTATGGTGCATGATAAATAGTATTTTAAAGAACTTAATCTACC 540
Qy 3732 ACTGAACCTTAAATCATCAAGAGCAGTGGCCTCTACGTTTAACTCTCTTTGCT 3785
Db 541 ACTGAACCTTAAATCATCAAGAGCAGTGGCCTCTACGTTTAACTCTCTTTGCT 594

RESULT 8
US-11-266-748A-152365/c
; Sequence 152365, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18

; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 152365
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-152365

Query Match 15.0%; Score 570; DB 8; Length 594;
Best Local Similarity 99.7%; Pred. No. 3e-149; Indels 2; Gaps 2;
Matches 592; Conservative 0; Mismatches 0;
QY 3194 APTCAGAAGTTTGTAAACAG-AAACATATGGAAAGATACATCACCGG-AGAAAAGAG 3251
Db 594 APTCAGAAGTTTGTAAACAGAAACTATGGAAAGATACATCACCGGAGAAAAGAG 535
QY 3252 TTTCTGAAGAAAACACACACCATGCAATGAAGAAATGCTATTTTCATGGGTCTCTTTTG 3311
Db 534 TTTCTGAAGAAAACACACACCATGCAATGAAGAAATGCTATTTTCATGGGTCTCTTTTG 475
QY 3312 TGAATGCAATTTATCCACAAAGGCTTTTGATGAAGGCGATGCGTACATAGTGTGTATGTTG 3371
Db 474 TGAATGCAATTTATCCACAAAGGCTTTTGATGAAGGCGATGCGTACATAGTGTGTATGTTG 415
QY 3372 GAGCTGGCAATTTATTTTGTGAAAACTCTTCCAAAAGCAATCAATATATGTATGGAATTG 3431
Db 414 GAGCTGGCAATTTATTTTGTGAAAACTCTTCCAAAAGCAATCAATATATGTATGGAATTG 355
QY 3432 GAGGAGGTACTGGGTGTCAGTTTCAAAAGACAGATCTTTGTATACATTTTGGCCACAGGAGC 3491
Db 354 GAGGAGGTACTGGGTGTCAGTTTCAAAAGACAGATCTTTGTATACATTTTGGCCACAGGAGC 295
QY 3492 TGCTCTTTTGGCGGTAACTTTGGGAAAGTCTTCTCCAGTTTCAGTTCAGTCAATGAAATGG 3551
Db 294 TGCTCTTTTGGCGGTAACTTTGGGAAAGTCTTCTCCAGTTTCAGTTCAGTCAATGAAATGG 235
QY 3552 CACATTCCTCCAGGTCACTCAGTCAGTCTGTAGGCCAGTGAATGAGCCCTAGCAT 3611
Db 234 CACATTCCTCCAGGTCACTCAGTCAGTCTGTAGGCCAGTGAATGAGCCCTAGCAT 175
QY 3612 TAGCTGAATATGTTATTTACAGAGAGAACAGGCTTATCCTGAGTATTTAATTAATCTTACC 3671
Db 174 TAGCTGAATATGTTATTTACAGAGAGAACAGGCTTATCCTGAGTATTTAATTAATCTTACC 115
QY 3672 AGATTATGAGGCTCAAGGTATGTCGATGATTAATAGTATTAATTAAGAACTAATTC 3731
Db 114 AGATTATGAGGCTCAAGGTATGTCGATGATTAATAGTATTAATTAAGAACTAATTC 55
QY 3732 ACTGAACCTTAAATCATCAAGCAGCAGTGGCTCTAGCTTTTACTCTCTTTGCT 3785
Db 54 ACTGAACCTTAAATCATCAAGCAGCAGTGGCTCTAGCTTTTACTCTCTTTGCT 1

RESULT 9
US-11-266-748A-189602
; Sequence 189602, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 189602
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-189602

Query Match 14.1%; Score 535.6; DB 8; Length 929;
Best Local Similarity 74.0%; Pred. No. 1.7e-139;
Matches 679; Conservative 0; Mismatches 239; Indels 0; Gaps 0;
QY 1688 CAATTGCTGGAGCTGCAGAGGCTGGAGATGTCGAAACTGTAAATAAACTGTGTACTGTT 1747
Db 12 CGACTCTTTAGAGGCATCTTAAAGCTGGAGACTTGGAAACTGTGAAGCAACTTTGACGCTCT 71
QY 1748 CAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCACTGTACACCACTTTCATTTTGCAGCT 1807
Db 72 CAAATGTGATTTGTAGAGACTTAGAGGGCGGCATTCACGCCCTTACACTTCGCAGCA 131
QY 1808 GGGTATACAGAGTGTCCGTTGGAATATCTGTACAGCATGGAGCTGTGTGATGCT 1867
Db 132 GGCTACAAACCGGTGCTGTTGTAGAGTACCTGTCTACACACGGTGGCGATGTCCATGCC 191
QY 1868 AAGNTAAAGAGGCGCTTGTACCTTTGCACATGCATGCTTCTTATGGACATTAAGAATT 1927
Db 192 AAAGACAAGGTGGCTTGGTGGCCCTTTCATAATGCTGTTTATATGGACACTATGAGGTG 251
QY 1928 GCAGAACTTCTTGTGTTAAACATGGAGCAGTGTGTAATGTAGCTGTATTTATGGAAATTTACA 1987
Db 252 GCTGAGCTTTTAGTAAGGCATGGGCTTCTGTCAATGTGGCGGACTTATGGAAATTTACC 311
QY 1988 CTTTATCATGAAGCAGCAGCAAAAAGAAATATGAAATTTTGCAAACTTCTGCTCCAGAT 2047
Db 312 CCTCTCATGAAGCAGCAGCTTAAAGGAAATATGAAATCTGCAAGCTCCTTTTAAAGAT 371
QY 2048 GGTGCAGACCTTACCACCAAAAACAGGATGGAATCTCTTGGATCTTGTGTAAGAT 2107
Db 372 GGACAGATCCAACTTAAAGAAACAGAGATGGAATACACCTTTTGGATTTGGTAAAGGAA 431
QY 2108 GGAGATACAGATATTCAAGATCTGCTTAGGGGAGATGAGCTTTGTAGATGCTGCCAAG 2167
Db 432 GGAGACACAGATATTAGGACTTACTGAGGGGAGTGTGCTTTTGGTGTGCTGCCAAG 491
QY 2168 AAGGTTGTTTAGCCAGAGTGAAGAAGTTGCTTCTCTGTGATAATGTAAATTTGGCGCAT 2227
Db 492 AAGGCTGCTGGCAAGAGTGCAGAGCTCTGTACCCAGAGAAATATCAACTGCAGAGAC 551
QY 2228 ACCCAAGGCACACATTCAACACCTTTTACATTTAGCAGCTGGTTATTAATTTAGAACTT 2287
Db 552 ACCCAGGGCGAAATTCACCCCTCTGCACCTGGCAGCAGGCTATATAAATCTGGAAGTA 611
QY 2288 GCAGAGTATTTGTTTACACACGAGCTGATGTGAATGCCAAGCAAAAGGAGGACTTATT 2347
Db 612 GCTGAATATCTTCTAGAGCATGGAGCTGTATTAATGCCAGGACACAGGGTGTGTTAAT 671
QY 2348 CTTTATCATATAGCAGCATTTTACGGGCATGTAGATGTAGAGCTCTTACTACTATAAAGTAT 2407
Db 672 CTTCTTCATATGCGGCATCTTATGGGCATGTGACATAGCGGCTTTTATTGATAAATAAC 731
QY 2408 AATGATGTGTCAATGCCACGACAAATGGGCTTTTACACCTTTTGCACAGACAGCCCAA 2467
Db 732 AACACGTGTGTAATGCAACAGATAAGTGGCGGCTTTACTCCCTCCATGAAGAGCCGAC 791


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Query Match      13.6%; Score 515.6; DB 8; Length 668;
Best Local Similarity 97.6%; Pred. No. 5.9e-134;
Matches 518; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1644 TCCTCCAAAGAGGGTATCTCATTAGGTAAATTCAGAGGCGAGACAGCAATTCGTGGAAGCTG 1703
DB 23 TCCTACAAAGAGGGTATCTCATTAGGTAAATTCAGAGGCGAGACAGCAATTCGTGGAAGCTG 82

QY 1704 CAAAGGCTGGAGATGTCGAAATCTGTAAAAAAAATCTGTACTGTTTCAGAGTGTCAACTGCA 1763
DB 83 CAAAGGCTGGAGATGTCGAAATCTGTGTAAAAAAATCTGTACTGTTTCAGAGTGTCAACTGCA 142

QY 1764 GAGACATTTGAAGGCGTCACTACACCTTCATTTTTCAGCTGGGTATTAACAGAGTGT 1823
DB 143 GAGACATTTGAAGGCGTCACTACACCTTCATTTTTCAGCTGGGTATTAACAGAGTGT 202

QY 1824 CCGTGGTGGAAATATCTCTACAGCATGAGCTGATGTGCATGCTTAAAGATATAAGGAGGCC 1883
DB 203 CCGTGGTGGAAATATCTCTACAGCATGAGCTGATGTGCATGCTTAAAGATATAAGGAGGCC 262

QY 1884 TTGTACCTTTGCACAAATGCAATGCTTTTATGACATTTATGAAGTTGCGAAATCTTCTGTTA 1943
DB 263 TTGTACCTTTGCACAAATGCAATGCTTTTATGACATTTATGAAGTTGCGAAATCTTCTGTTA 322

QY 1944 AACATGAGCAGTAGTTAATGTAGCTGATTTATGGAATTTACACCTTTACATGGAAGCAG 2003
DB 323 AACATGAGCAGTAGTTAATGTAGCTGATTTATGGAATTTACACCTTTACATGGAAGCAG 382

QY 2004 CAGCAAAAGGAAATATGAATTTGCAAACTTCTGCTCCAGCATGTCGACCCCTACCA 2063
DB 383 CAGCAAAAGGAAATATGAATTTGCAAACTTCTGCTCCAGCATGTCGACCCCTACCN 442

QY 2064 AAAAAACAGGGATGGAATACTCTCTTTGGATCTTTTAAAGATGAGATACAGATATTC 2123
DB 443 NNNNNNCCAGGATGGAATACTCTCTTTGGATCTTTTAAAGATGAGATACAGATATTC 502

QY 2124 AAGATCTGCTTAGGGGAGATGACGCTTTGCTAGATGCTGCCAAGGGTT 2174
DB 503 AAGATCTGCTTAGGGGAGATGACGCTTTGCTAGATGCTGCCAAGGGTT 553
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RESULT 14
US-11-266-748A-116071
; Sequence 116071, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Karl
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 116071

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; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-116071

Query Match      13.3%; Score 503.2; DB 8; Length 1000;
Best Local Similarity 76.2%; Pred. No. 2.3e-130;
Matches 619; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 2878 GGATATATTTTGGAGAGAAACAGATCACTTTTGGATGTATTAGTTGAGATGGGGCAACAGGA 2937
DB 3 GGATATCTTTTGAACAGAAACAGATTAACACTAGATGTGTGGCTGATATGGGTCAATGAAGA 62

QY 2938 GCTGAAGAGATTTGGAATCAATGCTTATGACATAGCACAACAACTAATTAAGAGATCGA 2997
DB 63 GTTGAAGAAATAGGCATCAATGCATATGGGCCCGCCACAAAATTAATCAAGAGAGTAGA 122

QY 2998 GAGACTTATCTCCGGACAACAAGGTCTTAAACCATATTTAACTTTTGAACACCTCTGGTAG 3057
DB 123 AAGACTCTTAAAGTGGACAACAGGCCCAATCTCTTATTTGACTTTTCACTGTGTATCA 182

QY 3058 TGAACAACAATTTTATAGATCTGTCTCTGATGATAAGAGTTTTCAGTCTGTGGAGGAAGA 3117
DB 183 GGGACGATTTTCTGCTGATCTTCTCCAGAAGATAAAGATATACAGTCAGTGGGAAGAAGA 242

QY 3118 GATGCAAAAGTACAGTTTCGAGAGACAGAGATGAGAGTCATGCGAGTGGAAATCTTCAACAG 3177
DB 243 GATGCAAAAGTACTATTTCGAGAACACAGAGATGAGTGGTAAATGCTTGGCGGCATCTTTCAACAG 302

QY 3178 ATACAATATTTCTCAAGATTCAGAAAGTTTCTTAAACAAGAAATATGGAAGAGATACACTCA 3237
DB 303 ATACAATGTCATTTTCAAAATTTCAAAAGTTTGTCAACAGAGAGTTGAGGAGCGGTTCTGCCA 362

QY 3238 CCGGAGAAAAAGAGTTTCTGAAGAAAAACCAACCAATGCCAATGAACAAATGCTTATTTC 3297
DB 363 CCGACAGAAAGAGTGTCTGAGGAGAAATCAACCAATCAACAATGAGGCGCATGTTGTTTCA 422

QY 3298 TGGGTCTCTTTTGTGAATGCAATTTATCAACAAAGGCTTTGATGAAAGGCAATGCGTACAT 3357
DB 423 TGGTCTCTCTTTTCAATTAATGCCATTTATTCATAAAGGGTTTGTATGAGCGACATGCATACAT 482

QY 3358 AGGTGGTATGTTTGGAGCTGGCATTTATTTTGTCTGAAAACTCTTCCAAAAGCAATCAATA 3417
DB 483 AGGAGGAATGTTTGGGCCCGGGATTTATTTTGTCTGAAAACTCTTCCAAAAGCAACCAATA 542

QY 3418 TGTATATGGAATTTGGAGAGGTACTGGGTGTCAGTTTCACAAAGACAGATCTTGTTCAT 3477
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DB 663 CACATGAAAAATGGCCACCGGCTCCAGGCGCCACTCAGTCATTGGTAGACCGAGCGT 722

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QY 3658 TTTAATTTACTTACCAGATTTATGAGGCTCTGAAG 3689
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RESULT 15
US-11-266-748A-158235/c
; Sequence 158235, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick


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; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 158235
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-158235

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Query Match	13.3%	Score 503.2	DB 8	Length 1000
Best Local Similarity	76.2%	Pred. No. 2.3e-130		
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2938	GCTGAAGGAGATTGGAAATCAATGCTTTATGACATATAGGCACAAAACCTAATTAAAGGAGTCGA	2997		
938	GTTTGAAGAATAAGGCATCAATGCATATGGCACCGCCACAAAATTAATCAAGAGAGTAGA	879		
2998	GAGACTTATCTCCGGACAAACAAGGCTCTTAACCCATATTTAACTTTGACACACCTCTGGTAG	3057		
878	AAGACTCTTAGTGGGACAAACAGGCACCAATCCTTATTTCACITTTTCACCTGTGTTAATCA	819		
3058	TGGAACAAATCTTTATAGATCTGTCTCTGATGATAAAGAGTTTCAGTCTCTGGAGGAAGA	3117		
818	GGGACGATTTTGTCTGGATCTTGTCTCAGAAGATAAAGAAATATCAGTCAGTGGAGGAGA	759		
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3178	ATACAAATATTCTCAAGATTCAGAAAGTTTGTACAAGAAACTATGGGAAAGATACACTCA	3237		
698	ATCAATGTCAITTCGAATTCAAAAGTTGTCAACAGAAAGTTGAGGGAGCGGTTCTGCCA	639		
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3298	TGGGTCTCTTTTGTGNAATGCAATTATCCACAAAGGCTTTGATGAAAGGCATCGGTACAT	3357		
578	TGGTCTCTCTTTTCATTAAATGCCATTATTCATAAGGGTTTGTAGAGCGCATGCATACAT	519		
3358	AGGTGGTATGTTTGGAGCTGGCATTTATTTTGTGTGAAAACCTCTTCCAAAAGCAATCAATA	3417		
518	AGAGGNAATGTTTGGGGCCGGATTATTTTGTGTGAAAACCTCTTCCAAAAGCAACCAATA	459		
3418	TGTATATGGAATTTGGAGAGGATCTCGGGTCTCAGTTTCAAAAGACAGATCTTTGTTACAT	3477		
458	TGTTTATGGAATTTGGAGAGGAAACAGGCTGCCCTTACACAAAGGACAGGTCATGCTATAT	399		

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Result No.	Score	Match	Length	DB	ID	Description
1	3816	100.0	3816	3	US-09-696-668-2	Sequence 2, Appli
2	3816	100.0	3816	3	US-09-843-1598-2	Sequence 2, Appli
3	3791.4	99.4	4275	3	US-09-972-115A-5	Sequence 5, Appli
4	3788.4	99.3	6018	3	US-09-849-602-11	Sequence 11, Appli
5	3770.8	98.8	5075	3	US-09-799-451-556	Sequence 556, App
6	3594.8	94.2	4512	3	US-09-350-982C-3	Sequence 3, Appli
7	3488.8	91.4	3498	3	US-09-350-982C-4	Sequence 4, Appli
8	3393.4	88.9	3797	3	US-09-696-668-1	Sequence 1, Appli
9	3393.4	88.8	3797	3	US-09-843-1598-1	Sequence 1, Appli
10	3387.6	88.8	3394	3	US-09-427-154-1	Sequence 1, Appli
11	3341	87.6	4297	3	US-09-972-115A-3	Sequence 3, Appli
12	3039	79.6	4493	3	US-09-972-115A-1	Sequence 1, Appli
13	1885	49.4	4134	3	US-09-196-387-1	Sequence 1, Appli
14	1885	49.4	4134	3	US-09-841-835-1	Sequence 1, Appli
15	1885	49.4	4134	3	US-09-972-115A-7	Sequence 7, Appli
16	1521.2	39.9	4491	3	US-09-196-387-7	Sequence 7, Appli
17	1521.2	39.9	4491	3	US-09-841-835-7	Sequence 7, Appli
18	1369.4	35.9	4657	3	US-09-196-387-9	Sequence 9, Appli
19	1369.4	35.9	4657	3	US-09-841-835-9	Sequence 9, Appli
20	1192.6	31.3	2409	3	US-09-964-899-40	Sequence 40, Appli
21	518.4	13.6	520	3	US-09-972-115A-10	Sequence 10, Appli
22	380.4	10.0	384	3	US-09-972-115A-9	Sequence 9, Appli
23	249.4	6.5	770	3	US-09-270-767-13625	Sequence 13625, Appli

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Qy 3181 GTGGAACTTCAACAGATCAATATTTCTCAAGATTCAGAAAGTTTGTAAACAAGAACTAT 3240
Db 3181 GTGGAACTTCAACAGATCAATATTTCTCAAGATTCAGAAAGTTTGTAAACAAGAACTAT 3240
Qy 3241 GGGAAAGATACACTACCCGGAGAAAGAGTTTCTGAAGAAACCAACACCATGCAATG 3300
Db 3241 GGGAAAGATACACTACCCGGAGAAAGAGTTTCTGAAGAAACCAACACCATGCAATG 3300
Qy 3301 AACGAATGCTATTTCAATGGTCTCTTTTGTGAATGCAATTTATCAAAAGGCTTTGATG 3360
Db 3301 AACGAATGCTATTTCAATGGTCTCTTTTGTGAATGCAATTTATCAAAAGGCTTTGATG 3360
Qy 3361 AAAGGATGCTACATAGTGTGTATGTTGGAGTGGCAATTTATTTGTGAAACTCTT 3420
Db 3361 AAAGGATGCTACATAGTGTGTATGTTGGAGTGGCAATTTATTTGTGAAACTCTT 3420
Qy 3421 CCAAAAGCAATCAATATGATATGGAATTTGGAGGAGTACTGGGTGTCAGTTCAAAAG 3480
Db 3421 CCAAAAGCAATCAATATGATATGGAATTTGGAGGAGTACTGGGTGTCAGTTCAAAAG 3480
Qy 3481 ACAGATCTTTGATATTTGCAAGCAGCTGCTTTTTCGGGGTAACTTTGGGAAAGT 3540
Db 3481 ACAGATCTTTGATATTTGCAAGCAGCTGCTTTTTCGGGGTAACTTTGGGAAAGT 3540
Qy 3541 CTTTCTGAGTTCAGTGAATGGAATGCAATTTCTCTCAGTCACTCACTCAGTCA 3600
Db 3541 CTTTCTGAGTTCAGTGAATGGAATGCAATTTCTCTCAGTCACTCACTCAGTCA 3600
Qy 3601 CTGAGGAGGAGTGAATGAGCTTACGATTTAGCTGAATATGTTATTTACAGAGGAGAC 3660
Db 3601 CTGAGGAGGAGTGAATGAGCTTACGATTTAGCTGAATATGTTATTTACAGAGGAGAC 3660

Qy 3661 AGGCTTATCTGAGTATTTAAATTTACTTACAGATTATGAGGCTGAAGTATGTTCTGATG 3720
Db 3661 AGGCTTATCTGAGTATTTAAATTTACTTACAGATTATGAGGCTGAAGTATGTTCTGATG 3720
Qy 3721 GATAAATAGTATTTTAAAGAACTAAATTTCCACTGAACCTAAATCATCAAGCAGCAGTG 3780
Db 3721 GATAAATAGTATTTTAAAGAACTAAATTTCCACTGAACCTAAATCATCAAGCAGCAGTG 3780
Qy 3781 GCCTCTAGTATTTACTCTCTTGTCTGAAAAAATAA 3816
Db 3781 GCCTCTAGTATTTACTCTCTTGTCTGAAAAAATAA 3816

RESULT 3
US-09-972-115A-5
; Sequence 5, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; PRIORITY FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 4275
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (284)..(3781)
; OTHER INFORMATION:
US-09-972-115A-5

Query Match 99.4%; Score 3791.4; DB 3; Length 4275;
Best Local Similarity 99.8%; Pred No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 1 CGCGTGTCTCCGCGCCCGCGCGGCGAGCCGGGGGCGAGGAGCCAGAGGGGCGCG 60
Db 61 CGCGTGTCTCCGCGCGCGCGCGGCGAGCCGGGGGCGAGGAGCCATCGAGGGGCGCG 120
Qy 61 TGGGCGCGCGCCATGGGACTGGCCCGGATCCGTCACAGCAGGAGCCAGAGCGCCGCG 120
Db 121 TGGGCGCGCG-CCATGGGACTGGCCCGGATCCGTCACAGCAGGAGCCAGAGCGCCG 179
Qy 121 CCTCAGCAGCGCTTCTCTCGGGGGGCTCGCCCTCTCTGTCGCGGGGCGCGGGCTCTG 180
Db 180 CCTCAGCAGCGCTTCTCTCGGGGGGCTCTCGCCCTCTCTGTCGCGGGGCGCGGGCTCTG 239
Qy 181 TCCGGTGTCTGCGCTGTGTGCTGGGCGGCGCCAGGATCATGTGCGGTTCGCGCT 240
Db 240 TCCGGTGTCTGCGCTGTGTGCTGGGCGGCGCCAGGATCATGTGCGGTTCGCGCT 299
Qy 241 GCGCGCGGGGAGCGGCTGCGGAGCGCGCGCGCGCGGCGCGCGCGCGCGCG 300
Db 300 GCGCGCGGGGAGCGGCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 359
Qy 301 GAGAGCTGTTGAGGCGCTGCGCAACGGGAGCTGAAACAGTCAAGAGCTGTTGACGC 360
Db 360 GAGAGCTGTTGAGGCGCTGCGCAACGGGAGCTGAAACAGTCAAGAGCTGTTGACGC 419
Qy 361 CTGAGAAGTGAACAGCGCGGACAGCGGGGCGAGGAAATCCACCCGCTTGCACTTCGCG 420

Db 420 CTGAGAGGTGAAAGCAGCGCGGACAGCGGGGCGAGGAAATCCACCCCGCTGCACCTTCGCG 479
Qy 421 CAGGTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAAATGTCGAAG 480
Db 480 CAGGTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAAATGTCGAAG 539
Qy 481 CACGTGATGATGGGGGCTTATTCCTCTTCATATATGATGCTCTTTTGGTCATGCTGAAG 540
Db 540 CACGTGATGATGGGGGCTTATTCCTCTTCATATATGATGCTCTTTTGGTCATGCTGAAG 599
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Qy 601 CTCCTCTCCATGAAAGCTGCAATTAAGAGAAAGATTGATTTTGCATTTGTGCTTTACAGC 660
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Db 720 ATGGAGCTGAGCCCAACCATCCGAATACAGATGAAGAGACAGCATTTGGATTTAGCAGATC 779
Qy 721 CATCTGCCAAGCAGTGTCTTACTGCTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCA 780
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Qy 781 GGAGTGGCAATGAAGAAATAATGATGCTCTTACACCAATTAATTTGTCAACTGCCACG 840
Db 840 GGAGTGGCAATGAAGAAATAATGATGCTCTTACACCAATTAATTTGTCAACTGCCACG 899
Qy 841 CAAGTATGGCAGAAAGTCAACTCCATACATTTATTTGGCAGCAGGATATAACAGAGTAAGA 900
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Qy 901 TTGTACAGCTGTACTGCAACATGAGCTGATGCTCAATGCTTAAAGATAAAGGTGATCTGG 960
Db 960 TTGTACAGCTGTACTGCAACATGAGCTGATGCTCAATGCTTAAAGATAAAGGTGATCTGG 1019
Qy 961 TACCATTACAAATGCCCTGTTTATGGTCAATTAATGAAGTAACCTGAACTTTTGGTCAAGC 1020
Db 1020 TACCATTACAAATGCCCTGTTTATGGTCAATTAATGAAGTAACCTGAACTTTTGGTCAAGC 1079
Qy 1021 ATGGTGCCTGTGAATGCAATGACATTTGGGCAATTCACCTCTTCATGAGCAGCTT 1080
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Qy 1081 CTAAGAACAGGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGACAGACCAACACTGC 1140
Db 1140 CTAAGAACAGGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGACAGACCAACACTGC 1199
Qy 1141 TCAATTTGTCACAATAAAGTGTCTATAGACTTTGGCTCCACACCAAGATTAAAGAAAGAT 1200
Db 1200 TCAATTTGTCACAATAAAGTGTCTATAGACTTTGGCTCCACACCAAGATTAAAGAAAGAT 1259
Qy 1201 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAGAGCTGATGTTACTC 1260
Db 1260 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAGAGCTGATGTTACTC 1319
Qy 1261 GAATCAAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCTTCAAAACATGAAA 1320
Db 1320 GAATCAAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCTTCAAAACATGAAA 1379
Qy 1321 CAGCATTTGCTGCTGCATCTCCATATCCCAAGAAAGCAAAATATGTGAATGTT 1380
Db 1380 CAGCATTTGCTGCTGCATCTCCATATCCCAAGAAAGCAAAATATGTGAATGTT 1439
Qy 1381 TGCTAAGAAAGGAGCAACATCAATGAAGATTAAGGAATTTGACTCTCTGCAAG 1440
Db 1440 TGCTAAGAAAGGAGCAACATCAATGAAGATTAAGGAATTTGACTCTCTGCAAG 1499
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Qy 1501 TTAATGCTCTGGATAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTTCATC 1560
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Qy 1561 TACAAACCTCCGCCCTACTCTCAGAGCTATGGGTGTGATCTTAACATTATATCCCTTCAGG 1620
Db 1620 TACAAACCTCCGCCCTACTCTCAGAGCTATGGGTGTGATCTTAACATTATATCCCTTCAGG 1679
Qy 1621 GCTTTACTGCTTTTACAGATGGGAAATGAAAATGTACAGCAACTCTCTCAAGAGGGTATCT 1680
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Qy 1681 CATTAGTAAATTCAGAGGAGACAGACAATTTGCTGGAGCTGCAGAGCTGGAGATGTCG 1740
Db 1740 CATTAGTAAATTCAGAGGAGACAGACAATTTGCTGGAGCTGCAGAGCTGGAGATGTCG 1799
Qy 1741 AAACGTGAAAAAATCTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGGCTC 1800
Db 1800 AAACGTGAAAAAATCTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGGCTC 1859
Qy 1801 AGTCTACACCACTTCAATTTTTCAGCTGGGTATTAACAGAGTGTCCGTGGTGGAAATATCTGC 1860
Db 1860 AGTCTACACCACTTCAATTTTTCAGCTGGGTATTAACAGAGTGTCCGTGGTGGAAATATCTGC 1919
Qy 1861 TACAGCATGAGAGCTGATGTCATGCTTAAAGATAAAGAGGSCCTTGTTACCTTTGCACATG 1920
Db 1920 TACAGCATGAGAGCTGATGTCATGCTTAAAGATAAAGAGGSCCTTGTTACCTTTGCACATG 1979
Qy 1921 CATGTTCTTATGACATTTATGAAGTTGCAGAACTTCTTTTAAACATGGAGCAGTAGTTA 1980
Db 1980 CATGTTCTTATGACATTTATGAAGTTGCAGAACTTCTTTTAAACATGGAGCAGTAGTTA 2039
Qy 1981 ATGTAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATG 2040
Db 2040 ATGTAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATG 2099
Qy 2041 AAATTTGCAAACTTCTGCTCCAGATGGTGAGACCTTACCAAAAAAAGAGGATGGA 2100
Db 2100 AAATTTGCAAACTTCTGCTCCAGATGGTGAGACCTTACCAAAAAAAGAGGATGGA 2159
Qy 2101 ATACTCTTTTGGATCTTGTTTAAAGATGAGATACAGATATTTCAAGATCTGCTTAGGGAG 2160
Db 2160 ATACTCTTTTGGATCTTGTTTAAAGATGAGATACAGATATTTCAAGATCTGCTTAGGGAG 2219
Qy 2161 ATGCAGCTTTGCTAGATGCTGCAAGAAAGGGTGTTTAGCCAGAGTGAAGTGTGCTT 2220
Db 2220 ATGCAGCTTTGCTAGATGCTGCAAGAAAGGGTGTTTAGCCAGAGTGAAGTGTGCTT 2279
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Db 2280 CTCTGTATATGTAATTTGCGGATACCCAGGAGACATTTCAACACCTTTTACATTTAG 2339
Qy 2281 CAGCTGTTTATTAATTTTAAAGTTTGCAGATATTTTGTACAAACAGGAGCTGATGTA 2340
Db 2340 CAGCTGTTTATTAATTTTAAAGTTTGCAGATATTTTGTACAAACAGGAGCTGATGTA 2399
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Db 2400 ATGCCAAGCAAAAGGAGGACTTATTCCTTTTACATAATGAGCATCTTACGGGATGTAG 2459
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Db 2580 CCCATGAGCTGACCCGACTCTTTAAATAATCAGGAAGGACAAAACCTTTTAGATTTAGTTT 2639

Qy	2581	CAGCGGATGATGTCTCAGCGCTCTTCTTGACAGGACGCATGCCCCCAATTCGTCTCTGGCCCTCTTT	2644
Db	2640	CAGCGGATGATGTCTCAGCGCTCTTCTTGACAGGACGCATGCCCCCAATTCGTCTCTGGCCCTCTTT	2699
Qy	2641	GTTACAAGCCCTCAAGTCTCTCAAATGGTGTGAGAAGCCCCAGGAGCACCTGCAGATGCTCTCT	2700
Db	2700	GTTACAAGCCCTCAAGTCTCTCAAATGGTGTGAGAAGCCCCAGGAGCACCTGCAGATGCTCTCT	2759
Qy	2701	CTTCAGGTTCCATCTTAGGCCCATCAAGCCCTTTCTGCAGCCAGCAGTCTTTGACAACTTATCTG	2760
Db	2760	CTTCAGGTTCCATCTTAGGCCCATCAAGCCCTTTCTGCAGCCAGCAGTCTTTGACAACTTATCTG	2819
Qy	2761	GGAGTTTTTCAGAACTGTCTTCAGTAGTGTAGTTTCAAGTGGAAACAGAGGGTGTCTTCAAGTT	2820
Db	2820	GGAGTTTTTCAGAACTGTCTTCAGTAGTGTAGTTTCAAGTGGAAACAGAGGGTGTCTTCAAGTT	2879
Qy	2821	TGGAGAAAAGGAGGTTCCAGGAGTGTAGTTTATAGCATAACTCAATTTCGTAAAGNAATCTTG	2880
Db	2880	TGGAGAAAAGGAGGTTCCAGGAGTGTAGTTTATAGCATAACTCAATTTCGTAAAGNAATCTTG	2939
Qy	2881	GACTTTGAGCACCTAANTGGATATATTTTGAGAGAGAACAGATCACTTTTGGATGTATTAGTTTG	2940
Db	2940	GACTTTGAGCACCTAANTGGATATATTTTGAGAGAGAACAGATCACTTTTGGATGTATTAGTTTG	2999
Qy	2941	AGATGGGGCACAAGGAGCTGAAGAGATTGGAATCAATGCTTATGGACATAGGCAACAAC	3000
Db	3000	AGATGGGGCACAAGGAGCTGAAGAGATTGGAATCAATGCTTATGGACATAGGCAACAAC	3059
Qy	3001	TAAATTAAGAGNCTCGAGAGCTTATCTCCGGACAAACAGTCTTTAACCATATTTAACTTT	3060
Db	3060	TAAATTAAGAGNCTCGAGAGCTTATCTCCGGACAAACAGTCTTTAACCATATTTAACTTT	3119
Qy	3061	TGAACACTCTGTGTAGTGGAACTTCTTATAGATCTGTCTCTGTATGATAAAGAGTTTC	3120
Db	3120	TGAACACTCTGTGTAGTGGAACTTCTTATAGATCTGTCTCTGTATGATAAAGAGTTTC	3179
Qy	3121	AGTCTGTGGAGGAAGAGATGCAAAAGTACAGTTCTGAGAGCACAGAGATGGAGTCAATGCAG	3180
Db	3180	AGTCTGTGGAGGAAGAGATGCAAAAGTACAGTTCTGAGAGCACAGAGATGGAGTCAATGCAG	3239
Qy	3181	GTGGAACTCTTCACAGATACAATATTTCTCAAGATTTCAGAGGTTCTGTAACAAGAACTAT	3240
Db	3240	GTGGAACTCTTCACAGATACAATATTTCTCAAGATTTCAGAGGTTCTGTAACAAGAACTAT	3299
Qy	3241	GGGAAAGATACACTCACCGGAGAAAAAGTTTCTGAAGAAAAACCACCAACCATGCCAATG	3300
Db	3300	GGGAAAGATACACTCACCGGAGAAAAAGTTTCTGAAGAAAAACCACCAACCATGCCAATG	3359
Qy	3301	AACGAATGCTATTTTCATGGGTCTCTCTTTGTGAATGCAATTTATCCAAAGGCTTTGATG	3360
Db	3360	AACGAATGCTATTTTCATGGGTCTCTCTTTGTGAATGCAATTTATCCAAAGGCTTTGATG	3419
Qy	3361	AAAGGCATGGGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTCTGAAAACTCTT	3420
Db	3420	AAAGGCATGGGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTCTGAAAACTCTT	3479
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Db	3480	CCAAAAGCAATCAATATGTATATGGAATTTGGAGAGGTACTTGGGTGTCCAGTTTCACAAAG	3539
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Db	3540	ACAGATCTTGTTTACATTTGGCCACAGGAGCTGTCTTTTTCGGGTAAACCTTCGGGAAAGT	3599
Qy	3541	CTTTCCTGCAAGTTCAAGTGCATGGAATGGAATGGACATTTCTCTCCAGGTCACTCAGTCA	3600
Db	3600	CTTTCCTGCAAGTTCAAGTGCATGGAATGGAATGGACATTTCTCTCCAGGTCACTCAGTCA	3659
Qy	3601	CTGGTAGGCCAGTGAATGGCCCTAGCATTTAGCTGAAATGTTTATTTTACAGAGGAGAAC	3660
Db	3660	CTGGTAGGCCAGTGAATGGCCCTAGCATTTAGCTGAAATGTTTATTTTACAGAGGAGAAC	3719
Qy	3661	AGGCTTATCTCTGAGTATTTAAATTTACTTACCAGATTTATGAGGCCCTGGAAGTATGGTCGATG	3720

Db	3720	AGGCTTATCTGAGTATTTAAATTTACAGATTATGAGCCCTGAAGGTATGTCGATG	3779
Qy	3721	GATAAAATAGTTATTTAAAGAACTAAATTCCACTGAACCTAAAATCATCAAAGCAGCAGTG	3780
Db	3780	GATPAAATAGTTATTTAAAGAACTAAATTCACCTGAACCTAAAATCATCAAAGCAGCAGTG	3839
Qy	3781	GCCTCTACGTTTACTCTCTTGTGTAATAAAAA 3813	
Db	3840	GCCTCTACGTTTACTCTCTTGTGTAATAAAAA 3872	
RESULT 4			
US-09-849-602-11			
; Sequence 11, Application US/09849602			
; Patent No. 6794501			
; GENERAL INFORMATION:			
; APPLICANT: Scanlan, Matthew J.			
; APPLICANT: Old, Lloyd J.			
; APPLICANT: Stockert, Elisabeth			
; APPLICANT: Chen, Yao-Tseng			
; TITLE OF INVENTION: Colon Cancer Antigen Panel			
; FILE REFERENCE: L0461/7105(JRV)			
; CURRENT APPLICATION NUMBER: US/09/849,602			
; CURRENT FILING DATE: 2001-05-04			
; NUMBER OF SEQ ID NOS: 30			
; SOFTWARE: Patentin version 3.0			
; SEQ ID NO 11			
; LENGTH: 6018			
; TYPE: DNA			
; ORGANISM: Homo sapien			
US-09-849-602-11			
Query Match 99.3%; Score 3788.4; DB 3; Length 6018;			
Best Local Similarity 99.8%; Pred. No. 0;			
Matches 3803; Conservative 0; Mismatches 6; Indels 1; Gaps 1;			
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Db	1	GCTGCTTCGCGCGCGCGGGCAGCCGGGGGCGAGGCCAGCGAGCCAGCGAGCGCGCGTGG	60
Qy	64	CGCGCGGCCATGGGACTCGCGCGGATCCGGTGACAGCAGCGAGCCAGCGCGCGCGCGCC	123
Db	61	CGCGCG-CCATGGGACTCGCGCGGATCCGGTGACAGCAGCGAGCCAGCGCGCGCGCC	119
Qy	124	TGACGCGCTCTTCTTCGCGGGGGCTCGCCCTCTCTGTCGCGGGGCCCGGGGCTCTCTGCTCC	183
Db	120	TGACGCGCTCTTCTTCGCGGGGGCTCGCCCTCTCTGTCGCGGGGCCCGGGGCTCTCTGCTCC	179
Qy	184	GTTTGTGCGCGCTGTTGCTGGCTGTGGCGGGGCCAGGATCATGTTCGGGTGCGCGCTGCG	243
Db	180	GTTTGTGCGCGCTGTTGCTGGCTGTGGCGGGGCCAGGATCATGTTCGGGTGCGCGCTGCG	239
Qy	244	CCGCGCGGAGCGGCTGCGCGAGCCCGCGGCCAGCGCGCTGGAGCCGCGCGCCCGCGAG	303
Db	240	CCGCGCGGAGCGGCTGCGCGAGCCCGCGGCCAGCGCGCTGGAGCCGCGCGCCCGCGAG	299
Qy	304	AGCTGTTTCGAGGCGTGCCGCAACGGGGAACGTGGAACCAAGAGCTGCTGTGACGCGCTG	363
Db	300	AGCTGTTTCGAGGCGTGCCGCAACGGGGAACGTGGAACCAAGAGCTGCTGTGACGCGCTG	359
Qy	364	AGAGGTGAACCGCGGACCGCGGGCAGGAAATCCACCCGCTGCACCTTCGCCCGCAG	423
Db	360	AGAGGTGAACCGCGGACCGCGGGCAGGAAATCCACCCGCTGCACCTTCGCCCGCAG	419
Qy	424	GTTTTCGGCGGAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAATGTCCAAAGCAC	483
Db	420	GTTTTCGGCGGAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGCAAATGTCCAAAGCAC	479
Qy	484	GTGAATGATGGGCGCTTATTCCTCTTCATATGATGCTCTTTTGGTCACTGCTGAAGTAG	543
Db	480	GTGAATGATGGGCGCTTATTCCTCTTCATATGATGCTCTTTTGGTCACTGCTGAAGTAG	539

QY 544 TCAATCTCCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAAATGGNAATTATACTC 603
Db 540 TCAATCTCCTTTTGGGACATGGTGCAGACCCCAATGCTCGAGATAAATGGNAATTATACTC 599
QY 604 CTCTCCATGAAGCTGCAATTAAGGAAAGATTGATGTTTGGCATTGTGCTGTACAGCATG 663
Db 600 CTCTCCATGAAGCTGCAATTAAGGAAAGATTGATGTTTGGCATTGTGCTGTACAGCATG 659
QY 664 GAGCTGAGCCAAACATCCGAAATAACAGATGGAAGGACAGCATTTGGATTTAGCAGATCCAT 723
Db 660 GAGCTGAGCCAAACATCCGAAATAACAGATGGAAGGACAGCATTTGGATTTAGCAGATCCAT 719
QY 724 CTGCCAAGCAGTCTTACTGGTGAATATAGAAAGATGAACCTTTAGAAAGTGCCAGGA 783
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QY 784 GTGGCAATGAAGAAAAAATGATGGCTCTACTCACCAATTAATGTCAACTGCCACGCCAA 843
Db 780 GTGGCAATGAAGAAAAAATGATGGCTCTACTCACCAATTAATGTCAACTGCCACGCCAA 839
QY 844 GTGATGGCAGAAAGTCAATCCATTAATTTGGCAGCAGGATATAACAGAGTAAAGATTG 903
Db 840 GTGATGGCAGAAAGTCAATCCATTAATTTGGCAGCAGGATATAACAGAGTAAAGATTG 899
QY 904 TACAGCTGTACTGCAACATGGAGCTGATGCTCCATGCTTAAGATAAAGGTGATCTGTAC 963
Db 900 TACAGCTGTACTGCAACATGGAGCTGATGCTCCATGCTTAAGATAAAGGTGATCTGTAC 959
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QY 1024 GTGCTGTGTAATGCAATGGAATGTGGCAATTCATCTCTTTTCATGAGCAGCTTCTA 1083
Db 1020 GTGCTGTGTAATGCAATGGAATGTGGCAATTCATCTCTTTTCATGAGCAGCTTCTA 1079
QY 1084 AGAAGGGTTGAAGTATGTTCTTCTTTAAGTTATGGTGAGACCCACACATGCTCA 1143
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QY 1144 ATGTGCAATATAAAGTGCTATAGACTTGGCTCCACACACACAGTTAAAGAAAGATTAG 1203
Db 1140 ATGTGCAATATAAAGTGCTATAGACTTGGCTCCACACACAGTTAAAGAAAGATTAG 1199
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Db 1200 CATATGAATTTAAAGGCCACTCGTTGTGTCGAAGCTGCAAGAGAGCTGATGTTACTCGAA 1259
QY 1264 TCAAAAACATCTCTCTGGAATGTTGAATTTCAAGCATCTCTCAACACATGAAACAG 1323
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QY 1324 CATTGCAATTTGCTGCTGCATCTCCATATCCAAAAGAAAGCAATATGTGAACCTGTGC 1383
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Db 1680 TAGGTAATTCAGAGGCAGACAGACAATTTGCTGGAAGCTGCAAGGGCTGGAGATGTGAAA 1739
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RESULT 6
US-09-350-982C-3
; Sequence 3, Application US/09350982C
; Patent No. 6455290
; GENERAL INFORMATION:
; APPLICANT: Berthelsen, Jens
; APPLICANT: Toma, Salvatore
; APPLICANT: Isacchi, Antonella
; TITLE OF INVENTION: Tankyrase Homolog Protein(THP), Nucleic Acids, and Methods Relat
; FILE OF INVENTION: Same
; FILE REFERENCE: PHRM-0043
; CURRENT APPLICATION NUMBER: US/09/350,982C
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4512
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PCR Primers
; NAME/KEY: misc feature
; LOCATION: (1124)..(1124)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (2672)..(2672)
; OTHER INFORMATION: n is any nucleic acid
US-09-350-982C-3
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 3593; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
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Qy 2670 AGAAGCCAGAGGACCTGAGATGCTCTCTCTTTCAGTGTGATGTAGCCCATCAAGCCTT 2729
Db 2468 AGAAGCCAGAGGACCTGAGATGCTCTCTCTTTCAGTGTGATGTAGCCCATCAAGCCTT 2527
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Db 2528 TCTGACCCAGAGTCTTGACAACTTATCTGGGAGTTTTTTCAGAACTGTCTTCAAGTAGTT 2587
Qy 2790 AGTTTCAAGTGGAAACAGAGGGTGTCTTCCAGTTTGGAGAAAAAGGAGGTTTCCAGGAGTAGAT 2849
Db 2588 AGTTTCAAGTGGAAACAGAGGGTGTCTTCCAGTTTGGAGAAAAAGGAGGTTTCCAGGAGTAGAT 2647


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QY 2850 TTTAGCATAACTCAATTCGTAGGAATCTTGGACTTGGACACCTAATGGATATATTGAG 2909
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QY 2970 GGAATCAATGCTTATGGACATAGGACACAACTAATTAAGAGAGTGGAGAGACTTATCTCC 3029
Db 2768 GGAATCAATGCTTATGGACATAGGACACAACTAATTAAGAGAGTGGAGAGACTTATCTCC 2827
QY 3030 GGACAAACAGGCTTAAACCCATATTTAACTTTGAAACACTCTCTGGTAGTGGAACTTCTT 3089
Db 2828 GGACAAACAGGCTTAAACCCATATTTAACTTTGAAACACTCTCTGGTAGTGGAACTTCTT 2887
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Db 2888 ATAGATCTGCTCTGATGATGAAGAGTTTCAGTCTGTGGAGGAAGAGATGCAAGTACA 2947
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Db 3548 CACTGAACTTAAATCATCAAGCAGAGTGGCCTCTACGTTTCTCTTCTGCTGAAA 3607
QY 3810 AAAA 3813
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RESULT 7
US-09-350-982C-4
; Sequence 4, Application US/09350982C
; Patent No. 6455290

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; GENERAL INFORMATION:  
; APPLICANT: Berthelsen, Jens  
; APPLICANT: Tona, Salvatore  
; APPLICANT: Isacchi, Antonella  
; TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, and Methods Relat  
; FILE REFERENCE: PHRM-0043  
; CURRENT APPLICATION NUMBER: US/09/350,982C  
; CURRENT FILING DATE: 1999-07-09  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 4  
; LENGTH: 3498  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: PCR Primers  
; NAME/KEY: CDS  
; LOCATION: (1)..(3498)  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Xaa is any amino acid  
; NAME/KEY: misc feature  
; LOCATION: (1102)..(1102)  
; OTHER INFORMATION: n is any nucleic acid  
; NAME/KEY: misc feature  
; LOCATION: (2650)..(2650)  
; OTHER INFORMATION: n is any nucleic acid  
US-09-350-982C-4
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Query Match 91.4%; Score 3488.8; DB 3; Length 3498;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3487; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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QY 285 GTGGAGCGCGCGCGCGCGAGAGCTGTTGAGCGGTGCGCAACGGGGAGCTGGAAAGAGTC 344  
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QY 345 AAGAGGCTGTGAGCGCTGGAAGGTGAACAGCGCGCACACAGCGCGGCGAGAAATCCACC 404  
Db 121 AAGAGGCTGTGAGCGCTGGAAGGTGAACAGCGCGCACACAGCGCGGCGAGAAATCCACC 180  
QY 405 CCGCTGCACTTCGCGCGAGGTTTTGGCGGGAAGACAGTAGTTGAATATTTGCTTCAGAA 464  
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QY 465 GGTCAAAATGTCCAAAGCACGTGATGATGGGGGCTTATTCCTCTTCAATGCAATGCTCT 524  
Db 241 GGTCAAAATGTCCAAAGCACGTGATGATGGGGGCTTATTCCTCTTCAATGCAATGCTCT 300  
QY 525 TTTGGTCATGCTGAAGTAGTCAATCTCTTTTGGCACATGCGTGCAGACCCCAATGCTCGA 584  
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DB 661 TATAACAGAGTAAAGATTGTACAGCTGTATTCTGCAACATGGAGCTGATGTCCTGCTAAA 720
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DB 721 GATAAAGGTGATCTGGTACCATTACAAATGCCCTGTTCTTTATGTCATATTGAAGTAACT 780
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RESULT 8
US-09-696-668-1
; Sequence 1, Application US/0969668
; Patent No. 6617102
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ososovskaya, Valeria
; TITLE OF INVENTION: TANKYRASE H. COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS
; CURRENT APPLICATION NUMBER: US/09/696,668
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3797
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-696-668-1
Query Match 88.9%; Score 3393.4; DB 3; Length 3797;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 2082 AATTTGCACAACTTCTGCTCCAGCATGTGCGAGACCTTACCNAAAAAACAGGGATGAAA 2082
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DB 2142 TACTCCTTTGGATCTTGTAAAGATGGAGATACAGATATTAAGATCTGCTTAGGGGAGA 2142
QY 2221 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGATTTGCTTTC 2221
DB 2202 TGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTAGCCAGAGTGAAGATTTGCTTTC 2202
QY 2281 TCCTGATAATGTAATTTGCCGCGATACCCAGGCAGACATTTCAACCTTTTACATTTAGC 2281
DB 2262 TCCTGATAATGTAATTTGCCGCGATACCCAGGCAGACATTTCAACCTTTTACATTTAGC 2262
QY 2341 AGCTGGTTATAATTAATTTAGAAATTTGAGAGTATTTGTTTACAAACCGAGCTGATGTGAA 2341
DB 2322 AGCTGGTTATAATTAATTTAGAAATTTGAGAGTATTTGTTTACAAACCGAGCTGATGTGAA 2322
QY 2401 TGCCCAAGACAAAGGAGACTTATTCCTTTACATAAATGCAAGCATCTTACGGGCATGTAGA 2401
DB 2382 TGCCCAAGACAAAGGAGACTTATTCCTTTACATAAATGCAAGCATCTTACGGGCATGTAGA 2382
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DB 2442 TGTAGCAGCTCTACTAATAAGTATATGCAATGTCTCAATGCCACGACAAATGGGCTTT 2442
QY 2521 CACACCTTTGCAAGAGCAGCCCAAAAGGGACGAACACAGCTTTGTGCTTTGTGCTAGC 2521
DB 2502 CACACCTTTGCAAGAGCAGCCCAAAAGGGACGAACACAGCTTTGTGCTTTGTGCTAGC 2502

QY 2522 CCATGAGAGCTGACCCGACTCTTAAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC 2581
DB 2503 CCATGAGAGCTGACCCGACTCTTAAAAATCAGGAAGGACAAACACCTTTAGATTTAGTTTC 2562
QY 2582 AGCGGATGATGTGAGCGCTCTTCTGACAGCAGCATGCCCCCATCTGCTCTGCCCTCTTG 2641
DB 2563 AGCGGATGATGTGAGCGCTCTTCTGACAGCAGCATGCCCCCATCTGCTCTGCCCTCTTG 2622
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DB 2623 TTACAAGCCTCAAGTGTCAATGGTGTGAGAAGCCCAAGGAGCCACTGACAGATGCTCTC 2682
QY 2702 TTCAAGTCCATCTAGCCCATCAAGCCTTTCTGACGCCAGCAGTCTTTGACAACTATCTGG 2761
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QY 2762 GAGTTTTTCAAGAACTGTCTTCAAGTGTAGTTCAAGTGGAAACAGAGGCTGCTCCAGTTT 2821
DB 2743 GAGTTTTTCAAGAACTGTCTTCAAGTGTAGTTCAAGTGGAAACAGAGGCTGCTCCAGTTT 2802
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DB 2863 ACTTGAGCACCTAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGTTATAGTTGA 2922
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DB 3102 GAACACCTCTGGTAGTGGAAACAATTTCTTATAGATCTGTCTCTCGATGATATAAGAGTTTCA 3102
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DB 3282 GGAAGATACACTCACCGGAGAAAGAAAGTTCCTGAGAAACCAACCAATGCCAATGA 3282
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DB 3462 CAAAAGCAATCAATATGATATGGAATTTGGAGGAGTACTGGGGTGTCCAGTTTCAACAAGA 3462
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3643 GCGTTATCTGAGTATTTAACTTACTTACAGATTTATGAGCCCTGAAGGTATGGTCGATGG 3702
3722 ATAAATAGTATTTTAAAGAACTAAATTCACCTGAACCTAAATCATCAAGCAGCAGTGG 3781
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3763 CCTCTACGTTTTACTCTCTTTGCTGAAAAA 3797

RESULT 9
US-09-843-159B-1
; Sequence 1, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Ewan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-843-159B-1

Query Match 88.9%; Score 3393.4; DB 3; Length 3797;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1063 TAAGAACAGGGTTGAAGTATGTTCTTCTTAAAGTTATGCTGAGACCCCAACACTGCT 1122
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2023 AATTGCAAACTTCTGCTCAGCATGTTGCGAGCCCTTACCAAAAAAACAAGGATGAAA 2082
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3782 CCTCTAGTTTTTACTCTCTTTGCTGAAAAAATAAAAA 3816
3763 CCTCTAGTTTTTACTCTCTTTGCTGAAAAAATAAAAA 3797

RESULT 10

US-09-427-154-1

; Sequence 1, Application US/09427154

; Patent No. 6589725

; GENERAL INFORMATION:

; APPLICANT: Luo, Ying

; APPLICANT: Chan, Eva

; APPLICANT: Xu, Xiang

; APPLICANT: Huang, Betty

; TITLE OF INVENTION: TANKYRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND

; TITLE OF INVENTION: METHODS OF USE

; FILE REFERENCE: A-68292-DJB/RMS/DAV

; CURRENT APPLICATION NUMBER: US/09/427,154

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 3394

[illegible]

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RESULT 11

US-09-972-115A-3
; Sequence 3, Application US/099721115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4297
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; ORGANISM: Homo sapiens
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RESULT 12

US-09-972-115A-1
; Sequence 1, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
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; TITLE OF INVENTION: A Second Mammalian Telomerase
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; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
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US-09-972-115A-1

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RESULT 13
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; Sequence 1, Application US/09196387
; Patent No. 6277613
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; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN T
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2946	Db	TCCACCCCTCTCGCCTCTCGGCTGCCAGACATAGACAACTCACTGCGCCCTTTAGCA	3005
2772	Qy	GAACTGTCTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGGTGCTTCCAGTTGGGAGAAAAAG	2831
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[illegible]

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RESULT 15
US-09-972-115A-7
; Sequence 7, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972.115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-115A-7

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Query Match	49.4%;	Score 1885;	DB 3;	Length 4134;
Best Local Similarity	72.1%;	Pred. No. 0;		
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QY	312	GAGGCGTGGCGCAACGGGGACGTTGGAAACGAGTCAAGAGGCTGGTGACGCGTGAAGAGGTG	371	
DB	567	GAGGCTGTGCGAAATGGGACGCTGTCCCGGTAAAGAGGCTGGTGACGCGGCAACGTA	626	
QY	372	AACAGCGCGACACGCGGGGAGGAAATCCACCCCGCTGCACTTCGCGCGAGGTTTGGG	431	
DB	627	AATGCAAGGACATGCGCGCGCGGAAGTCTTCTCCCTGCACTTCGCTGCGAGTTTGGG	686	
QY	432	CGGAAGAGCTAGTTGAAATATTTGCTTCGAATGGTGCAAATGCTCCAAACACGATGAT	491	
DB	687	AGGAAGGATGTTGTGAACAACCTTACTACAGATGGGTGCTAAATGTCACGCTCGTGATGAT	746	
QY	492	GGGGGCTTATTCTCTCATATATGATGCTCTTTTGGTCACTGCTCAAGTAGTCAATCTC	551	
DB	747	GGAGGTCTATCCGCTTCATATGCTGTTCTTTTGGCCATGCTGAGTTGTGAGTCTG	806	
QY	552	CTTTTCGACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTATACTCTCTCCAT	611	
DB	807	TTATTGTGCCAAGGAGCTGATCCAAATGCCAGGATAACTGGAACATATACACCTCGCAT	866	
QY	612	GAGCTGCAATTAAGGAAGATGTGATTTGCAATTTGCTGTTTACAGCATGAGCTGAG	671	
DB	867	GAGCTGCTATTAAGGGGAAGATCGATGTGTGCAITTTGCTGTGACGACGAGCTGAC	926	
QY	672	CCAAACCATCGAAATACAGATGGAAGCAGCATTCGATTTAGCAGATCCATCTGCCTGCAAA	731	
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QY	732	GCAGTCTTACTGGTGAATATAAGAAAGATGAACCTTTAGAAAAGTCCAGGAGTGCAAT	791	
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QY	912	TTACTGCAACATGGAGCTGATGTCATGTCTAAAGATAAAAGGTGATCTGGTACCATTAAC	971	
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RESULT 2
ABQ77067
ID ABQ77067 standard; DNA; 3816 BP.
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AC ABQ77067;
XX 08-APR-2003 (first entry)
XX Tankyrase H, isotype 2 TaHo-2 DNA from clone K23.
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3121	Db		AGTCTGTGGAG	GAAGATGCAAA	AGTTCGAGAC	CAGAGATGGAGGTCTATGCAG	3180
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3241	Qy		GGGAAAGATAC	ACTCACCGGAG	AAAGAGTTTCTG	AAAGAAACCAACCACTGCCANTG	3300
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3601	Qy		CTGGTAGGCC	CCAGTGTAAAT	TGGCCTAGCAT	TAGCTGAATATGTTATTACAGAGGAGAAC	3660
3601	Db		CTGGTAGGCC	CCAGTGTAAAT	TGGCCTAGCAT	TAGCTGAATATGTTATTACAGAGGAGAAC	3660
3661	Qy		AGGCTTATCT	GAGTATTTAA	TCTTACAGAT	TATTAGGCCCTGGAAGGTATGGTGCATG	3720

Db	3661	AGCCTATCTCTAGTATTTAAATTTACTTACAGATTATGAGCCCTGAAGGTATGTCATG	3780
Qy	3721	GATAAATAGTATTTATTTAAAGAAACAAATATCCACTGAAACCTAAATATCATCAAGCAGCAGTG	3780
Db	3721	GATAAATAGTATTTATTTAAAGAAACAAATATCCACTGAAACCTAAATATCATCAAGCAGCAGTG	3780
Qy	3781	GCCTCTACGTTTACTCTCTTTCCTTTCCTGCTGAAAAA	3816
Db	3781	GCCTCTACGTTTACTCTCTTTCCTTTCCTGCTGAAAAA	3816
RESULT 5			
AAC85294			
XX	AAC85294 standard; cDNA; 6019 BP.		
XX	AAC85294;		
XX	29-MAR-2001 (first entry)		
XX	Human SPANK cDNA.		
XX	SPANK; SAM; sterile alpha motif; PARP; insulin resistance;		
KW	poly adenosine diphosphate-ribose polymerase; catalytic domain; ANK;		
KW	ankyrin repeat; cytosol; insulin-responsive aminopeptidase; IRAP; GLUT4;		
KW	adipocyte; insulin signalling pathway; hyperlipidaemia;		
KW	glucose intolerance; atheromatous disease; atherosclerosis; obesity;		
KW	cardiac insufficiency; coronary insufficiency; stroke;		
KW	high blood pressure; non-insulin dependent diabetes; hypertension;		
KW	hyperuricemia; Syndrome X; muscular dystrophy; muscle atrophy; ds.		
XX	Homo sapiens.		
XX	Location/Qualifiers		
Key	252..3735		
FT	/tag= a		
FT	/product= "Human SPANK"		
FT	/transl_except= (pos:768..878,aa:173..209)		
FT	/transl_except= (pos:1230..1337,aa:327..362)		
FT	/transl_except= (pos:1374..1445,aa:375..398)		
FT	/transl_except= (pos:1695..1823,aa:482..524)		
FT	/transl_except= (pos:2172..2282,aa:641..677)		
XX	WO200077225-A1.		
XX	21-DEC-2000.		
XX	09-JUN-2000; 2000WO-US015926.		
XX	11-JUN-1999; 99US-0138957P.		
XX	(WHEO) WHITEHEAD INST BIOMEDICAL RES.		
PA	(GEO) GEN HOSPITAL CORP.		
XX	Chi N, Lodish HF;		
XX	WPI; 2001-091404/10.		
DR	P-PSDB; AAB47022.		
XX	New insulin signaling protein SPANK, useful for reducing body mass,		
PT	glucose intolerance or insulin resistance and for preventing or treating		
PT	obesity-related and muscle-related diseases.		
XX	Claim 3; Fig 4; 65pp; English.		
XX	This sequence represents the human SPANK cDNA. The SPANK protein		
CC	comprises 3 domains: (a) a SAM (sterile alpha motif) domain; (b) a PARP		
CC	(poly adenosine diphosphate-ribose polymerase) catalytic domain; and (c)		
CC	an ANK domain composed of ankyrin repeats. SPANK is a cytosolic protein		
CC	which can poly(ADP-ribosyl)ate itself. SPANK binds insulin-responsive		
CC	aminopeptidase (IRAP) and modulates translocation of GLUT4 in the		
CC	perinuclear region of adipocytes. It is an effector in the insulin		
CC	signalling pathway in eukaryotic cells. SPANK is useful for reducing body		
CC	mass, reducing glucose intolerance or insulin resistance, for preventing		

PN WO20061813-A1.
XX 19-OCT-2000.
XX 10-APR-2000; 2000WO-US009558.
XX 09-APR-1999; 99US-0128577P.
PR 13-APR-1999; 99US-0129123P.
XX (GERO-) GERON CORP.
XX Morin GB, Funk WD, Piatyszek MA;
PI WPI; 2000-679503/66.
XX P-PSDB; AAB27211.
XX Novel mammalian Tankyrase II polypeptide and the polynucleotide encoding
PT the polypeptide useful for modulating or maintaining telomere length,
PT replicative capacity, apoptosis, chromosome packing or gene expression.
XX Claim 1; Fig 4; 52pp; English.
XX The present sequence is a version of the human tankyrase II coding
CC sequence. Its protein is thought to be involved in signal transduction in
CC the cell, and to have binding activity for other telomere-associated
CC proteins. It is possible that it plays a role in the regulation of
CC telomere length, thus affecting the replicative ability of the cell. The
CC protein is useful for ribosylating target proteins, for determining
CC tankyrase II binding activity in a sample, and for modulating telomere
CC length in a cell
XX
SQ Sequence 4275 BP; 1247 A; 889 C; 1025 G; 1114 T; 0 U; 0 Other;
Query Match 99.4%; Score 3791.4; DB 3; Length 4275;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 1 CGCGCTGCTCCGCCCGCGGGGAGCCGGGGGAGGAGCCAGCGAGGGGCGCGG 60
DB 61 CGCGCTGCTCCGCCCGCGGGGAGCCGGGGGAGGAGCCAGCGAGGGGCGCGG 120
QY 61 TGGCGCGCGCCATGGGATCGCGCCGGATCCGGTGACAGAGGAGCCAGCGCGCGG 120
DB 121 TGGCGCGCGG-CCATGGGATCGCGCCGGATCCGGTGACAGAGGAGCCAGCGCGG 179
QY 121 CCTGAGCGGCTTCTCGGGGGGCTCGCCCTCTGCTCGGGGGCGGGGCTCCTGC 180
DB 180 CCTGAGCGGCTTCTCGGGGGGCTCGCCCTCTGCTCGGGGGCGGGGCTCCTGC 239
QY 181 TCCGGTTGCTGGCGCTGTTGCTGGCTGTGGCGCGGCGGAGGATCATGTCCGGTCCGCGT 240
DB 240 TCCGGTTGCTGGCGCTGTTGCTGGCTGTGGCGCGGCGGAGGATCATGTCCGGTCCGCGT 299
QY 241 GCGCGCGCGGGAGCGGCTTGGCGAGCGCGCGCGCGCGGCGGAGCGCGCGCGCGCC 300
DB 300 GCGCGCGCGGGAGCGGCTTGGCGAGCGCGCGCGCGCGGCGGAGCGCGCGCGCGCC 359
QY 301 GAGAGCTGTTGAGGGCTGCGGCAACCGGGAGCGTGGAAAGAGTCAAGAGCTGGTGA 360
DB 360 GAGAGCTGTTGAGGGCTGCGGCAACCGGGAGCGTGGAAAGAGTCAAGAGCTGGTGA 419
QY 361 CTGAGAAGGTGAACAGCGCGGAGCGGCGGAGGAAATCCACCCGCTGCATCTCGCGG 420
DB 420 CTGAGAAGGTGAACAGCGCGGAGCGGCGGAGGAAATCCACCCGCTGCATCTCGCGG 479
QY 421 CAGGTTTGGCGGGAAGACGTAGTTGAAATATTTGCTTCAGAAATGCTGCAAAATGTC 480
DB 480 CAGGTTTGGCGGGAAGACGTAGTTGAAATATTTGCTTCAGAAATGCTGCAAAATGTC 539
QY 481 CAGGTGATGATGGGGCCTTATTCCTTCATTAATGCTATGCTTTTGGTCAATGCTGA 540
DB 540 CAGGTGATGATGGGGCCTTATTCCTTCATTAATGCTATGCTTTTGGTCAATGCTGA 599
QY 541 TAGTCAATCTCCTTTTGGACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTATA 600
DB 600 TAGTCAATCTCCTTTTGGACATGGTGCAGACCCCAATGCTCGAGATAATTTGGAATTATA 659
QY 601 CTCCTCTCCATGAAGCTGCAATTAAGGAAGATTGATGTTTGCATTTGCTGCTTACAGC 660
DB 660 CTCCTCTCCATGAAGCTGCAATTAAGGAAGATTGATGTTTGCATTTGCTGCTTACAGC 719
QY 661 ATGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATC 720
DB 720 ATGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATC 779
QY 721 CATCTGCCAAAGCAGTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCA 780
DB 780 CATCTGCCAAAGCAGTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCA 839
QY 781 GGAGTGGCAATGAAGAAAAATGATGGCTCTACTCAGACCATTAATGTCACATGCCAGC 840
DB 840 GGAGTGGCAATGAAGAAAAATGATGGCTCTACTCAGACCATTAATGTCACATGCCAGC 899
QY 841 CAAGTGATGGCAGAAAGTCACTCCATTTACATTTTGGCAGCAGGATATAACAGAGTAAAGA 900
DB 900 CAAGTGATGGCAGAAAGTCACTCCATTTACATTTTGGCAGCAGGATATAACAGAGTAAAGA 959
QY 901 TTGTACAGCTGTTACTGCAACATGAGCTGATGTCCTATGCTTAAAGATAAAGGTGATCTGG 960
DB 960 TTGTACAGCTGTTACTGCAACATGAGCTGATGTCCTATGCTTAAAGATAAAGGTGATCTGG 1019
QY 961 TACCATTAACAAATGCCCTGTTCTTATGTCATTAATGAAGTAACTGAATTTTGGTCAAGC 1020
DB 1020 TACCATTAACAAATGCCCTGTTCTTATGTCATTAATGAAGTAACTGAATTTTGGTCAAGC 1079
QY 1021 ATGGTGCCTGTGTAATGCAATGGAATGTCGCAATTCACCTCTCTCATGAGGAGCTT 1080
DB 1080 ATGGTGCCTGTGTAATGCAATGGAATGTCGCAATTCACCTCTCTCATGAGGAGCTT 1139
QY 1081 CTAAGAACAGGGTTGAAGTATGTTCTTCTTAAAGTTATGGTGCAGACCCCAACTGC 1140
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QY 1141 TCAATGTCACAAATAAAGTGTATAGACTTGGCTCCACACACAGTAAAGAAAGAT 1200
DB 1200 TCAATGTCACAAATAAAGTGTATAGACTTGGCTCCACACACAGTAAAGAAAGAT 1259
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DB 1260 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCGAGAGCTGATGTTACTC 1319
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QY 1321 CAGCATTTGCTGCTGCTGCTCATATCCCAAAAGAAAGCAATATGTAAGTGT 1380
DB 1380 CAGCATTTGCTGCTGCTGCTCATATCCCAAAAGAAAGCAATATGTAAGTGT 1439
QY 1381 TGCTAAGAAAAGGAGCAACATCAATGAAAGACTTAAAGAAATTTTGACTCTCTGCGAG 1440
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QY 1441 TGGCATCTGAGAAAGCTCAATATGATGTTGTTGAAGTGTGTTGAACATGAAGCAAGG 1500
DB 1500 TGGCATCTGAGAAAGCTCAATATGATGTTGTTGAAGTGTGTTGAACATGAAGCAAGG 1559
QY 1501 TTAATGCTCTGGAATATCTTGGTCAAGCTTCTCTCAACAGAGCTGCATATTTGGTCAATC 1560
DB 1560 TTAATGCTCTGGAATATCTTGGTCAAGCTTCTCTCAACAGAGCTGCATATTTGGTCAATC 1619
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DB 1620 TACAAACCTCGCGCTACTCTCTGAGCTATGGTGTGATCCCTAACATATATCCCTTCAGG 1679
QY 1621 GCTTTACTGCTTTACAGATGGGAAATGAAATGTATACAGCAACTCTCTCCAAGAGGATCT 1680

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Db 1680 GCCTTACTGCTTTACAGATGGAAATGAAATGTACAGCAACTCCTCAAGAGGGTATCT 1739
Qy
1681 CATTAGGTAAATTCAGAGGCAGACAGACAAATGCTGGAGCTGCAAGGCTGGAGATGCG 1740
Db
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1741 AAACGTGTAATAAAAACTGTGTAATCTGTTAGAGTGTCAAACCTGCAGAGAGACATTGAAGGGCGTC 1800
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Qy
1801 AGTCTACACCACTTCAATTTTGCAGCTGGGTATACAGAGTGTCCGTTGGTAATATCTGC 1860
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2221 CTCCTGATAATGTAAATGTCGCGATACCCAGGCAGACATTTCAACACCTTTACATTTAG 2280
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2281 CAGCTGGTTATAATTAATTTAGAAAGTTGAGAGTATTTGTTACAAACAGAGCTGATGTGA 2340
Db
2340 CAGCTGGTTATAATTAATTTAGAAAGTTGAGAGTATTTGTTACAAACAGAGCTGATGTGA 2399
Qy
2341 ATGCCCAAGACAAAGGAGGACTTATCTTTTACATAATGAGCATCTTTACGGGCATGTAG 2400
Db
2400 ATGCCCAAGACAAAGGAGGACTTATCTTTTACATAATGAGCATCTTTACGGGCATGTAG 2459
Qy
2401 ATGTAGCAGCTCTACTAATAAGTATATATGATGTGTCAATGCCACGACAAATGGGCTT 2460
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2460 ATGTAGCAGCTCTACTAATAAGTATATATGATGTGTCAATGCCACGACAAATGGGCTT 2519
Qy
2461 TCACACCTTTGTCACGAGAGCCCAAGAGGACGAAACAGCTTTGTGTTGTGCTAG 2520
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2521 CCCATGGAGCTGACCCGACTCTTAAATCAGGAGGACAAACCTTTAGATTTAGTTT 2580
Db
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Db
2640 CAGCGGATGATGTGAGGGCTCTTCTGACAGAGCCATGCCCCCATCTGCTCGCCCTCTT 2699
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2641 GTTACAGACCTCAAGTGTCTCAATGGTGTGAGAGGCCAGAGGCCACTGCGAGATGCTCTCT 2700
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2700 GTTACAGACCTCAAGTGTCTCAATGGTGTGAGAGGCCAGAGGCCACTGCGAGATGCTCTCT 2759
Qy
2701 CTTACAGGTCCATCTAGCCCATCAAGCCTTTCTGAGCCAGCAGCTTTGACAACTTATCTG 2760
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2760 CTTACAGGTCCATCTAGCCCATCAAGCCTTTCTGAGCCAGCAGTCTTTGACAACTTATCTG 2819
Qy
2761 GGAGTTTTTTCAGAACTGTCTTTCAAGTAGTTAGTTCAAGTGGAAACAGAGGGTCTTTCCAGTT 2820
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Qy
2821 TGGAGAAAAAGGAGGTTCAGAGGTAGATTTTACATAAATCTCAATTCGTAGGGAATCTTG 2880
Db
2880 TGGAGAAAAAGGAGGTTCAGAGGTAGATTTTACATAAATCTCAATTCGTAGGGAATCTTG 2939
Qy
2881 GACTTGAGCACCTAAATGGATATATTTGAGAGAGAAACAGATCACTTTGGATGTATAGTTG 2940
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Qy
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Qy
3481 ACAGATCTTGTACATTTGCCACAGGAGCTGTCTTTTGGCGGGTAAACCTTTGGGAAGT 3540
Db
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Qy
3541 CTTTCTGCAAGTTCAGTGCATGAAATGGCAATCTCTCCAGGTCATCAGTCAGTCA 3600
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Db
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3661 AGGCTTATCTGAGTATTTAAATTTACTTTACAGATTATGAGGCTGGAAGGTATGTCGATG 3720
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Qy
3781 GCCTCTACGTTTTTACTCTCTTTTGTGTAATAAAAA 3813
Db
3840 GCCTCTACGTTTTTACTCTCTTTTGTGTAATAAAAA 3872
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1446 TGCTAAGAAAAGGAGCAAAACATCAATGAAAAGACTAAGAAATCTTGACTCCTCTGCACG 1505
Qy
1441 TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACACATGAAGCAAGG 1500
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1506 TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAGCAAGG 1565
Qy
1501 TTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTCAATC 1560
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1566 TTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGGTCAATC 1625
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1561 TACAAACCTGCGCCTACTCTCTGAGCTATGGTGTGATCCTTAAATATATATCCCTTCAGG 1620
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1626 TACAAACCTGCGCCTACTCTCTGAGCTATGGTGTGATCCTTAAATATATATCCCTTCAGG 1685
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1686 GCTTTACTGCTTTACAGATGGAAATGAAATGTACAGCAACTCCTCCAAGAGGGTATCT 1745
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1681 CATTAGGTAAATTCAGAGCAGACAGACAATTTGCTGGAGCTGCAAGAGCTGGAGATGTG 1740
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1746 CATTAGGTAAATTCAGAGCAGACAGACAATTTGCTGGAGCTGCAAGAGCTGGAGATGTG 1805
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Db
1806 AAACCTGTAAAAAATCTGTACTCTTCAGAGTGTCAACTGCAGAGACATTTGAAAGGGGCTC 1865
Qy
1801 AGTCTACACCACTTCATTTTCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGC 1860
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Qy
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1926 TACAGATGGAGCTGTGTGATGCTAAAGATAAAGAGGCGCTTGTACCTTTGCACAATG 1985
Qy
1921 CATGCTCTTATGGACATATGAAAGTTCAGAACTTCTTGTAAACATGGAGCAGTACTTA 1980
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1981 ATGTAGCTGATTTATGAAAATTTACACCTTTACATGAAGCAGACGAAAGAAAATATG 2040
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2401 ATGTAGCAGCTCTACTAATAAAGTATATGATGATGTGTCAATGCGACGCAAAATGGGGCTT 2460
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Qy
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Db
|||||

Db
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2521 CCATATGAGCTGACCCGACTCTTTAAAAATCAGAAAGCAAAAACACCTTTTAGATTTAGTTT 2580
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2586 CCATATGAGCTGACCCGACTCTTTAAAAATCAGAAAGCAAAAACACCTTTTAGATTTAGTTT 2645
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2581 CAGCGGATGATGTACGGGCTCTTTGACAGCAGCCATGCCCCCATCTGCTCTGCCCCCTT 2640
Db
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2706 GTTACAAAGCCTCAAGTGTCTCAATGGTGTGAAAGCCAGGAGCCACTGCGAGATGCTCTCT 2765
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2766 CTTTCAGTCCATCTAGCCCCATCAAGCCTTTCTGACAGCAGCAGTCTTTGACAACTTATCTG 2825
Qy
2761 GGAGTTTTTTCAGAACTGTCTTCAGTAGTTAGTTTCAAGTGGAACAGAGGGTGTCTTCCAGTT 2820
Db
2826 GGAGTTTTTTCAGAACTGTCTTCAGTAGTTAGTTTCAAGTGGAACAGAGGGTGTCTTCCAGTT 2885
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2886 TGCAGAAAAAGGAGGTTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAAGGAATCTTG 2945
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2881 GACTTGAGCACCCTAAATGGATATATTTTGAGAGAGAAACAGATCACTTTTGGATGTATTAGTTG 2940
Db
2946 GACTTGAGCACCCTAAATGGATATATTTTGAGAGAGAAACAGATCACTTTTGGATGTATTAGTTG 3005
Qy
2941 AGATGGGGCACAAGGAGCTGAAAGGAGATTGGATCAATGCTTATGGACATAGGCACAAAC 3000
Db
3006 AGATGGGGCACAAGGAGCTGAAAGGAGATTGGATCAATGCTTATGGACATAGGCACAAAC 3065
Qy
3001 TAAATTAAGGAGTTCGAGAGACTTATCTCCGGAACAAAGGCTTTAAACCCATATTTAACTT 3060
Db
3066 TAAATTAAGGAGTTCGAGAGACTTATCTCCGGAACAAAGGCTTTAAACCCATATTTAACTT 3125
Qy
3061 TGAACACCTCTGCTAGTGGAAACAATTTCTTATAGATCTGTCTCTGATGATAAAGAGTTTC 3120
Db
3126 TGAACACCTCTGCTAGTGGAAACAATTTCTTATAGATCTGTCTCTGATGATAAAGAGTTTC 3185
Qy
3121 AGTCTGTGGAGGAGAGATGCAAGTACAGTTTCGAGAGCAGACAGATGGAGGTCATCCAG 3180
Db
3186 AGTCTGTGGAGGAGAGATGCAAGTACAGTTTCGAGAGCAGACAGATGGAGGTCATCCAG 3245
Qy
3181 GTGGAATCTTTCAACAGATACAATATTTCTCAAGATTTCAGAAAGTTTGTAAACAGAAACTAT 3240
Db
3246 GTGGAATCTTTCAACAGATACAATATTTCTCAAGATTTCAGAAAGTTTGTAAACAGAAACTAT 3305
Qy
3241 GGGAAAGATACACTCACCGGAGAAAAAGAGTTTCTGAAAGAAAACCAACATGCCCAATG 3300
Db
3306 GGGAAAGATACACTCACCGGAGAAAAAGAGTTTCTGAAAGAAAACCAACATGCCCAATG 3365
Qy
3301 AACGAATGCTATTTTCATGGGTCCTCTTTGTAATGCAATTTTCCACAAAGGCTTTGATG 3360
Db
3366 AACGAATGCTATTTTCATGGGTCCTCTTTGTAATGCAATTTTCCACAAAGGCTTTGATG 3425
Qy
3361 AAAGGCAATGCGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTGAAACTCTT 3420
Db
3426 AAAGGCAATGCGTACATAGGTGGTATGTTTGGAGCTGGCATTTATTTTGTGAAACTCTT 3485
Qy
3421 CCAAAAGCAATCAATATGATATGGAATTTGGAGAGGTACTGGGTGTCAGTTTCAAAAG 3480
Db
3486 CCAAAAGCAATCAATATGATATGGAATTTGGAGAGGTACTGGGTGTCAGTTTCAAAAG 3545
Qy
3481 ACAGATCTCTGTACATTTTCCACAGGAGTGTCTTTTCCGGGTAACTTGGGAAGT 3540
Db
3546 ACAGATCTCTGTACATTTTCCACAGGAGTGTCTTTTCCGGGTAACTTGGGAAGT 3605
Qy
3541 CTTTCTTCAGAGTTCAGTGCATGAAATGGAATTCCTCTCCAGGTCATCAGTTCAGTCA 3600
Db
3606 CTTTCTTCAGAGTTCAGTGCATGAAATGGAATTCCTCTCCAGGTCATCAGTTCAGTCA 3665

QY 3601 CTGGTAGCCAGTGTAAATGCGCTAGCATTAAGCTGAATATGTTATTTACAGAGGAGAAC 3660
DB |||||
DB 3666 CTGGTAGGCCAGTGTAAATGCGCTAGCATTAAGCTGAATATGTTATTTACAGAGGAGAAC 3725
QY 3661 AGGCTTATCCTGAGTATTAAATTAATTAACAGATTATGAGCCTGAAGTATGTCGATG 3720
DB |||||
DB 3726 AGGCTTATCCTGAGTATTAAATTAATTAACAGATTATGAGCCTGAAGTATGTCGATG 3785
QY 3721 GATAAATAGTATTATTAAGAACTAAATTCCTCACTGAACCTTAAATCATCAAGCAGCAGTG 3780
DB |||||
DB 3786 GATAAATAGTATTATTAAGAACTAAATTCCTCACTGAACCTTAAATCATCAAGCAGCAGTG 3845
QY 3781 GCGTCTACGTTTACTCTCTTCTGCAAAAAAA 3813
DB |||||
DB 3846 GCGTCTACGTTTACTCTCTTCTGCAAAAAAA 3878

RESULT 8
AAF63953
ID AAF63953 standard; DNA; 4992 BP.
XX
AC AAF63953;
XX
DT 05-APR-2001 (first entry)
XX Human tankyrase2 TANK2-SHORT coding sequence SEQ ID NO: 134.
XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
KW inflammatory disorder; ds.
XX Homo sapiens.
XX OS
XX WO200100849-A1.
XX PD 04-JAN-2001.
XX 28-JUN-2000; 2000WO-US017827.
XX 29-JUN-1999; 99US-0141582P.
XX (ICOS-) ICOS CORP.
XX Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
XX WPI; 2001-102896/11.
XX P-PSDB; AAB66295.
XX New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
PT inflammatory and autoimmune disorders.
XX Claim 6; Page 195-200; 242pp; English.
XX The present invention provides the protein and coding sequence for the
CC human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
CC ribosylation activity and is involved in the modification of TRF1, which
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
XX disorders
XX
SQ Sequence 4992 BP; 1454 A; 1064 C; 1191 G; 1283 T; 0 U; 0 Other;
Query Match 99.4%; Score 3791.4; DB 5; Length 4992;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 1 CCGCTGTCTCCCGCCCGCGGCGAGCGGGGCGAGGCCCGAGCGGGCGCGCG 60
DB |||||
DB 653 CCGCTGTCTCCCGCCCGCGGCGAGCGGGGCGAGGCCCGAGCGGGCGCGCG 712

QY 61 TGGCGCGCGGCCATGAGGACTGCGCGGATCGGTGACAGAGGAGCAAGCGCCGGG 120
DB |||||
DB 713 TGGCGCGCGG-CCATGAGGACTGCGCGGATCGGTGACAGAGGAGCAAGCGCCGGG 771
QY 121 CCCTGAGCGGCTTTCTCCGGGGGGCCCTCGCCCTCTCTGCTCGCGGGCGCGGGCTCTGCG 180
DB |||||
DB 772 CCCTGAGCGGCTTTCTCCGGGGGGCCCTCGCCCTCTCTGCTCGCGGGCGCGGGCTCTGCG 831
QY 181 TCCGCTTGTCTGGCGCTGTTGCTGCTGCTGCGCGGGCGCAGGATCATGTCGGGTGCGCGCT 240
DB |||||
DB 832 TCCGCTTGTCTGGCGCTGTTGCTGCTGCTGCGCGGGCGCAGGATCATGTCGGGTGCGCGCT 891
QY 241 GCGCGCGCGGGGAGCGGCTGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 300
DB |||||
DB 892 GCGCGCGCGGGGAGCGGCTGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 951
QY 301 GAGAGCTGTTGAGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 360
DB |||||
DB 952 GAGAGCTGTTGAGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1011
QY 361 CTGAGAAAGGTGAACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 420
DB |||||
DB 1012 CTGAGAAAGGTGAACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1071
QY 421 CAGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGTCGCAATGTCGAAG 480
DB |||||
DB 1072 CAGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGTCGCAATGTCGAAG 1131
QY 481 CAGGTATGATGGGGGCTTATTCCTCTTCAATATGATGCTCTTTGGTGCATGCTGAAG 540
DB |||||
DB 1132 CAGGTATGATGGGGGCTTATTCCTCTTCAATATGATGCTCTTTGGTGCATGCTGAAG 1191
QY 541 TAGTCAATCTCTTTTGGGACATGTCGAGACCCCAATGCTCGAGATAATTTGGAATATA 600
DB |||||
DB 1192 TAGTCAATCTCTTTTGGGACATGTCGAGACCCCAATGCTCGAGATAATTTGGAATATA 1251
QY 601 CTCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATTTTGCATTTGTGCTGTACAGC 660
DB |||||
DB 1252 CTCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATTTTGCATTTGTGCTGTACAGC 1311
QY 661 ATGAGCTGAGCCCAACCATTCGAAATACAGATGGAAGGACAGATTTGATTTAGCAGATC 720
DB |||||
DB 1312 ATGAGCTGAGCCCAACCATTCGAAATACAGATGGAAGGACAGATTTGATTTAGCAGATC 1371
QY 721 CATCTGCAAGCAGTCTTACTGCTGAATATAAGAAAGATGAACCTCTTGAAGAGTGCCA 780
DB |||||
DB 1372 CATCTGCAAGCAGTCTTACTGCTGAATATAAGAAAGATGAACCTCTTGAAGAGTGCCA 1431
QY 781 GGAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACCAATTAATTAATGTCACCGCAG 840
DB |||||
DB 1432 GGAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACCAATTAATTAATGTCACCGCAG 1491
QY 841 CAAGTATGAGCAGAAAGTCAACTCCATTAATTTGGGAGCAGGATATAACAGAGTAAAGA 900
DB |||||
DB 1492 CAAGTATGAGCAGAAAGTCAACTCCATTAATTTGGGAGCAGGATATAACAGAGTAAAGA 1551
QY 901 TTGTACAGCTGTTACTCCACATGAGCTGATGCCATGCTTAAAGATAAGGCTGATCTGG 960
DB |||||
DB 1552 TTGTACAGCTGTTACTCCACATGAGCTGATGCCATGCTTAAAGATAAGGCTGATCTGG 1611
QY 961 TACCATTACAAATGCTGTTCTTATGCTCATTAATGAAGTAACTGAACCTTTTGGTCAAGC 1020
DB |||||
DB 1612 TACCATTACAAATGCTGTTCTTATGCTCATTAATGAAGTAACTGAACCTTTTGGTCAAGC 1671
QY 1021 ATGTTGCTGTGTAATGCAATGAGCTTGTGGCAATTCATCTCTTTCATGAGGCGAGTT 1080
DB |||||
DB 1672 ATGTTGCTGTGTAATGCAATGAGCTTGTGGCAATTCATCTCTTTCATGAGGCGAGTT 1731
QY 1081 CTAGAAGCAGGGTTGAAGTATGTTCTCTCTTAAAGTATGTTGTCGAGGCGGCGGCGGCG 1140
DB |||||
DB 1732 CTAGAAGCAGGGTTGAAGTATGTTCTCTCTTAAAGTATGTTGTCGAGGCGGCGGCGGCG 1791
QY 1141 TCAATTTGTCAAAATAAAAAAGTCTATAGACTTGGGCTCCACACCAACAGTTAAAAAGAGAT 1200

Db 1792 TCAATGTGCATAAAGTGTCTATAGACTTGGCTCCACACCAAGTTAAAGAAAGAT 1851
Qy |||||
Db 1201 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTC 1260
Qy |||||
Db 1852 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTC 1911
Qy |||||
Db 1261 GAATCAAAAAACATCTCTCTGGAATATGGTGAATTTCAAGCATCTCTCAACACATGAAA 1320
Qy |||||
Db 1912 GAATCAAAAAACATCTCTCTGGAATATGGTGAATTTCAAGCATCTCTCAACACATGAAA 1971
Qy |||||
Db 1321 CAGCATTCGATTTGCTGCTGCATCTCCATATCCAAAAAGAAACAAATATGTCAACTGT 1380
Qy |||||
Db 1972 CAGCATTCGATTTGCTGCTGCATCTCCATATCCAAAAAGAAACAAATATGTGAACTGT 2031
Qy |||||
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Qy |||||
Db 2032 TGCTAAGAAAAGGAGCAACATCAATGAAAAGACTAAAGAAATCTTGACTCTCTCGCACG 2091
Qy |||||
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Qy |||||
Db 2092 TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAACAAAGG 2151
Qy |||||
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Qy |||||
Db 2152 TTAATGCTCTGATAATCTTCTGCTCAGACTTCTCTACACAGAGCTGCATATTTGTGCTCATC 2211
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Db 2212 TACAAACCTGCGCCTACTCTCTGAGCTATGGGTGTGATCTTAAACATATATATCCCTTCAGG 2271
Qy |||||
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Qy |||||
Db 2272 GCTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCT 2331
Qy |||||
Db 1681 CATTAGGTAAATTCAGAGCAGACAGCAATTTGCTGGAAGCTGCAAGCTGGAGATGTGCG 1740
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Qy |||||
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Db 2392 AAACGTAAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTC 2451
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Qy |||||
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Db 1861 TACAGCATGGAGCTGATGTGCAATGCTAAAGATAAAGAGGCGCTTGTACCTTTGCACAAATG 1920
Qy |||||
Db 2512 TACAGCATGGAGCTGATGTGCAATGCTAAAGATAAAGAGGCGCTTGTACCTTTGCACAAATG 2571
Qy |||||
Db 1921 CATGTTCTTATGGACATTTAAGATTGAGAACTTCTTTGTTAAACATGGAGCAGTAGTTA 1980
Qy |||||
Db 2572 CATGTTCTTATGGACATTTAAGATTGAGAACTTCTTTGTTAAACATGGAGCAGTAGTTA 2631
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Qy |||||
Db 2632 ATGTAGCTGATTTATGGAATTTTACACTTTTACATGAAGAGCAGCAAAAGGAAAAATATG 2691
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Db 2041 AAAATTTGCAAACTTCTGCTCCAGCATGTGCGAGCCCTTACCAAAAAAAACAGGGATGAAA 2100
Qy |||||
Db 2692 AAAATTTGCAAACTTCTGCTCCAGCATGTGCGAGCCCTTACCAAAAAAAACAGGGATGAAA 2751
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Db 2101 ATACTCTTTTGGATCTTGTTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAG 2160
Qy |||||
Db 2752 ATACTCTTTTGGATCTTGTTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAG 2811
Qy |||||
Db 2161 ATGCAAGCTTTGCTAGATGCTGCCAAGAAGGTTGTTTAGCCAGAGTGAAGATGTGCTTT 2220
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Db 2812 ATGCAAGCTTTGCTAGATGCTGCCAAGAAGGTTGTTTAGCCAGAGTGAAGATGTGCTTT 2871
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Db 2872 CTCTCTGATAATGTAAATTTGCCGCGATACCCACGAGACATTTCAAACACCTTTTACATTTAG 2931
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Qy |||||
Db 2932 CAGCTGGTTTATAATAATTTAGAAAGTTGCGAGAGTATTTGTTTACAACACGAGAGCTGATGTGA 2991
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Db 2341 ATGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGCAGCATCTTACGGGCATCTAG 2400
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Db 2992 ATGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGCAGCATCTTACGGGCATCTAG 3051
Qy |||||
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Qy |||||
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Qy |||||
Db 3172 CCCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGACAAACACCTTTTATAGATTTAGTTT 3231
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Qy |||||
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Qy |||||
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Qy |||||
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Qy |||||
Db 3832 GTGGAATCTTCAACAGATACAAATATTTCTCAAGATTGAGAAGGTTTGTAAACAGAAACTAT 3891
Qy |||||
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Qy |||||
Db 3892 GGGAAAGATACACTCACCGGAGAAAGAGTTCCTGAAGAAACCAACCAATGCCAATG 3951
Qy |||||
Db 3301 AACGAATGCTATTTTCAATGGGCTCTCTTTGTGAATGCAATTTATCCACAAAGGCTTTGATG 3360
Qy |||||
Db 3952 AACGAATGCTATTTTCAATGGGCTCTCTTTTGTGAATGCAATTTATCCACAAAGGCTTTGATG 4011
Qy |||||

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QY 3361 AAAGCATCGTACATAGTGTATGTTTGGAGCTGGCATTTATTTTGTGTAAGAACTCTT 3420
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QY 4012 AAAGCATCGTACATAGTGTATGTTTGGAGCTGGCATTTATTTTGTGTAAGAACTCTT 4071
DB |||||||
QY 3421 CCAAAGCAATCAATATATGATGTAATTTGGAGGAGTACTGGGTGTCCAGTTCAAAAG 3480
DB |||||||
QY 4072 CCAAAGCAATCAATATGATGTAATTTGGAGGAGTACTGGGTGTCCAGTTCAAAAG 4131
DB |||||||
QY 3481 ACAGATCTGTACATTTGCCACAGCAGCTCTCTTTTGGCCGGGTACCTTGGGAAAGT 3540
DB |||||||
QY 4132 ACAGATCTGTACATTTGCCACAGCAGCTCTCTTTTGGCCGGGTACCTTGGGAAAGT 4191
DB |||||||
QY 3541 CTTTCTCGAGTTTCAAGTCAATGAAATGCGACATTTCTCTCCAGGTCACTCACTCAGTCA 3600
DB |||||||
QY 4192 CTTTCTCGAGTTTCAAGTCAATGAAATGCGACATTTCTCTCCAGGTCACTCACTCAGTCA 4251
DB |||||||
QY 3601 CTGGTAGGCCAGTGTAAATGCCCTAGCATTTAGCTGAATATGTTTATACAGAGAGAAC 3660
DB |||||||
QY 4252 CTGGTAGGCCAGTGTAAATGCCCTAGCATTTAGCTGAATATGTTTATACAGAGAGAAC 4311
DB |||||||
QY 3661 AGGCTTATCTCGAGTATTTAATTTACTTACCAGATTTAGGGCTGAAGTATGTCGATG 3720
DB |||||||
QY 4312 AGGCTTATCTCGAGTATTTAATTTACTTACCAGATTTAGGGCTGAAGTATGTCGATG 4371
DB |||||||
QY 3721 GATAAATAGTATTTTAAAGAACTAATTCCTGAACTGAACCTTAAATCATCAAAGCAGCAGTG 3780
DB |||||||
QY 4372 GATAAATAGTATTTTAAAGAACTAATTCCTGAACTGAACCTTAAATCATCAAAGCAGCAGTG 4431
DB |||||||
QY 3781 GCCTCTAGCTTTTACTCTCTTTGCTGAAAAAAA 3813
DB |||||||
QY 4432 GCCTCTAGCTTTTACTCTCTTTGCTGAAAAAAA 4464
DB |||||||
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RESULT 9

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AAF63952
ID AAF63952 standard; DNA; 5002 BP.
XX AC AAF63952;
XX DT 05-APR-2001 (first entry)
XX DE Human tankyrase2 TANK2-LONG coding sequence SEQ ID NO: 132.
XX KW Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
XX KW inflammatory disorder; db.
XX OS Homo sapiens.
XX PN WO200100849-A1.
XX PD 04-JAN-2001.
XX PF 28-JUN-2000; 2000WO-US017827.
XX PR 29-JUN-1999; 99US-0141582P.
XX PA (ICOS-) ICOS CORP.
XX PI Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
XX WPI: 2001-102896/11.
XX DR P-PSDB; AAB66294.
XX CC New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
PT inflammatory and autoimmune disorders.
XX Claim 5; Page 185-190; 242pp; English.
XX The present invention provides the protein and coding sequence for the
CC human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
```

CC ribosylation activity and is involved in the modification of TRF1, which
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders

XX SQ Sequence 5002 BP; 1456 A; 1065 C; 1196 G; 1285 T; 0 U; 0 Other;

Query Match 99.4%; Score 3791.4; DB 5; Length 5002;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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QY 1 CGCGTGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
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QY 663 CGCGTGTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 722
DB |||||||
QY 61 TGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
DB |||||||
QY 723 TGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 781
DB |||||||
QY 121 CCCTGAGCGCGCTCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB |||||||
QY 782 CCCTGAGCGCGCTCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 841
DB |||||||
QY 181 TCCTGAGCGCGCTCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB |||||||
QY 842 TCCTGAGCGCGCTCTCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 901
DB |||||||
QY 241 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB |||||||
QY 902 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 961
DB |||||||
QY 301 GAGAGCTGTTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB |||||||
QY 962 GAGAGCTGTTTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1021
DB |||||||
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DB |||||||
QY 1022 CTGAGAGGTGAACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1081
DB |||||||
QY 421 CAGGTTTGGCGGGAAGACGCTAGTTGAATTTTGTCTTCAGATGTTGTCGAATGTCGAAG 480
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QY 1082 CAGGTTTGGCGGGAAGACGCTAGTTGAATTTTGTCTTCAGATGTTGTCGAATGTCGAAG 1141
DB |||||||
QY 481 CAGGTTGATGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
DB |||||||
QY 1142 CAGGTTGATGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1201
DB |||||||
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DB |||||||
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DB |||||||
QY 601 CTCTCTCCATGAAGCTGCAATTTAAAGAAAGATTGATGTTTGTGATTTGCTGTTTACAGC 660
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QY 1262 CTCTCTCCATGAAGCTGCAATTTAAAGAAAGATTGATGTTTGTGATTTGCTGTTTACAGC 1321
DB |||||||
QY 661 ATGGAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
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QY 1322 ATGGAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1381
DB |||||||
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DB |||||||
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DB |||||||
QY 781 GGAGTGGCAATGAAGAAAAGATGATGCTCTACTCACAACCATTAATTAATGTCGAAGCGCAG 840
DB |||||||
QY 1442 GGAGTGGCAATGAAGAAAAGATGATGCTCTACTCACAACCATTAATTAATGTCGAAGCGCAG 1501
DB |||||||
QY 841 CAAGTGTGCGCAGAAAGTCAACTCCATTACATTTTGGCAGCAGGATATTAACAGAGTAAAGA 900
DB |||||||
QY 1502 CAAGTGTGCGCAGAAAGTCAACTCCATTACATTTTGGCAGCAGGATATTAACAGAGTAAAGA 1561
DB |||||||
QY 901 TTGTACAGCTGTACTGCAACATGGAGCTGATGTCCATGCTAAAGATAAAGGTGATCTGCG 960
DB |||||||
```


QY 3121 AGTCTGTGAGGAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGGTCATGCAG 3180
DB |||||
QY 3782 AGTCTGTGAGGAGAGATGCAAAAGTACAGTTTCGAGAGCACAGAGATGGAGGTCATGCAG 3841
DB |||||
QY 3181 GTGGAATCTTTCAACAGATCAATATTTCTCAAGATTCAGAAAGTTTGTATCAAGAAACTTAT 3240
DB |||||
QY 3842 GTGGAATCTTTCAACAGATCAATATTTCTCAAGATTCAGAAAGTTTGTATCAAGAAACTTAT 3901
DB |||||
QY 3241 GGGAAAGATACACTACCGGAGAAAGAGTTCTGAAAGAAACACACACCAATGCCAATG 3300
DB |||||
QY 3902 GGGAAAGATACACTACCGGAGAAAGAGTTCTGAAAGAAACACACCAATGCCAATG 3961
DB |||||
QY 3301 AACGAATGCTATTTTCATGGGTCTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATG 3360
DB |||||
QY 3962 AACGAATGCTATTTTCATGGGTCTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGATG 4021
DB |||||
QY 3361 AAAGGATCGGTACATAGGTGTATGTTTGGAGCTGGCAATTTATTTTGTGAAAACCTTT 3420
DB |||||
QY 4022 AAAGGATCGGTACATAGGTGTATGTTTGGAGCTGGCAATTTATTTTGTGAAAACCTTT 4081
DB |||||
QY 3421 CAAAAGCAATCAATATGATATGTAATGGAGGAGTACTGGGTCTCCAGTTTCAAAAG 3480
DB |||||
QY 4082 CAAAAGCAATCAATATGATATGTAATGGAGGAGTACTGGGTCTCCAGTTTCAAAAG 4141
DB |||||
QY 3481 ACAGATCTTTGTACATTTGCCACAGGCAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGT 3540
DB |||||
QY 4142 ACAGATCTTTGTACATTTGCCACAGGCAGCTGCTCTTTTGGCGGGTAACTTTGGGAAAGT 4201
DB |||||
QY 3541 CTTTCTCGAGTTCAGTCAATGAAATGGCAATTTCTCTCCAGGTTCATCACTCAGTCA 3600
DB |||||
QY 4202 CTTTCTCGAGTTCAGTCAATGAAATGGCAATTTCTCTCCAGGTTCATCACTCAGTCA 4261
DB |||||
QY 3601 CTGTAGGCCAGTGTAAATGGCTAGCATTTAGCTGAATATGTTTATTTACAGAGGAGAC 3660
DB |||||
QY 4262 CTGTAGGCCAGTGTAAATGGCTAGCATTTAGCTGAATATGTTTATTTACAGAGGAGAC 4321
DB |||||
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DB |||||
QY 4322 AGGCTTATCTCAGTATTTAAATTTACTTACAGATTTAGAGGCTTGAAGTATGGTTCGATG 4381
DB |||||
QY 3721 GATAAATAGTTATTTTAAAGAACTAATTCACATGAACTTAAATCATCAAAACAGCAGTG 3780
DB |||||
QY 4382 GATAAATAGTTATTTTAAAGAACTAATTCACATGAACTTAAATCATCAAAACAGCAGTG 4441
DB |||||
QY 3781 GCCTCTACGTTTACTCTCTTTGCTGAAAAAAA 3813
DB |||||
QY 4442 GCCTCTACGTTTACTCTCTTTGCTGAAAAAAA 4474
DB |||||

RESULT 10
ADRI14766
ID ADRI14766 standard; DNA; 6189 BP.
XX AC ADRI14766;
XX DT 04-NOV-2004 (first entry)
XX DE Nucleotide sequence of human MAPCAX orthologue #24.
XX KW adenomatous polyposis coli protein; APC; axin pathway;
XX KW modifier of APC and axin; MAPCAX; cancer; human; gene; ss.
XX OS Homo sapiens.
XX PH Key
XX FT CDS
XX FT Location/Qualifiers
XX FT 380..3880
XX FT /*tag= a
XX FT /product= "MAPCAX orthologue"
XX PN WO2004066948-A2.
XX PD 12-AUG-2004.

XX 28-JAN-2004; 2004WO-US002338.
XX PF
XX 29-JAN-2003; 2003US-0443484P.
PR 11-FEB-2003; 2003US-0447358P.
PR 10-APR-2003; 2003US-0461789P.
PR 14-MAY-2003; 2003US-0470684P.
PR 19-JUN-2003; 2003US-0479650P.
XX (EXEL-) EXELIXIS INC.
XX Gendreau SB, Morabianco EL, Lickteig K, Zhang H;
PI P-PSDB; ADR14792.
XX WPI; 2004-580849/56.
DR DR
XX. Identifying a candidate adenomatous polyposis coli protein (APC) and axin
PT pathways modulating agent for treating cancer by contacting an assay
PT system comprising a modifier of APC and axin polypeptide or nucleic acid
PT with a test agent.
XX Example 1; SEQ ID NO 24; 199pp; English.
XX The specification describes a method for identifying a candidate
CC adenomatous polyposis coli protein (APC) and axin pathways modulating
CC agents. The method comprises providing an assay system comprising a
CC modifier of APC and axin (MAPCAX) polypeptide or nucleic acid, contacting
CC the assay system with a test agent under conditions where, except for the
CC presence of the test agent, the system provides a reference activity, and
CC detecting a test agent-biased activity of the assay system, where a
CC difference between the test agent-biased activity and the reference
CC activity identifies the test agent as a candidate APC and axin pathways
CC modulating agent. The method is useful in identifying a candidate
CC adenomatous polyposis coli protein (APC) and a pathways modulating agent,
CC which are useful for preparing a composition for diagnosing or treating
CC cancer. The present sequence encodes a human orthologue of a
CC Caenorhabditis elegans MAPCAX polypeptide. The sequence was identified
CC using BLAST analysis.
XX SQ Sequence 6189 BP; 1772 A; 1233 C; 1386 G; 1798 T; 0 U; 0 Other;

Query Match 99.4%; Score 3791.4; DB 13; Length 6189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY 1 CGCGCTGCTCG 60
DB 157 CGCGCTGCTCG 216
QY 61 TGGCG 120
DB 217 TGGCG 275
QY 121 CCCTGAGCGCGCTCTTCTCCGGGGGCGCTTCGCCCTCTCTCTCGCGGGGCGCGGCTCTTCG 180
DB 276 CCCTGAGCGCGCTCTTCTCCGGGGGCGCTTCGCCCTCTCTCTCGCGGGGCGCGGCTCTTCG 335
QY 181 TCCGCTTGTCTGGCGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 336 TCCGCTTGTCTGGCGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 395
QY 241 CG 300
DB 396 CG 455
QY 301 GAGAGCTGTTTCGAGCGCTGCGCGCAACCGGGGACGTGGAAACGAGTCAAGAGGCTGTGACGC 360
DB 456 GAGAGCTGTTTCGAGCGCTGCGCGCAACCGGGGACGTGGAAACGAGTCAAGAGGCTGTGACGC 515
QY 361 CTGAGAGGTGAACAGCG 420
DB 516 CTGAGAGGTGAACAGCG 575

QY 421 CAGGTTTTGGCGGAAAGACGTAGTTGAATATTTGGCTTCAGAAATGGTGCAAAATGTCCAAG 480
DB 576 CAGGTTTTGGCGGAAAGACGTAGTTGAATATTTGGCTTCAGAAATGGTGCAAAATGTCCAAG 635
QY 481 CACGTGATGATGGGGGCTTATTCCTCTTCATAATGCATGCTCTTTTGGTTCATGCTGAAG 540
DB 636 CACGTGATGATGGGGGCTTATTCCTCTTCATAATGCATGCTCTTTTGGTTCATGCTGAAG 695
QY 541 TAGTCAATCTCCTTTTGGCAGCATGGTCAGACCCCAATGCTCGAGATAAATGGGAATTTATA 600
DB 696 TAGTCAATCTCCTTTTGGCAGCATGGTCAGACCCCAATGCTCGAGATAAATGGGAATTTATA 755
QY 601 CTCCTCTCCATGAAGCTGCAATTAAGGAAGATTGATTTGCAATTTGCTGTTACAGC 660
DB 756 CTCCTCTCCATGAAGCTGCAATTAAGGAAGATTGATTTGCAATTTGCTGTTACAGC 815
QY 661 ATGGAGCTGAGCCCAACATCCGAATACAGATGGAAGACAGACATTCGGATTTAGCAGATC 720
DB 816 ATGGAGCTGAGCCCAACATCCGAATACAGATGGAAGACAGACATTCGGATTTAGCAGATC 875
QY 721 CATCTGCCAAAGCAGTGTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCA 780
DB 876 CATCTGCCAAAGCAGTGTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCA 935
QY 781 GGAGTGGCAATGAAGAAATAATGATGCTCTACTCACACCATTAATGTCNACTGCCACG 840
DB 936 GGAGTGGCAATGAAGAAATAATGATGCTCTACTCACACCATTAATGTCNACTGCCACG 995
QY 900 CAAGTGTGGCAGAAAGTCAACTCCATTCACATTTGGCAGCAGGATATAAAGAGTAAGA 900
DB 1055 CAAGTGTGGCAGAAAGTCAACTCCATTCACATTTGGCAGCAGGATATAAAGAGTAAGA 1055
QY 901 TTGTACAGCTGTTACTGCAACATGAGAGCTGATGCCATGCTTAAAGATAAAGAGTGAATCTGG 960
DB 1056 TTGTACAGCTGTTACTGCAACATGAGAGCTGATGCCATGCTTAAAGATAAAGAGTGAATCTGG 1115
QY 961 TACCATTAACAATGCGCTGTTCTTATGGTCATTAATGAAGTAACCTGAACTTTGGTCAAGC 1020
DB 1116 TACCATTAACAATGCGCTGTTCTTATGGTCATTAATGAAGTAACCTGAACTTTGGTCAAGC 1175
QY 1021 ATGCTGCTGTGTAATGCAATGACCTTGTGGCAATTCACCTCTCTTCATGAGGACGCTT 1080
DB 1176 ATGCTGCTGTGTAATGCAATGACCTTGTGGCAATTCACCTCTCTTCATGAGGACGCTT 1235
QY 1081 CTAAGAACAGGGTTGAAGTATGTTCTCTCTCTTAAAGTTATGGTGCAGACCCACACTGC 1140
DB 1236 CTAAGAACAGGGTTGAAGTATGTTCTCTCTCTTAAAGTTATGGTGCAGACCCACACTGC 1295
QY 1141 TCAATTTGTCACAATAAAGTGCTATAGACTTGGCTCCACACACAGTTAAAGAAAGAT 1200
DB 1296 TCAATTTGTCACAATAAAGTGCTATAGACTTGGCTCCACACACAGTTAAAGAAAGAT 1355
QY 1201 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAGAGCTGATGTTACTC 1260
DB 1356 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAGAGCTGATGTTACTC 1415
QY 1261 GAATCAAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCTCTCAACACATGAAA 1320
DB 1416 GAATCAAAAAACATCTCTCTCGAAATGGTGAATTTCAAGCATCTCTCAACACATGAAA 1475
QY 1321 CAGCATTTGCATTTGCTGCTGCATCTCCATATCCCAAGAAAGCAAAATATGTTGAATCTGT 1380
DB 1476 CAGCATTTGCATTTGCTGCTGCATCTCCATATCCCAAGAAAGCAAAATATGTTGAATCTGT 1535
QY 1381 TGCTAAGAAAGAGGAGCAAAACATCAATGAAAAGACTTAAAGAAATCTTGACTCTCTGCAAG 1440
DB 1536 TGCTAAGAAAGAGGAGCAAAACATCAATGAAAAGACTTAAAGAAATCTTGACTCTCTGCAAG 1595
QY 1441 TGGCATCTGAGAAAGCTCATTAATGATGTTGTTGAAGTAGTGGTGAATCATGAAGCAAAAGG 1500
DB 1596 TGGCATCTGAGAAAGCTCATTAATGATGTTGTTGAAGTAGTGGTGAATCATGAAGCAAAAGG 1655
QY 1501 TTAATGCTCTGGATAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTTGGTCATC 1560

DB 1656 TTAATGCTCTGGATAATCTTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTTGGTCATC 1715
QY 1561 TACAAACCTGCCGCCCTACTCCTCAGACTATGGGTGATCCTTAACATTAATATCCCTTCAGG 1620
DB 1716 TACAAACCTGCCGCCCTACTCCTCAGACTATGGGTGATCCTTAACATTAATATCCCTTCAGG 1775
QY 1621 GCITTTACTGCTTTTACAGATGGGAAATGAATAATGTACAGCAACTCCTCCAAGAGGGTATCT 1680
DB 1776 GCITTTACTGCTTTTACAGATGGGAAATGAATAATGTACAGCAACTCCTCCAAGAGGGTATCT 1835
QY 1681 CATTAGTAAATTCAGAGGACAGACACAATTTGCTGGAAGCTGCAAGGGCTGGAGATGTCG 1740
DB 1836 CATTAGTAAATTCAGAGGACAGACACAATTTGCTGGAAGCTGCAAGGGCTGGAGATGTCG 1895
QY 1741 AAACTGTAAAAAATCTGTGTAATGTTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTC 1800
DB 1896 AAACTGTAAAAAATCTGTGTAATGTTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTC 1955
QY 1801 AGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGATATCTGC 1860
DB 1956 AGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGATATCTGC 2015
QY 1861 TACAGCATGAGCTGATGTCATGCTAAAGATAAAGGAGGCCCTTGTAACCTTTGCACAATG 1920
DB 2016 TACAGCATGAGCTGATGTCATGCTTAAGATAAAGGAGGCCCTTGTAACCTTTGCACAATG 2075
QY 1921 CATGTTCTTTATGGACATTAATGAAGTTGCAGAACTTCTTTGTTAAACATGGAGCAGTAGTTA 1980
DB 2076 CATGTTCTTTATGGACATTAATGAAGTTGCAGAACTTCTTTGTTAAACATGGAGCAGTAGTTA 2135
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DB 2136 ATGTAGCTGATTTTATGGAAATTTTACACCTTTTACATGAGCAGCAGCAAAAGGAAATATG 2195
QY 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACCAAAAAAACAAGGATCGAA 2100
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QY 2221 CTCTGTGATAATGTAATAATTTGCCGCGATACCCAAGCAGACATTCACACCTTTTACATTTAG 2280
DB 2376 CTCTGTGATAATGTAATAATTTGCCGCGATACCCAAGCAGACATTCACACCTTTTACATTTAG 2435
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DB 2616 TCACACCTTTGCAAGAGCAGCCCAAAAGGAGCAACACAGCTTTTGTGTTGTCTAG 2675
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DB 2676 CCNATGAGCTGACCCGACTCTTAAATAATCAGNAGGACAAACACCTTTAGATTTAGTTT 2735
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2701 CTTCAAGTGTCTCAAGTGTCTCAATGCTGTGAGAGCCACCCAGGAGCCACTGCAGATGCTCTCT 2760
Db
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Db
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2881 GACTTGGACCTCAATGGATATATTTGAGAGAGAACAGATCACTTTGGATGTATTAGTTG 2940
Db
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Qy
2941 AGATGGGGCAAGAGAGCTGAAGAGATTTGGAATCAATGCTTATGGACATAGGACAAAC 3000
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Db
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Db
3276 AGTCTGGAGAGAGAGATGCAAGTACAGTTCGAGAGCAAGAGATGGAGGTCAATGAG 3335
Qy
3181 GTGGAATCTTCAACAGATACATATTTCTCAAGATTCAGAGGTTTGTAAAGAACTAT 3240
Db
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3241 GGGAAAGATACATCACCGGAGAAAGAGTTTCTGAAAGAAACACCAACCATGCCAATG 3300
Db
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3456 AACGAATGCTATTTCAATGGTCTCTTTTGTGAATGCAATTTATCACAAGGCTTTGATG 3515
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Db
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Db
3576 CCAAGAACATCAATATGATGAAATGGAGAGGTACTGGGTGCTCCAGTTCACAAAG 3635
Qy
3481 ACAGATCTTGTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAAACCTTGGGAAAGT 3540
Db
3636 ACAGATCTTGTACATTTGCCACAGGAGCTGCTCTTTTGGCGGTAAACCTTGGGAAAGT 3695
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3541 CTTTCCTGAGTTCAGTCAATGAATGGACATTTCTCCTCCAGGTCACTCACTGATCA 3600
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3601 CTGCTAGGCCAGTGTAAATGCCCTAGCATTTAGCTGAATATGTTATTTACAGAGAGAAC 3660
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3756 CTGCTAGGCCAGTGTAAATGCCCTAGCATTTAGCTGAATATGTTATTTACAGAGAGAAC 3815
Qy
3661 AGGCTTATCTGAGTATTTAAATCTTACCAGATTTATGAGGCTTATGGTGCATG 3720
Db
3816 AGGCTTATCTGAGTATTTAAATCTTACCAGATTTATGAGGCTTATGGTGCATG 3875

Qy 3721 GATAAATAGTTATTTTAAAGAACTAAATTCACCTGAACCTAAAAATCATCAAGCAGCAGTG 3780
Db 3876 GATAAATAGTTATTTTAAAGAACTAAATTCACCTGAACCTAAAAATCATCAAGCAGCAGTG 3935
Qy 3781 GCCTCTACGTTTACTCTCTTGTGTAAGAAAAA 3813
Db 3936 GCCTCTACGTTTACTCTCTTGTGTAAGAAAAA 3968
RESULT 11
ADR66604
ID ADR66604 standard; DNA; 6189 BP.
XX AC ADR66604;
XX AC
XX AC
DT 02-DEC-2004 (first entry)
XX Human prostatic carcinoma derived DNA SEQ ID 116 #3.
XX human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis; ds.
XX Homo sapiens.
OS
XX
XX
PN WO2004076614-A2.
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004WO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
XX (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T;
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
PI Xinzhang L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
PT New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
XX Claim 1; Page 976-978; 1607pp; German.
PS
XX
CC This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated

Db 2076 CATGTTCTTATGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTA 2135
 Qy 1981 ATGTAGCTGATTTATGGAATTTTACACCTTTTACATGACGACGACCAAAAGGAAATATG 2040
 Db 2136 ATGTAGCTGATTTATGGAATTTTACACCTTTTACATGAGCAGCAGCAAAAGGAAATATG 2195
 Qy 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTGACAGCCCTACCAAAAAAAGGAGTGGAA 2100
 Db 2196 AAATTTGCAAACTTCTGCTCCAGCATGGTGACAGCCCTACCAAAAAAAGGAGTGGAA 2255
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 Db 2256 ATATCTCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGAG 2315
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 Db 2316 ATGACGCTTTGCTAGATGCTGCCAAGAGGGTTGTTAGCCAGAGTGAGAGATTTGCTT 2375
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 Db 2376 CTCTCTGATAATGTAAATTCGCCGCGATACCCAAAGGAGACATTCACACCTTTTACATTTAG 2435
 Qy 2281 CAGCTGGTTATTAATTAATTTAGAAATTTGAGATTTTGTGTTCAACCGAGCTGATGTGA 2340
 Db 2436 CAGCTGGTTATTAATTAATTTAGAAATTTGAGATTTTGTGTTCAACCGAGCTGATGTGA 2495
 Qy 2341 ATGCCCAAGACAAAGGAGCTTATTCCTTTTACATAATGCACGATCTTACGGGCATGTAG 2400
 Db 2496 ATGCCCAAGACAAAGGAGCTTATTCCTTTTACATAATGCACGATCTTACGGGCATGTAG 2555
 Qy 2401 ATGTAGCAGCTCTACTTAATAAGTATAATGCATGTGTCAATGCCACGACAAATGGGCTT 2460
 Db 2556 ATGTAGCAGCTCTACTTAATAAGTATAATGCATGTGTCAATGCCACGACAAATGGGCTT 2615
 Qy 2461 TCACACCTTTGCAAGAGCAGCCCAAAAGGGAGCGAACACAGCTTTGTGTTGCTGAG 2520
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 Db 2676 CCCATGGAGCTCACCGACTCTTAAATATCAGGAAGGACAAACACTTTAGATTTAGTTT 2735
 Qy 2581 CAGCGGATGATGTCAGCGCTCTTCTGACAGCAGCATGCCCCATCTGCTGCGCCTCTT 2640
 Db 2736 CAGCAGATGATGTCAGCGCTCTTCTGACAGCAGCATGCCCCATCTGCTGCGCCTCTT 2795
 Qy 2641 GTTACAAGCCTCAAGTGCTCAATGTGTGAGAGGCCAGAGGCCACTGACAGATGCTCTCT 2700
 Db 2796 GTTACAAGCCTCAAGTGCTCAATGTGTGAGAGGCCAGAGGCCACTGACAGATGCTCTCT 2855
 Qy 2701 CTTCAAGTCCATCTAGCCCATCAAGCCTTTCTGACGCCAGCAGTCTTGACACTTTATCTG 2760
 Db 2856 CTTCAAGTCCATCTAGCCCATCAAGCCTTTCTGACGCCAGCAGTCTTGACACTTTATCTG 2915
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 Db 2916 GGAGTTTTTTCAGAACTGCTCTCAGTAGTTAGTTTCAAGTGGAAACAGAGGGTGTCTCCAGTT 2975
 Qy 2821 TGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTATGATATACTCAATTCGTAAGGAATCTTTG 2880
 Db 2976 TGGAGAAAAAGGAGGTTCCAGGAGTAGATTTTATGATATACTCAATTCGTAAGGAATCTTTG 3035
 Qy 2881 GACTTGGACCACTTAATGGATATATTGAGAGAGACAGATCACTTTGGATGTATTAGTTG 2940
 Db 3036 GACTTGGACCACTTAATGGATATATTGAGAGAGACAGATCACTTTGGATGTATTAGTTG 3095
 Qy 2941 AGATGGGACACAGGAGCTGAAGGAGATTGGAAATCAATGCTTTATGACATAGGCACAAAC 3000
 Db 3096 AGATGGGACACAGGAGCTGAAGGAGATTGGAAATCAATGCTTTATGACATAGGCACAAAC 3155
 Qy 3001 TAAATTAAGGAGCTCGAGAGACTTATCTCCGGACAAAGGCTCTTAACCCATATTTAACTT 3060
 Db 3156 TAAATTAAGGAGCTCGAGAGACTTATCTCCGGACAAAGGCTCTTAACCCATATTTAACTT 3215

Qy 3061 TGAACACCTCTGGTAGTGGAACAAATTTCTTATAGATCTGCTCTCTGATGATAAAGAGTTTC 3120
 Db 3216 TGAACACCTCTGGTAGTGGAACAAATTTCTTATAGATCTGCTCTCTGATGATAAAGAGTTTC 3275
 Qy 3121 AGTCTGCGAGGAAGAGATGCAAAAGTACAGTTCGAGAGACACAGAGATGGAGGTCTATGCA 3180
 Db 3276 AGTCTGCGAGGAAGAGATGCAAAAGTACAGTTCGAGAGACACAGAGATGGAGGTCTATGCA 3335
 Qy 3181 GTGGATCTTCAACAGATACAAATTTCTCAAGATTCAGAAAGTTCGAAAGAACTAT 3240
 Db 3336 GTGGATCTTCAACAGATACAAATTTCTCAAGATTCAGAAAGTTCGAAAGAACTAT 3395
 Qy 3241 GGGAAAGATACACTCACCGGAGAAAGAAAGTTTCTGAAAGAAACCAACCAATGCAATG 3300
 Db 3396 GGGAAAGATACACTCACCGGAGAAAGAAAGTTTCTGAAAGAAACCAACCAATGCAATG 3455
 Qy 3301 AACGAATCTATTTCAATGGGTCTCTCTTTTGAATGCAATTTATCCAAAGGCTTTGATG 3360
 Db 3456 AACGAATCTATTTCAATGGGTCTCTCTTTTGAATGCAATTTATCCAAAGGCTTTGATG 3515
 Qy 3361 AAAGCATGCGTACATAGTGTATGTTTGGAGCTGGCATTTATTTGCTGAAACTCTT 3420
 Db 3516 AAAGCATGCGTACATAGTGTATGTTTGGAGCTGGCATTTATTTGCTGAAACTCTT 3575
 Qy 3421 CCMAAGCAATCAATATGATATGAAATTTGAGGAGGTACTGGGTGTCCAGTTCCAAAG 3480
 Db 3576 CCMAAGCAATCAATATGATATGAAATTTGAGGAGGTACTGGGTGTCCAGTTCCAAAG 3635
 Qy 3481 ACAGATCTTGTACATTTGCCACAGGAGCTGCTCTTTTGGCGGGTAAACCTTTGGGAAAGT 3540
 Db 3636 ACAGATCTTGTACATTTGCCACAGGAGCTGCTCTTTTGGCGGGTAAACCTTTGGGAAAGT 3695
 Qy 3541 CTTTCTCGAGTTCAGTCAATGAAATGGACATCTCTCTCCAGGTCACTCACTCAGTCA 3600
 Db 3696 CTTTCTCGAGTTCAGTCAATGAAATGGACATCTCTCTCCAGGTCACTCACTCAGTCA 3755
 Qy 3601 CTGTTAGGCCCAGTGTAAATGGCCCTAGCATTTAGCTGAATATGTTTATACAGAGGAGAAC 3660
 Db 3756 CTGTTAGGCCCAGTGTAAATGGCCCTAGCATTTAGCTGAATATGTTTATACAGAGGAGAAC 3815
 Qy 3661 AGGCTTATCTCGAGTATTTAATTTACTTACCAGATTTATGAGGCTTGAAGGTATGGTCGATG 3720
 Db 3816 AGGCTTATCTCGAGTATTTAATTTACTTACCAGATTTATGAGGCTTGAAGGTATGGTCGATG 3875
 Qy 3721 GATAAATAGTTATTTTAAAGAACTTAATTTCCACTGAACCTTAAATCATCAAAAGCAGCAGTG 3780
 Db 3876 GATAAATAGTTATTTTAAAGAACTTAATTTCCACTGAACCTTAAATCATCAAAAGCAGCAGTG 3935
 Qy 3781 GCCTCTAGCTTTTACTCCTCTTGTGCAAAAAA 3813
 Db 3936 GCCTCTAGCTTTTACTCCTTTGCTGAAAAA 3968

RESULT 12

ID ADR66262 standard; DNA; 6189 BP.
 XX

AC ADR66262;

DT 02-DEC-2004 (first entry)

DE Human prostatic carcinoma derived DNA SEQ ID 116 #2.

XX human; cytostatic; diagnosis; prostatic cancer;
 KW differential expression analysis; ds.
 XX

OS Homo sapiens.

PN WO2004076614-A2.

XX 10-SEP-2004.

XX

Db 1416 GAATCAAAAAACATCTCTCTCGAAATGGTGAAATTTCAAGCATCTCTCAAAACACATGAAA 1475
Qy 1321 CAGCATTGATTTGCTGCTGCTGATCTCCATATCCCAAAAGAAAGCAATATCTGAACTGT 1380
Db 1476 CAGCATTGATTTGCTGCTGCTGATCTCCATATCCCAAAAGAAAGCAATATCTGAACTGT 1535
Qy 1381 TGTCTAGAAAAGGAGCAAAACATCAATGAAAAGACTAAAGAAATTTTGACTCTCTCTGCACG 1440
Db 1536 TGTCTAGAAAAGGAGCAAAACATCAATGAAAAGACTAAAGAAATTTTGACTCTCTCTGCACG 1595
Qy 1441 TGGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGTGAAAACATGAAAGCAAGG 1500
Db 1596 TGGCATCTGAGAAAGCTCATATATGATGTTGTTGAAGTAGTGTGAAAACATGAAAGCAAGG 1655
Qy 1501 TTAATGCTCTGATATCTTTGCTGACATCTCTACACAGAGCTGCATATCTGCTGATC 1560
Db 1656 TTAATGCTCTGATATCTTTGCTGACATCTCTACACAGAGCTGCATATCTGCTGATC 1715
Qy 1561 TACAAAACCTGCCGCCCTACTCTCTGAGCTATGGGTGTGATCCTTAACATTTATATCCCTTCAGG 1620
Db 1716 TACAAAACCTGCCGCCCTACTCTCTGAGCTATGGGTGTGATCCTTAACATTTATATCCCTTCAGG 1775
Qy 1621 GCTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAATCTCTCCAAGAGGATATCT 1680
Db 1776 GCTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAATCTCTCCAAGAGGATATCT 1835
Qy 1681 CATTAGGTAAATTCAGAGGCAGACAGCAATTCCTGGAAGCTGCAAGGCTGGAGATGTCG 1740
Db 1836 CATTAGGTAAATTCAGAGGCAGACAGCAATTCCTGGAAGCTGCAAGGCTGGAGATGTCG 1895
Qy 1741 AAATCTGTAATAAAAACTGTCTGCTGAGTGTCAATGTCAGAGACATTTGAAGGCGCTC 1800
Db 1896 AAATCTGTAATAAAAACTGTCTGAGTGTCAATGTCAGAGACATTTGAAGGCGCTC 1955
Qy 1801 AGCTTACACCACTTCATTTTCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGC 1860
Db 1956 AGCTTACACCACTTCATTTTCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGC 2015
Qy 1861 TACAGCTGGAGCTGATGTGCTTAAGATTAAGGAGGCTGTACCTTTTGCAATG 1920
Db 2016 TACAGCTGGAGCTGATGTGCTTAAGATTAAGGAGGCTGTACCTTTTGCAATG 2075
Qy 1921 CATGTTCTTATGGACATTAAGTTGACAGACTCTCTGTTAAACATGAGCAGTAGTTA 1980
Db 2076 CATGTTCTTATGGACATTAAGTTGACAGACTCTCTGTTAAACATGAGCAGTAGTTA 2135
Qy 1981 ATGTAGCTGATTTATGGAAATTTACACCTTTATGAAAGCAGCAGCAAAAGGAAATATG 2040
Db 2136 ATGTAGCTGATTTATGGAAATTTACACCTTTATGAAAGCAGCAGCAAAAGGAAATATG 2195
Qy 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTGAGACCTTACCACCAAAAAACAGGGATGGAA 2100
Db 2196 AAATTTGCAAACTTCTGCTCCAGCATGGTGAGACCTTACCACCAAAAAACAGGGATGGAA 2255
Qy 2101 ATACTCTTTTGGATCTTTGTTAAAGATGGAGATACAGATTTCAAGATCTGTTAGGGAG 2160
Db 2256 ATACTCTTTTGGATCTTTGTTAAAGATGGAGATACAGATTTCAAGATCTGTTAGGGAG 2315
Qy 2161 ATGCAGCTTTTGTAGTGTGCCAAGAGGGTTGTTTAGCCAGAGTGAAAGATTTGTCTT 2220
Db 2316 ATGCAGCTTTTGTAGTGTGCCAAGAGGGTTGTTTAGCCAGAGTGAAAGATTTGTCTT 2375
Qy 2221 CTCCTGATTAATGTAATTCGCGGATACCCAGGCGAGACATTTCAACACCTTTACATTTAG 2280
Db 2376 CTCCTGATTAATGTAATTCGCGGATACCCAGGCGAGACATTTCAACACCTTTACATTTAG 2435
Qy 2281 CAGCTGGTTTAAATTAATTTAGAAAGTTGCAGAGTATTTGTTTCAACACGAGCTGATGTA 2340
Db 2436 CAGCTGGTTTAAATTAATTTAGAAAGTTGCAGAGTATTTGTTTCAACACGAGCTGATGTA 2495
Qy 2341 ATGCCCAAGACAAAGAGGAGCTTATTTCTTTTACATAATGCAGCATCTTTACGGGCGATGTA 2400
Db 2496 ATGCCCAAGACAAAGAGGAGCTTATTTCTTTTACATAATGCAGCATCTTTACGGGCGATGTA 2555

Qy 2401 ATGTAGCAGCTCTACTAATAAAGTATAATGATGTGTCATGCCACGACGAATGGGCTT 2460
Db 2556 ATGTAGCAGCTCTACTAATAAAGTATAATGATGTGTCATGCCACGACGAATGGGCTT 2615
Qy 2461 TCACACCTTTTGCACGAAGCAGCCCCAAAAGGAGCGAACACAGCTTTTGTGCTAG 2520
Db 2616 TCACACCTTTTGCACGAAGCAGCCCCAAAAGGAGCGAACACAGCTTTTGTGCTAG 2675
Qy 2521 CCCATGGAGCTGACCCGACTCTTAATAATCAGGAGGACAAACACCTTTAGATTTAGTTT 2580
Db 2676 CCCATGGAGCTGACCCGACTCTTAATAATCAGGAGGACAAACACCTTTAGATTTAGTTT 2735
Qy 2581 CAGCGGATGATGTACAGCGCTCTTCTGACAGAGCCATGCCCCCTCTGCTCGCCCTCTT 2640
Db 2736 CAGCAGATGATGTACAGCGCTCTTCTGACAGAGCCATGCCCCCTCTGCTCGCCCTCTT 2795
Qy 2641 GTTACAAGCCTCAAGTGTCTCAATGGTGTGAGAGCCCGAGGAGCCACTGCAGATGCTCT 2700
Db 2796 GTTACAAGCCTCAAGTGTCTCAATGGTGTGAGAGCCCGAGGAGCCACTGCAGATGCTCT 2855
Qy 2701 CTTCAAGTTCATCTAGCCCATCAAGCCTTTCTGAGCAGCAGAGTCTTTGACAACTTATCTG 2760
Db 2856 CTTCAAGTTCATCTAGCCCATCAAGCCTTTCTGAGCAGCAGAGTCTTTGACAACTTATCTG 2915
Qy 2761 GGAGTTTTTTCAGAACTGTCTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGCTGCTCCAGTT 2820
Db 2916 GGAGTTTTTTCAGAACTGTCTTCAGTAGTTAGTTTCAAGTGGAAACAGAGGCTGCTCCAGTT 2975
Qy 2821 TGGGAAAAAGGAGGTTCCAGGAGTAGATTTTGTAGCAATCACTCAATTCGTAAAGGAATCTTG 2880
Db 2976 TGGGAAAAAGGAGGTTCCAGGAGTAGATTTTGTAGCAATCACTCAATTCGTAAAGGAATCTTG 3035
Qy 2881 GACTTGAGCACCCTAATGTGATATATTTGAGAGAGACAGATCACTTTGATGTATTTAGTTG 2940
Db 3036 GACTTGAGCACCCTAATGTGATATATTTGAGAGAGACAGATCACTTTGATGTATTTAGTTG 3095
Qy 2941 AGATGGGGCAACAAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCAACAAC 3000
Db 3096 AGATGGGGCAACAAGGAGCTGAAGGAGATTGGAATCAATGCTTATGGACATAGGCAACAAC 3155
Qy 3001 TAAATTAAGGAGTCGAGAGACTTATCTCCGACAAACAAGGCTTTAAACCCATATTTAACTT 3060
Db 3156 TAAATTAAGGAGTCGAGAGACTTATCTCCGACAAACAAGGCTTTAAACCCATATTTAACTT 3215
Qy 3061 TGAAACACCTCTGTTAGTGGAAACAATTTCTTATAGATCTGCTCTCTGATGATAAAGATTTT 3120
Db 3216 TGAAACACCTCTGTTAGTGGAAACAATTTCTTATAGATCTGCTCTCTGATGATAAAGATTTT 3275
Qy 3121 AGTCTGTGGAGAGAGATGCAAGTACAGTTTCGAGAGCAGACAGATGGAGGTCATGCAAG 3180
Db 3276 AGTCTGTGGAGAGAGATGCAAGTACAGTTTCGAGAGCAGACAGATGGAGGTCATGCAAG 3335
Qy 3181 GTGGAATCTTCAACAGATACAAATTTCTCAAGATTCAGAAGGTTTGTAAACAGAACTAT 3240
Db 3336 GTGGAATCTTCAACAGATACAAATTTCTCAAGATTCAGAAGGTTTGTAAACAGAACTAT 3395
Qy 3241 GGGAAAGATACACTCACCGGAGAAAGAGTTTCTGAAAGAAAACCAACCAATGCCAATG 3300
Db 3396 GGGAAAGATACACTCACCGGAGAAAGAGTTTCTGAAAGAAAACCAACCAATGCCAATG 3455
Qy 3301 AACGAATGCTATTTTCATGGGCTCTCTTTTGTGAATGCAATTTATCCAAAAGGCTTTGATG 3360
Db 3456 AACGAATGCTATTTTCATGGGCTCTCTTTTGTGAATGCAATTTATCCAAAAGGCTTTGATG 3515
Qy 3361 AAAGCATGCGTACATAGTGTGATTTTGGAGCTGGCATTTTATTTTGTGAAAACCTCTT 3420
Db 3516 AAAGCATGCGTACATAGTGTGATTTTGGAGCTGGCATTTTATTTTGTGAAAACCTCTT 3575
Qy 3421 CCAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTGGGTGTCAGTTTCAAAAG 3480
Db 3576 CCAAAAGCAATCAATATGTATATGGAATTTGGAGGAGGTACTGGGTGTCAGTTTCAAAAG 3635

Qy 3481 ACAGATCTTGTACATTTGCCACAGGAGCTGCTCTTTTGGCGGGTAACCTTGGGAAGT 3540
Db |||||||
Qy 3636 ACAGATCTTGTACATTTGCCACAGGAGCTGCTCTTTTGGCGGGTAACCTTGGGAAGT 3695
Db |||||||
Qy 3541 CTTTCTGCGAGTTCAGTGCATGAAATGGCACATTTCTCTCCAGGTATCAGTCACTCA 3600
Db |||||||
Qy 3596 CTTTCTGCGAGTTCAGTGCATGAAATGGCACATTTCTCTCCAGGTATCAGTCACTCA 3755
Db |||||||
Qy 3601 CTGTAGGCCAGGTGTAATGGCCCTAGCATTTAGCTGAATATGTTATTTATACAGAGGAAC 3660
Db |||||||
Qy 3756 CTGTAGGCCAGGTGTAATGGCCCTAGCATTTAGCTGAATATGTTATTTATACAGAGGAAC 3815
Db |||||||
Qy 3661 AGGCTTATCTGAGTATTAATTAATTTACAGATTTAGAGCCCTGAAGGTATGTCATG 3720
Db |||||||
Qy 3916 AGGCTTATCTGAGTATTAATTAATTTACAGATTTAGAGCCCTGAAGGTATGTCATG 3875
Db |||||||
Qy 3721 GATAAATAGTATTTTAAAGAACTTAATTTCCACTGAACCTTAATCATCAAAAGCAGCAGTG 3780
Db |||||||
Qy 3876 GATAAATAGTATTTTAAAGAACTTAATTTCCACTGAACCTTAATCATCAAAAGCAGCAGTG 3935
Db |||||||
Qy 3781 GCCTCTACGTTTTACTCTCTTTGCTGAAAAAAA 3813
Db |||||||
Qy 3936 GCCTCTACGTTTTACTCTCTTTGCTGAAAAAAA 3968
Db |||||||

RESULT 13
ID ADW86202
XX ADW86202 standard; DNA; 6189 BP.

AC ADW86202;

DT 21-APR-2005 (first entry)

DE Human Tankyrase 2 DNA.

KW ds; gene; cancer; tankyrase 2; Cytostatic; Gene Therapy; Neoplasm.

OS Homo sapiens.

XX WO2005012524-A1.

XX 10-FEB-2005.

XX 23-JUL-2004; 2004WO-GB003235.

XX 25-JUL-2003; 2003GB-00017466.

XX (UYSH-) UNIV SHEFFIELD.

XX Helleday T;

XX WPI; 2005-132664/14.

PT A poly(ADP-ribose)ylation polymerase (PARP) inhibitor of activity of an
PT enzyme that mediates repair of a DNA strand break, useful in treating
PT diseases with gene defects on homologous recombination.

PS Disclosure; Fig 13; 52pp; English.

XX The invention relates to the use of an agent that inhibits the activity
CC of an enzyme that mediates repair of a DNA strand break in the
CC manufacture of a medicament for the treatment of diseases caused by a
CC defect in a gene that mediates homologous recombination (HR). The use is
CC for the treatment of cancer, preferably lung, colon, pancreatic, gastric,
CC ovarian, cervical, breast and prostate cancer. The cancer is in a human,
CC and is gene-linked hereditary cancer. The cancer is specifically breast
CC cancer, where the cancer cells to be treated are defective in BRCA1 or
CC BRCA2 expression, and are partially or totally deficient in BRCA1 and/or
CC BRCA2 expression. The gene that mediates HR is a tumor suppressor gene
CC that is BRCA1 or BRCA2. The PARP inhibitor is useful in the manufacture
CC of a medicament for inducing apoptosis in HR defective cells that are
CC cancer cells, where the cancer cells defective in HR are partially or
CC totally deficient in HR. The present sequence represents human tankyrase

CC 2 DNA.
XX
SQ Sequence 6189 BP; 1772 A; 1233 C; 1386 G; 1798 T; 0 U; 0 Other;
Query Match 99.4%; Score 3791.4; DB 14; Length 6189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
Qy 1 CGCGCTGCTCCGCCCGCGCGGAGCCGCGGGGGAGGAGCCAGCGAGGGGCGCGCG 60
Db |||||||
Qy 157 CGCGCTGCTCCGCCCGCGCGGAGCCGCGGGGGAGGAGCCAGCGAGGGGCGCGCG 216
Db |||||||
Qy 61 TGGGCGGCGCCATGGGACTGCCCGATCCGCTGACAGCAGGAGGAGCAAGCGGCCCGGG 120
Db |||||||
Qy 217 TGGGCGGCGG-CCATGGGACTGCCCGGATCCGCTGACAGCAGGAGGAGCAAGCGGCCCGGG 275
Db |||||||
Qy 121 CCCTGAGCGGCTCTTCTCCCGGGGGGCTCCGCCCTCTCTGCTCGGGGGCCCGGGCTCCTGC 180
Db |||||||
Qy 276 CCCTGAGCGGCTCTTCTCCCGGGGGGCTCCGCCCTCTCTGCTCGGGGGCCCGGGCTCCTGC 335
Db |||||||
Qy 181 TCCGGTTGCTGGCGCTGTTGCTGGCTGTGGCGGGCCAGGATCATGTCGGGTCCCGCT 240
Db |||||||
Qy 336 TCCGGTTGCTGGCGCTGTTGCTGGCTGTGGCGGGCCAGGATCATGTCGGGTCCCGCT 395
Db |||||||
Qy 241 GCGCGCGGGGGAGCGGCTGCGGAGCGCGCGGCGGAGGCGGCGGCGCGGCC 300
Db |||||||
Qy 396 GCGCGCGGGGGAGCGGCTGCGGAGCGCGCGGCGGCGGAGGCGGCGGCGGCC 455
Db |||||||
Qy 301 GAGAGCTGTTTCGAGGGCTGCGCAACCGGGACGCTGGAAACGAGTCAAGAGGCTGGTGACGC 360
Db |||||||
Qy 456 GAGAGCTGTTTCGAGGGCTGCGCAACCGGGACGCTGGAAACGAGTCAAGAGGCTGGTGACGC 515
Db |||||||
Qy 361 CTGAGAAAGTGAAACAGCCGCGACACGCGGGGAGGAAATCCACCCCGCTGCACATTCGCGC 420
Db |||||||
Qy 516 CTGAGAAAGTGAAACAGCCGCGACACGCGGGGAGGAAATCCACCCCGCTGCACATTCGCGC 575
Db |||||||
Qy 421 CAGGTTTTGGGCGGAAAGAGCTAGTTGAATATTTGCTTCAGAAATGGTGCAGTTCGCAAG 480
Db |||||||
Qy 576 CAGGTTTTGGGCGGAAAGAGCTAGTTGAATATTTGCTTCAGAAATGGTGCAGTTCGCAAG 635
Db |||||||
Qy 481 CAGTGATGATGGGGGCTTTATCTCTTCATATGATGCTCTTTTGGTTCATGCTGAAG 540
Db |||||||
Qy 636 CAGTGATGATGGGGGCTTTATCTCTTCATATGATGCTCTTTTGGTTCATGCTGAAG 695
Db |||||||
Qy 541 TAGTCAATCTCTTTTTCGACATGCTGCAGACCCCAATGCTCGAGATAATTTGGAATATA 600
Db |||||||
Qy 696 TAGTCAATCTCTTTTTCGACATGCTGCAGACCCCAATGCTCGAGATAATTTGGAATATA 755
Db |||||||
Qy 601 CTCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATGTTTGCATGCTGCTTTACAGC 660
Db |||||||
Qy 756 CTCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATGTTTGCATGCTGCTTTACAGC 815
Db |||||||
Qy 661 ATGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGCAGCATTTGGATTTAGCAGATC 720
Db |||||||
Qy 816 ATGGAGCTGAGCCCAACCATCCGAAATACAGATGGAAGCAGCATTTGGATTTAGCAGATC 875
Db |||||||
Qy 721 CATCTGCCAAAGCAGTCTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCA 780
Db |||||||
Qy 876 CATCTGCCAAAGCAGTCTCTTACTGGTGAATATAAGAAAGATGAATCTTTAGAAAGTGCCA 935
Db |||||||
Qy 781 GGAGTGGCAATGAAGAAATGATGGCTCTACTCACACCATTAATGTCACCTGCCACG 840
Db |||||||
Qy 936 GGAGTGGCAATGAAGAAATGATGGCTCTACTCACACCATTAATGTCACCTGCCACG 995
Db |||||||
Qy 841 CAAGTGATGGCAGAAAGTCAATTCATTTACATTTGGCAGCAGGATATAACAGAGTAAAGA 900
Db |||||||
Qy 996 CAAGTGATGGCAGAAAGTCAATTCATTTACATTTGGCAGCAGGATATAACAGAGTAAAGA 1055
Db |||||||
Qy 901 TTGTACAGCTGTTACTGCAACATGAGAGCTGATGTCATGCTAAAGATAAAGGTGATCTGG 960
Db |||||||
Qy 1056 TTGTACAGCTGTTACTGCAACATGAGAGCTGATGTCATGCTAAAGATAAAGGTGATCTGG 1115
Db |||||||
Qy 961 TACCATTACAAATGCGCTGTTCTTTATGGTCATTATGAAGTAAGTGAACCTTTTGGTCAAGC 1020
Db |||||||

Db 1116 TACCAATACAAATGCCCTGTTCTTATGTCATTAATGAAGTAACCTTTTGGTCAAGC 1175
Qy 1021 ATGGTCCTGTGTAATGCAATGGACCTTTGGCAATTCACCTCTTTCATGAGCAGCTT 1080
Db 1176 ATGGTCCTGTGTAATGCAATGGACCTTTGGCAATTCACCTCTTTCATGAGCAGCTT 1235
Qy 1081 CTAAGAACAGGGTTGAAGTATGTTCTCTCTTAAAGTTATGGTGCAGACCCCAACACTGC 1140
Db 1236 CTAAGAACAGGGTTGAAGTATGTTCTCTCTTAAAGTTATGGTGCAGACCCCAACACTGC 1295
Qy 1141 TCAATGTCAACAATAAAGTCTATAGACTTTGGCTCCCAACAGCTTAAAGAAAGAT 1200
Db 1296 TCAATGTCAACAATAAAGTCTATAGACTTTGGCTCCCAACAGCTTAAAGAAAGAT 1355
Qy 1201 TAGCATATGAAATTAAGGCCACTGTTGCTGCAAGCTGCAGAGACTGATGTTACTC 1260
Db 1356 TAGCATATGAAATTAAGGCCACTGTTGCTGCAAGCTGCAGAGACTGATGTTACTC 1415
Qy 1261 GAATCAAAAAACATCTCTCTCGGAAATGGTGAATTTCAAGCATCTCAAAACACATGAAA 1320
Db 1416 GAATCAAAAAACATCTCTCTCGGAAATGGTGAATTTCAAGCATCTCAAAACACATGAAA 1475
Qy 1321 CAGCAATGCATTTGCTGCTGCATCTCCATATCCCAAGAAAGCAAAATATGTGAACGTG 1380
Db 1476 CAGCAATGCATTTGCTGCTGCATCTCCATATCCCAAGAAAGCAAAATATGTGAACGTG 1535
Qy 1381 TGCTAAGAAAGGAGCAACATCAATGAAGACTTAAAGAAATCTTGACTCTCTGCAAG 1440
Db 1536 TGCTAAGAAAGGAGCAACATCAATGAAGACTTAAAGAAATCTTGACTCTCTGCAAG 1595
Qy 1441 TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGTGAACATGAAGCAAAAGG 1500
Db 1596 TGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGTGAACATGAAGCAAAAGG 1655
Qy 1501 TTAATGCTCTGGATAATCTTGGTCAGACTCTCTACACAGAGCTGCATATTTGGTCAATC 1560
Db 1656 TTAATGCTCTGGATAATCTTGGTCAGACTCTCTACACAGAGCTGCATATTTGGTCAATC 1715
Qy 1561 TACAACCTCGCCCTACTCTCTGAGCTATGGTGTGATCCTAACTATATATCCCTTCAGG 1620
Db 1716 TACAACCTCGCCCTACTCTCTGAGCTATGGTGTGATCCTAACTATATATCCCTTCAGG 1775
Qy 1621 GCTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCCAAAGAGGTATCT 1680
Db 1776 GCTTTACTGCTTTACAGATGGGAATGAAATGTACAGCAACTCTCCAAAGAGGTATCT 1835
Qy 1681 CATTAGGTAATTCAGAGGCAGACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCG 1740
Db 1836 CATTAGGTAATTCAGAGGCAGACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCG 1895
Qy 1741 AAACGTGTAATAAATCTGTACTGTTACAGAGTGTCACTGACAGACATTTGAAGGGGCTC 1800
Db 1896 AAACGTGTAATAAATCTGTACTGTTACAGAGTGTCACTGACAGACATTTGAAGGGGCTC 1955
Qy 1801 AGTCACACCACTTCAATTTGAGCTGGGTATACAGAGTGTCCGTGGTGAATATCTGC 1860
Db 1956 AGTCACACCACTTCAATTTGAGCTGGGTATACAGAGTGTCCGTGGTGAATATCTGC 2015
Qy 1861 TACAGCATGGAGCTGATGTGCATGCTAAAGATTAAGAGGAGGCTTGATCCTTTGCACAATG 1920
Db 2016 TACAGCATGGAGCTGATGTGCATGCTAAAGATTAAGAGGAGGCTTGATCCTTTGCACAATG 2075
Qy 1921 CATGTTCTTATGGAATATGAAAGTTGAGAACTCTCTGTTTAAACATGGAGCAGTAGTTA 1980
Db 2076 CATGTTCTTATGGAATATGAAAGTTGAGAACTCTCTGTTTAAACATGGAGCAGTAGTTA 2135
Qy 1981 ATGTAGCTGATTTATGGAATTTACCTTTACATGAAGAGCGACCAAAAGAAATATG 2040
Db 2136 ATGTAGCTGATTTATGGAATTTACCTTTTACATGAAGAGCAGCAAAAGAAATATG 2195
Qy 2041 AAATTTGCAAACTCTGCTCCAGCATGGTGCAGACCTTACCACAAAAAAGAGGATGAAA 2100

Db 2196 AAATTTGCAAACTCTGCTCCAGCATGGTGCAGACCTTACAAAAAAGAGGATGAAA 2255
Qy 2101 ATACTCTCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAG 2160
Db 2256 ATACTCTCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGGAG 2315
Qy 2161 ATGCAGCTTTGCTAGATGCTGCGCAAGAGGGTGTGTTAGCCAGAGAGTGAAGAGTTGCTTT 2220
Db 2316 ATGCAGCTTTGCTAGATGCTGCGCAAGAGGGTGTGTTAGCCAGAGAGTGAAGAGTTGCTTT 2375
Qy 2221 CTCTGTATATGTAATTTGGCGGATACCCNAGGACAGATTTCAACACCTTTTACATTTAG 2280
Db 2376 CTCTGTATATGTAATTTGGCGGATACCCNAGGACAGATTTCAACACCTTTTACATTTAG 2435
Qy 2281 CAGCTGGTTATAATAATTTAGAGTTGCAGAGTATTTGTTACAAACAGGAGCTGATGTGA 2340
Db 2436 CAGCTGGTTATAATAATTTAGAGTTGCAGAGTATTTGTTACAAACAGGAGCTGATGTGA 2495
Qy 2341 ATGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGCAGCATCTTTACGGGATGTTAG 2400
Db 2496 ATGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGCAGCATCTTTACGGGATGTTAG 2555
Qy 2401 ATGTAGCAGCTCTACTAATAAAGTATTAATGATGTGTCATGTCGCAAGGACAAATGGGGCTT 2460
Db 2556 ATGTAGCAGCTCTACTAATAAAGTATTAATGATGTGTCATGTCGCAAGGACAAATGGGGCTT 2615
Qy 2461 TCACACCTTTGCGAAGAGCAGCCCAAGAGGAGCAACACACAGCTTTGCTTTGTTGCTAG 2520
Db 2616 TCACACCTTTGCGAAGAGCAGCCCAAGAGGAGCAACACACAGCTTTGCTTTGTTGCTAG 2675
Qy 2521 CCCATGGAGCTGACCCGACCTCTTAAAAATCAGGAAGGACAAACACCTTTTAGATTTAGTTT 2580
Db 2676 CCCATGGAGCTGACCCGACCTCTTAAAAATCAGGAAGGACAAACACCTTTTAGATTTAGTTT 2735
Qy 2581 CAGCGATGATGTGAGCGCTCTTCTGACAGAGCCATGCGCCCACTGCTCTCGCCCTCTT 2640
Db 2736 CAGCAGATGATGTGAGCGCTCTTCTGACAGAGCCATGCGCCCACTGCTCTCGCCCTCTT 2795
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Db 2856 CTTCAGGTCCATCTAGCCCATCAAGCCCTTTCTGACAGCCAGCAGCTTTTGACAACTTATCTG 2915
Qy 2761 GGAGTTTTTCAGAACTGTCTTTCAGTAGTTAGTTCAAGTGGAAACAGAGGGTCTTCCAGTT 2820
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RESULT 15
AAD54031
ID AAD54031 standard; DNA; 6018 BP.
XX

AC AAD54031;
XX 17-JUN-2003 (first entry)
XX Human colon cancer-associated polypeptide gene, TNKL (BC-203).
XX Human; colon cancer-associated polypeptide; immune response; therapy;
XX colon cancer; gene; ds.
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XX Key Location/Qualifiers
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XX /transl_except= (pos:262..265, aa:Asp)
XX /note= "CDS does not include start and stop codon"
XX /partial
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XX
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XX
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XX
XX 04-MAY-2001; 2001US-00849602.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (CORR) CORNELL RES FOUN INC.
XX
XX Chen Y, Old LJ, Scanlan MJ, Stockert E;
XX WPI; 2003-112003/10.
XX P-PSDB; AAE35352.
XX
XX Diagnosing colon cancer in a subject comprises identifying colon cancer-associated polypeptides as antigens that elicit immune response in colon cancer.
XX
XX Claim 1; Page 85-89; 122pp; English.
XX
XX The invention relates to a method for diagnosing colon cancer in a subject which comprises identifying colon cancer-associated polypeptides as antigens that elicit immune response in colon cancer. The method is useful for diagnosing, determining onset, progression, or regression of a colon cancer in a subject, or for selecting a course of treatment of a subject having or suspected of having colon cancer. The colon cancer-associated polypeptides are useful as markers for diagnosing colon cancer, and for following the course of treatment of colon cancer. The present sequence is human colon cancer-associated polypeptide gene
XX
XX Sequence 6018 BP; 1741 A; 1171 C; 1328 G; 1778 T; 0 U; 0 Other;
XX
XX Query Match 99.3%; Score 3788.4; DB 10; Length 6018;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 3803; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
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Db |||||
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Qy 124 TGAGCGGCTCTTCTCCGGGGGGCTCGCCCTCTCTGCTCGCGGGGCGCGGGCTCTGCTCC 183
Db 120 TGAGCGGCTCTTCTCCGGGGGGCTCGCCCTCTCTGCTCGCGGGGCGCGGGCTCTGCTCC 179
Qy 184 GGTGTGCTGGCGCTGTTGCTGGCTGTGGCGGGCAGGATCATGCGGTGCGCGCTGCG 243
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Search completed: December 18, 2006, 13:14:45
Job time : 2074.14 secs

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6	3791.4	99.4	4406	2	AX062247	Set	AX062247 Set
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8	3791.4	99.4	5002	2	AX062273	Set	AX062273 Set
9	3791.4	99.4	6189	2	CQ896544	Set	CQ896544 Set
10	3791.4	99.4	6189	2	CS019687	Set	CS019687 Set
11	3791.4	99.4	6189	2	CS023798	Set	CS023798 Set
12	3791.4	99.4	6189	5	AF438201	Hot	AF438201 Hot
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14	3770.8	98.8	5075	2	AR578380	Set	AR578380 Set
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Db	1861	TACAGCATGAGCTGATGTGCATCTCTAAAGATAAAGAGAGCCCTTGTAACCTTTGCACAATG	1920	1861	TACAGCATGAGCTGATGTGCATCTCTAAAGATAAAGAGAGCCCTTGTAACCTTTGCACAATG	1920
Qy	1921	CATGTTCTTATGACATTTAAGATTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTA	1980	1921	CATGTTCTTATGACATTTAAGATTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTA	1980
Db	1921	CATGTTCTTATGACATTTAAGATTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTA	1980	1921	CATGTTCTTATGACATTTAAGATTTGCAGAACTTCTTGTTAAACATGGAGCAGTAGTTA	1980
Qy	1981	ATGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAAATATG	2040	1981	ATGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAAATATG	2040
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Qy	2101	ATACTCCTTTGGATCTTGTTTAAAGATGGAGATACAGATATTCAGATCTCTTAGGGGAG	2160	2101	ATACTCCTTTGGATCTTGTTTAAAGATGGAGATACAGATATTCAGATCTCTTAGGGGAG	2160
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Qy	2281	CAGCTGGTTATAATATTTAAGATTTGCAGAGTATTTGTTTACAACCGGAGCTGATGTGA	2340	2281	CAGCTGGTTATAATATTTAAGATTTGCAGAGTATTTGTTTACAACCGGAGCTGATGTGA	2340
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[illegible]

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Qy	3661	AGGCTTATCTCTGAGTATTTAAATTAATTTACTTTACCAGATTATGAGCGCTGAAGGTATGTCGATG	3720			
Db	3661	AGGCTTATCTCTGAGTATTTAAATTAATTTACTTTACCAGATTATGAGCGCTGAAGGTATGTCGATG	3720			
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ACCESSION	AB653624					
VERSION	AB653624.1	GI:67584113				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 3816)					
AUTHORS	Luo, Y., Chan, E., Xu, X., Huang, B. and Ossoskaya, V.					
TITLE	Tanyrase H, compositions involved in the cell cycle and methods of use					
JOURNAL	Patent: US 6887675-A 2 03-MAY-2005;					
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Qy	181	TCCGGTTCGCGGCTCTTCTGCTGTGTGGCGGCGCAGGATCATGTGCGGTCGCGCT	240			
Db	181	TCCGGTTCGCGGCTCTTCTGCTGTGTGGCGGCGCAGGATCATGTGCGGTCGCGCT	240			
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ORGANISM Homo sapiens
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1 (bases 1 to 6028)
AUTHORS Chi, N.-W. and Lodish, H. F.
TITLE A novel homolog of Tankyrase
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 6028)
AUTHORS Chi, N.-W. and Lodish, H. F.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2000) Whitehead Institute for Biomedical
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[illegible]

[illegible]

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DEFINITION	AX057579		
ACCESSION	AX057579.1	GI:12310301	
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KEYWORDS			
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ORGANISM	Homo sapiens		
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AUTHORS	Chi, N.W. and Lodish, H.F.		
TITLE	A novel insulin signaling molecule		
JOURNAL	Patent: WO 0077225-A 21-DEC-2000;		
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	HOSPITAL CORPORATION (US)		
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QY	301	G	AGAGCTGTTGAGGGCGTGCCGCAACGGGGAACGTGGAACGAGTCAAGAGGCTGGTAGCGC	360			
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QY	901	T	TGTACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTTAAGATAAGAGTGAATCTGG	960			
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Db		
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Db		
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1348	CAGCATTGCAATTTGCTGCTGCATCTCCATATCCCAAAAGAAGCAAAATATGTGAACTGT	1407
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1408	TGCTAAGAAAAGGACCAACATCAATGAAGAAGCACTTAAAGAAATCTTGTGACTCCTCTGCACG	1467
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1468	TGGCATCTGAGAAAGCTCATAAATGATGTTGTTGAAAGTAGTGGTGAACATGAAGCAAAAGG	1527
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1648	GCTTTACTCTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGGGTATCT	1707
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1708	CATTAGGTTAATTCAGAGGCAGACAGACAATTCGTGGAAGCTGCAAAAGCTGGAGATGTGCG	1767
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1888	TACAGCATGGAGCTGATGTGCATGCTTAAAGATAAAGGAGGCCCTTGTACCTTTTGCACAATG	1947
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1948	CATGTTCTTTATGGACATTTAAGATTGCAAACTCTTGTATAACATGGAGCAGTAGTTTA	2007
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1981	ATGTAGCTCATTTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATG	2040
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2008	ATGTAGCTCATTTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATG	2067
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QY	2881	GACTTGCAGCACCTAATGGATATATTTTGAGAGAGAA CAGATCACTTTGGATGTATTAGTTTG	2940
DB	2908	GACTTGCAGCACCTAATGGATATATTTTGAGAGAGAA CAGATCACTTTGGATGTATTAGTTTG	2967
QY	2941	AGATGGGGCA CAGGAGCTGAAGAGATTGGATTCAA'TGCTTATGMCATPAGGCCACAAC	3000
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DEFINITION	Sequence 5 from patent US 6599728.		
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VERSION	AR361486.1	GI:33769334	
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AUTHORS	1 (bases 1 to 4275)		
TITLE	Morin,G.B., Funk,W.D. and Piatyszek,M.A.		
JOURNAL	Second mammalian tankyrase		
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QY	61	TGGGCGCGGCGCCATGGGACTCGCGCGGATCCGGTGAACAGCAGGAGAGCAAGCGCGCGG	120
Db	121	TGGGCGCGG--CCATGGGACTCGCGCGGATCCGGTGAACAGCAGGAGAGCAAGCGCGCGG	179

Qy	121	CCCTGAGCGGCTTTCTCCGGGGGCGCTCGCCCTCTGCTCGCGGGGCGGGGCTCCTGC	180
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Qy	181	TCGGGTTGCTGGCGCTGTGCTGCTGCTGGCGGGGCGGAGGATCATGTCCGGGTGCGCGCT	240
Ds	240	TCGGGTTGCTGGCGCTGTGCTGCTGCTGGCGGGGCGGAGGATCATGTCCGGGTGCGCGCT	299
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Ds	300	CGCGCGGGGGAGCGGCTTCGCGAGCGCGCGGGGCGGAGCGCGCGCGCGCC	359
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Ds	660	CTCTCTCCATGAAAGTCAATTAAGGAAAGATGATGTTTGGATGCTGCTTTACAGC	719
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Ds	720	ATGAGCTGAGCCCAACCAATCCGAAATACAGATGGAAGGACAGCATTTGATTTAGCAGATC	779
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Ds	900	CAAGTGATGGCAGAAAGTCAATCTGATTAATGAGGAGGATATTAACAGAGTAAGA	959
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LOCUS Sequence 106 from Patent WO0100849.
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ACCESSION AX062247
VERSION AX062247.1 GI:12540148
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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1 Christenson, E., Demaggio, A. J., Goldman, P. S. and Mcelligott, D. L.
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ORIGIN

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LOCUS AX062273 5002 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 132 from Patent WO0100849.
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KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Christenson, E., Denaggio, A. J., Goldman, P. S. and Mcelligott, D. L.
AUTHORS Tankyrase2 materials and methods
TITLE Patent: WO 0100849-A 132 04-JAN-2001;
JOURNAL ICOS CORPORATION (US)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Homnidae; Homo.			
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DEFINITION Sequence 5 from Patent WO2005012305.

ACCESSION CS023798

VERSION CS023798.1 GI:60222868

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Helleday,T. and Curtin,N.

TITLE Tricyclic parp inhibitors

JOURNAL Patent: WO 2005012305-A 5 10-FEB-2005;

Cancer Research Technology Limited (GB)

FEATURES

Location/Qualifiers

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RESULT 15
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LOCUS Homo sapiens tankyrase-related protein mRNA, partial cds.
DEFINITION AF305081
ACCESSION AF305081
VERSION AF305081.1 GI:10953951
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 4295)
AUTHORS Monz D., Munnia, A., Contesse, N., Fischer, U., Steudel, W. I.,
Feiden, W., Glas, B., and Meese, E. U.
TITLE Novel tankyrase-related gene detected with meningioma-specific sera
JOURNAL Clin. Cancer Res. 7 (1), 113-119 (2001)
PUBMED 11205898
REFERENCE 2 (bases 1 to 4295)
AUTHORS Monz D. W. and Meese, E.
TITLE Direct Submission
JOURNAL Saubermann, Geb. 60, Homburg 66421, Germany
FEATURES
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VDG"

ORIGIN
Query Match 97.9%; Score 3737; DB 5; Length 4295;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3798; Conservative 1; Mismatches 7; Indels 8; Gaps 5;
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82 CGCGCTGCTTCCGCGCGCGGCGAGCGCGGGCGAGCGAGGCCACGAGGGGCGCGCG 141

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RESULT 1	AK047094	1967 bp	linear	HTC 02-SEP-2005
LOCUS	AK047094	10 days neonate cerebellum cDNA, RIKEN full-length		
DEFINITION		enriched library, clone:B930018021 product:TANKYRASE-RELATED		
		PROTEIN (FRAGMENT) homolog [Homo sapiens], full insert sequence.		
ACCESSION	AK047094	1 GI:26338577		
VERSION	AK047094.1	GI:26338577		
KEYWORDS		HTC; CAP trapper.		
SOURCE		Mus musculus (house mouse)		
ORGANISM		Mus musculus		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		
		Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1	Carninci, P. and Hayashizaki, Y.		
AUTHORS		High-efficiency full-length cDNA cloning		
TITLE		Meth. Enzymol. 303, 19-44 (1999)		
JOURNAL		10349636		
PUBLISHED				
REFERENCE	2			
AUTHORS		Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K.,		
		Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
		Normalization and subtraction of cap-trapper-selected cDNAs to		
		prepare full-length cDNA libraries for rapid discovery of new genes		
		Genome Res. 10 (10), 1617-1630 (2000)		
		11042159		
REFERENCE	3			
AUTHORS		Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,		
		Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,		
		Suma, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,		
		Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,		
		Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,		
		Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,		
		Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
		RIKEN integrated sequence analysis (RISA) system-384-format		
		sequencing pipeline with 384 multicapillary sequencer		
		Genome Res. 10 (11), 1757-1771 (2000)		
		11076861		
JOURNAL				
PUBLISHED				
REFERENCE	4			
AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the		
		FANTOM Consortium.		
		Functional annotation of a full-length mouse cDNA collection		
TITLE				

JOURNAL
REFERENCE

5 Nature 409, 685-690 (2001)
The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL
REFERENCE

6 Nature 420, 563-573 (2002)
RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.
Antisense Transcription in the Mammalian Transcriptome

JOURNAL
REFERENCE

7 Science 309, 1564-1566 (2005)
The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
The Transcriptional Landscape of the Mammalian Genome

JOURNAL
REFERENCE

8 (bases 1 to 1967)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ighii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

JOURNAL
REFERENCE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

JOURNAL
REFERENCE

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

JOURNAL
REFERENCE

Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>
Location/Qualifiers

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REFERENCE

1. 1967
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JOURNAL
REFERENCE

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LQAREADVTRFKHLSLEWNPKHPOTHALHCAASPYPKRKQICELLRLKGAN
TNEKTKEFLTPLHVAENANDVVEVVKHEAKVNALDSLQTSIHRANHCGLQTCR

JOURNAL
REFERENCE

CDNAs

JOURNAL
REFERENCE

FEATURES

JOURNAL
REFERENCE

source

JOURNAL
REFERENCE

Query Match 43.6%; Score 1663.4; DB 6; Length 1967;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1782; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

JOURNAL
REFERENCE

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REFERENCE

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JOURNAL
REFERENCE

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RESULT 2

AK048860

LOCUS

DEFINITION

Mus musculus 0 day neonate cerebellum cdna, RIKEN full-length

3417 bp

mRNA

linear

HTC 02-SEP-2005

enriched library, clone: C230076L23 product: tankyrase,
 TRF1-interacting ankyrin-related ADP-ribose polymerase, full insert
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AK048860
 GI: 263339607
 HTC; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

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 RIKEN integrated sequence analysis (RISA) system-384-format
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 Phase I and II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
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 (Genome Network Core Team) and the FANTOM Consortium.
 Antisense Transcription in the Mammalian Transcriptome
 Science 309, 1564-1566 (2005)
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 The Transcriptional Landscape of the Mammalian Genome
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 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Ohsato, N.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
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RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsic.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>.

FEATURES

source

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423..3353

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/db_xref="GI:26339608"
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ORIGIN

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DB 399 AGGAGTGCATGAAGAAAAAATGATGCTCTACTCACACCACTTAAATGTCAACTGCCAT 458
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DB 1119 ATGAATGCATGGATAGTCTTGGTCAGACTGCTTTGCACAGAGCTGCTTAGCGGGCCAC 1178
QY 1560 CTACAAACCTGCCCTACTCTCTGAGCTATGGGTGTGATCTCTAAACATTTATATCCCTTCAG 1619
DB 1179 CTGCAGACCTGCCCTCTCTGCTGAGTTATGGCTCTGATCTCTTCATCATCTCTCCCTGCA 1238
QY 1620 GGCTTTACTGTTTACAGATGGGAAATGAAATGTACAGCAACTCTCTCAAGAGAGGTATC 1679
DB 1239 GGCTTTCAGGCGCAGATGGGGAATGAAGCAGTGCACACAGATTTCTGAGCGAGAGTACT 1298
QY 1680 TCATTAGGTAATTCAGAGGCGACAGACAAATGCTGGAAGCTGCAAGGCTGGAGATGTC 1739
DB 1299 CCTATGCGCATCTCGGACGTGGAATATCGTCTCTTAGAGGATCGAAAGCTGGTGACTTG 1358
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11076861 4	PUBMED REFERENCE AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Akawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Asahbuer, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayaashizaki, Y.
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		11217851
5	PUBMED REFERENCE AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osaio, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V., Chotha, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Naglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Maglott, H., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayaashizaki, Y.
		PANTOM Consortium
		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002)
		12466851
6	PUBMED REFERENCE AUTHORS	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, P., Down, T., Engstrom, P., Fagioli, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayaashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Humnietcki, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T.,
		Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuura, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, K., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Reid, J.F., Ring, B.Z., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reij, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sincalir, B., Sperling, S., Stupka, E., Sugiura, K., Sultana, R., M.S., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, C., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusci, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessy, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watahiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayaashizaki, Y.
		PANTOM Consortium
		The transcriptional landscape of the mammalian genome Science 309 (5740), 1559-1563 (2005)
7	PUBMED REFERENCE AUTHORS	16141072
		Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yag, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayaashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.
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		Antisense transcription in the mammalian transcriptome Science 309 (5740), 1564-1566 (2005)
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		Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayaashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayaashizaki, Y.
		Direct Submission
9	PUBMED REFERENCE AUTHORS	Submitted (30-MAR-2004) Yoshihide Hayaashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
		CNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
		Please visit our web site for further details.
		URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK080913

AK080913.1 GI:26099551

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

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High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

10349636

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prepare full-length cDNA libraries for rapid discovery of new genes

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Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, K.,

Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

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Nature 409, 685-690 (2001)

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The FANTOM Consortium, the RIKEN Genome Exploration Research Group

Phase I and II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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(Genome Network Core Team) and the FANTOM Consortium.

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Science 309, 1564-1566 (2005)

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The Transcriptional Landscape of the Mammalian Genome

Science 309, 1559-1563 (2005)

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Kasukawa, T.,

Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

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Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S.,

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of

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RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@res.riken.jp, URL:http://genome.gsc.riken.jp/, tel:81-45-503-9222, Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/

URL:http://fantom.gsc.riken.jp/.

FEATURES

source

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POLYMERASE homolog [Homo sapiens] (SPT905271, evidence:

FASTY, 95.9%ID, 80%length, match=3167)

putative"

ORIGIN

Query Match

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Matches 1934; Conservative 0; Mismatches 733; Indels 28; Gaps 3;

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RESULT 6
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1 (bases 1 to 3107)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civallo, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(ex) PLoS Biol. 3 (6), E170 (2005)
JOURNAL
PUBMED 15869325
REFERENCE 2 (bases 1 to 3107)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civallo, D.,

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Db 841 TCTTCCAAAAGCAATCAATATGATATATGAAATTTGGAGGAGTACTGGG 888

RESULT 8
LOCUS CR987822 RZPD no. 9016 Homo sapiens cDNA clone RZPDp901611435 5',
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ACCESSION CR987822
VERSION CR987822.1 GI:68281707
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Heil,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D.
AUTHORS Heil,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D.
TITLE Human T-Lymphocytes library
JOURNAL Unpublished (2005)
COMMENT Contact: Inge Arlt
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; RZPDp901611435.
RZPDLIB; (Human T-Lymphocytes) RZPD LIB No. 9016
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact:
Inge Arlt
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de

This clone is available from RZPD:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp901611435
contact RZPD (product- support@rzpd.de) for further information.
Primer name: qe3_4, Primer sequence: CGGATAACAATTCACACAG.

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NotI; vector:
http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml
; 1st strand cDNA was prepared from mRNA obtained from
human T-Lymphocytes with a NotI - oligo(dT) primer [5'
GACTAGTTCATAGTCGAGCGCGCCCTTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Sali adaptors.
digested with NotI and cloned into the NotI and Sali sites
of the pQE80LSN_cloned vector"

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Best Local Similarity 98.6%; Pred. No. 4.2e-215;
Matches 917; Conservative 0; Mismatches 8; Indels 5; Gaps 5;
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Qy 1887 AAAGATAAAGAGGCTTTGACCTTTGCACAAATGCATGTTCTTATGACACATTAAGAAGTT 1946
Db 240 AAAGATAAAGAGGCTTTGACCTTTGCACAAATGCATGTTCTTATGACACATTAAGAAGTT 299
Qy 1947 GCAGAACTCTTGTAAACATGGAGCAGTAGTAAATAGTAGTCTGATTTATGAAATTTACA 2006
Db 300 GCAGAACTCTTGTAAACATGGAGCAGTAGTAAATAGTAGTCTGATTTATGAAATTTACA 359
Qy 2007 CCTTTACATGAAGCAGCAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCCAGAT 2066
Db 360 CCTTTACATGAAGCAGCAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCCAGAT 419
Qy 2067 GGTGCAGACCTTACCAAAACACGGGATGGAATACTCTTTGGATCTTGTAAAGAT 2126
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Qy 2187 AAGGTTGTTTAGCCAGAGTGAAGAAGTTGTTCTCTCTGATATGTAATGTCGCGGAT 2246
Db 540 AAGGTTGTTTAGCCAGAGTGAAGAAGTTGTTCTCTCTGATATGTAATGTCGCGGAT 599
Qy 2247 ACCCAAGGCGACATTTCAACACCTTTTACATTTAGCAGCTGTTTATTAATTTAGAGTT 2306
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Qy 2487 AAGGAGCAACACACAGCTTTTGTGCTTTTGTGTAGCCCATGAGCTGACCCGACTCTTAAA 2546
Db 839 AAGGAGCAACACAGCTTTTGTGCTTTTGTGCTTTGCTGCTGCTGCTGCTT- AA 895

TITLE JOURNAL PUBMED REFERENCE AUTHORS	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Owata, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861
	4
	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaudo, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, R., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Hofmann, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Wittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 11217851
	5
CONSTRM JOURNAL PUBMED REFERENCE AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaudo, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Glessi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawagawa, Y., Kedzierski, R.M., King, B.L., Kongsawa, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Nunata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yangigawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. PANTOM Consortium Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12466851
	6
CONSTRM JOURNAL PUBMED REFERENCE AUTHORS	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L.,

TITLE JOURNAL PUBMED REFERENCE AUTHORS	Bansal, M., Baxter, L., Beisel, K.W., Bereano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Keiso, J., Kitamura, H., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuura, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavesi, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Sempke, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sincalir, B., Sperling, S., Stupka, E., Sugiyama, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamashita, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hilde, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusci, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watanabe, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y. PANTOM Consortium The transcriptional landscape of the mammalian genome Science 309 (5740), 1559-1563 (2005) 16141072
	7
CONSTRM JOURNAL PUBMED REFERENCE AUTHORS	Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yag, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C. RIKEN Genome Exploration Research Group Antisense transcription in the mammalian transcriptome Science 309 (5740), 1564-1566 (2005) 16141073
	8 (bases 1 to 1078)
CONSTRM JOURNAL PUBMED REFERENCE AUTHORS	Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, P., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
	9
TITLE JOURNAL PUBMED REFERENCE AUTHORS	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers 1. .1078
	10
CONSTRM JOURNAL PUBMED REFERENCE AUTHORS	

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VERSION	DT808067.1	GI:75739943	
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SOURCE	Bos taurus (cattle)		
ORGANISM	Bos taurus		
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AUTHORS	Moore, S., Alexander, L., Brownstein, M., Guan, L., Lobo, S., Meng, Y., Tanaguchi, M., Wang, Z., Yu, J., Prange, C., Schreiber, K., Shenmen, C., Wagner, L., Bala, M., Barbazuk, S., Barber, S., Babakair, R., Beland, J., Chun, E., Del Rio, L., Gibson, S., Hanson, R., Kirkpatrick, R., Liu, J., Matsuo, C., Mayo, M., Santos, R.R., Stott, J., Tsai, M., Wong, D., Siddiqui, A., Holt, R., Jones, S.J. and Marra, M.A.		
TITLE	Bovine Genome Sequencing Program: Full-length CDNA Sequencing		
JOURNAL	Unpublished (2005)		
COMMENT	Contact: Robert Kirkpatrick Canada's Michael Smith Genome Sciences Centre BC Cancer Agency Suite 100, 570 West 7th Avenue, Vancouver, British Columbia, Canada, V5Z 4S6 Tel: 1-604-707-5900 x5406 Fax: 1-604-876-3561 Email: robertk@bcgsc.ca Plate: LB0173 row: I column: 4 High quality sequence stop: 898.		
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DEFINITION
ACCESSION CK847047
VERSION CK847047.1 GI:45208162
KEYWORDS EST.
SOURCE Bos taurus (cattle)

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 834)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A.,
Chitko-McKown, C.G., Pettea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: 98 row: I column: 7
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/clone_lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 20 and day 40
embryos."

FEATURES

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Best Local Similarity 95.0%; Pred. No. 1.3e-190;
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Qy 1547 ATATTGTTGTCATCTACAAACCTGCCCTTACTCTGAGCTATGGGTGTGATCTTAAAT 1606
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.TITLE

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DN536421 848 bp mRNA linear EST 11-MAR-2005
 1372517 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
 DN536421

DN536421.1 GI:60988240

EST.

Bos taurus (cattle)

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 848)

Smith, T.P.L., Roberts, A.J., Ehternkamp, S.E., Chitko-McKown, C.G.,
 Wray, J.E. and Keelle, J.W.
 A second set of bovine ESTs from pooled-tissue normalized libraries
 Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and
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Plate: RLK8064 row: G column: 17

Seq primer: GTAATACGACTCACTATAGGG.

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Library made with RNA pooled from multiple tissues

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ORIGIN

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Best Local Similarity 91.5%; Pred. No. 2.6e-175;

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 VERSION
 DN533094.1 GI:81281747
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 Homnidae; Homo.
 1 (bases 1 to 819)

REFERENCE
 AUTHORS
 Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Teuritani, K., Wakaquri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
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 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)

JOURNAL
 PUBMED
 16344560
 COMMENT
 Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute

2-6-7 Karuse-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute (HRI); cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
HRI.

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LOCUS             AGENCOURT 11385409 NIH MGC 164 Mus musculus cDNA clone
DEFINITION        IMAGE:30244272 5', mRNA sequence.
ACCESSION         CB183123
VERSION           CB183123.1 GI:28191571
KEYWORDS          EST.
SOURCE            Mus musculus (house mouse)
ORGANISM          Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE         1 (bases 1 to 955)
AUTHORS          NIH-MGC http://mgc.nci.nih.gov/.
TITLE            National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL           Unpublished (1999)
COMMENT          Contact: Robert Strausberg, Ph.D.
                  Email: rgs@nih.gov
                  cDNA Library Preparation: Invitrogen Corp
                  DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at:
                  http://image.llnl.gov
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        directionally, priming method: Oligo-dT. cDNA enrichment:
        >1k bp, Average insert size 1.8k bp. Priming sequence:
        5'-GACTAGTCTTAGATCGAGCGCGCCCTT-3'. Tissue contributed
        by, David Rowe. Library constructed by ResGen, Invitrogen
        Corp."

ORIGIN
    Query Match          18.0%; Score 687.8; DB 4; Length 955;
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Job time : 16891.5 secs

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DB 1921 CATGTTCTTTATGACATTAATGAAGTTGCAAGACTTCTTGTAAACATGGAAGTAGTTA 1980
QY 1981 ATGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGAAATATG 2040
DB 1981 ATGTAGCTGATTTATGGAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGAAATATG 2040
QY 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTGACACCTTACCAAAAAAAGCAGGATGGAA 2100
DB 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTGACACCTTACCAAAAAAAGCAGGATGGAA 2100
QY 2101 ATACTCCTTTTGGATCTTTGTAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGAG 2160
DB 2101 ATACTCCTTTGGATCTTTGTAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGAG 2160
QY 2161 ATGCAGCTTTGCTAGATGCTGCCAAGAGGGTTGTTAGCCAGAGTGAAGATGTGCTT 2220
DB 2161 ATGCAGCTTTGCTAGATGCTGCCAAGAGGGTTGTTAGCCAGAGTGAAGATGTGCTT 2220
QY 2221 CTCCTGATTAATGTAATTTGCGCGATACCCAGGAGACATTTCAACACCTTTTACATTTAG 2280
DB 2221 CTCCTGATTAATGTAATTTGCGCGATACCCAGGAGACATTTCAACACCTTTTACATTTAG 2280
QY 2281 CAGCTGTTTATTAATTTAGAAAGTTTGCAGAGTATTTGTTTACAACACGAGCTGATGTGA 2340

D _b	180	CCCTGAGCGCGTCTTTCCGGGGGGGCTTCGCCCTTCCTGTCTGC GGGGGCGGGGGGCTCCTCGC	239
Q _y	181	TCCGGTTGCTGGCGCTGTTGCTGGCTGTGGCGGGCGCAGGATCATGT CGGGTGCGCGCT	240
D _b	240	TCCGGTTGCTGGCGCTGTTGCTGGCTGTGGCGGGCGGCGAGGATCATGT CGGGTGCGCGCT	299
Q _y	241	GCGCGGCGGGGGAGCGGCTTCGCGAGCGCGCGCGCGCGCGCGCGTGGAGCGCGCGCGCGCC	300
D _b	300	GCGCGGCGGGGGAGCGGCTTCGCGAGCGCGCGCGCGCGCGCGCGTGGAGCGCGCGCGCGCC	359
Q _y	301	GAGAGCTGTTTCGAGCGCTGCGCAACGSGGACGTGGAAACGAGTCAAGAGCGTGGTGACGC	360
D _b	360	GAGAGCTGTTTCGAGCGCTGCGCAACGSGGACGTGGAAACGAGTCAAGAGCGTGGTGACGC	419
Q _y	361	CTGAGAAGGTGAACAACGCGCGACACGCGCGGCGAGAAATCACCCGCTGCATCTTCGCGC	420
D _b	420	CTGAGAAGGTGAACAACGCGCGACACGCGGCGGCGAGAAATCACCCGCTGCATCTTCGCGC	479
Q _y	421	CAGTTTTTGGCGGAAAGACGTAGTTGAATAATTGCTTCAGAAATGGTGCAAAATGTC AAG	480
D _b	480	CAGTTTTTGGCGGAAAGACGTAGTTGAATAATTGCTTCAGAAATGGTGCAAAATGTC AAG	539
Q _y	481	CACGTGATGATGGGGCTTAATTCCTCTTCATATGCAATGCTCTTTTGGTGCATGCTGAAG	540
D _b	540	CACGTGATGATGGGGCTTAATTCCTCTTCATATGCAATGCTCTTTTGGTGCATGCTGAAG	599
Q _y	541	TAGTCAATCTCTTTTGGCAGCATGGTGAGACCCCAATGCTCGAGATAAATTTGGAATTA TA	600
D _b	600	TAGTCAATCTCTTTTGGCAGCATGGTGAGACCCCAATGCTCGAGATAAATTTGGAATTA TA	659
Q _y	601	CTCCTCTCCATGAAGTGC AATTAAGGAAAGATTGATTTGTCATTTGCTGTTTACAGC	660
D _b	660	CTCCTCTCCATGAAGTGC AATTAAGGAAAGATTGATTTGTCATTTGCTGTTTACAGC	719
Q _y	661	ATGAGCTGAGCCAAACCATCCGAATACAGATGGAAGCAGCATTCGATTTTAGCAGATC	720
D _b	720	ATGAGCTGAGCCAAACCATCCGAATACAGATGGAAGCAGCATTCGATTTTAGCAGATC	779
Q _y	721	CATCTGCCAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACCTTTAGAAAGTGCCA	780
D _b	780	CATCTGCCAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACCTTTAGAAAGTGCCA	839
Q _y	781	GGAGTGCAATGAAGAAAAATGATGCTCTACTCACCAATTAATTTCAACTGCCACG	840
D _b	840	GGAGTGCAATGAAGAAAAATGATGCTCTACTCACCAATTAATTTCAACTGCCACG	899
Q _y	841	CAAGTGATGGCAGAAAGTCAACTCATTAATTTGGCAGCAGGATATAACAGAGTAAAGA	900
D _b	900	CAAGTGATGGCAGAAAGTCAACTCATTAATTTGGCAGCAGGATATAACAGAGTAAAGA	959
Q _y	901	TTGTACAGCTGTACTGCAACATGGAGCTGATGCCATGTCAAAGATAAAGGTGATCTGG	960
D _b	960	TTGTACAGCTGTACTGCAACATGGAGCTGATGCCATGTCAAAGATAAAGGTGATCTGG	1019
Q _y	961	TACCATTACAAATTCSCCTGTTCTTATGGTCATTTATGAAGTAACATGAACCTTTTGGTCAAGC	1020
D _b	1020	TACCATTACAAATTCSCCTGTTCTTATGGTCATTTATGAAGTAACATGAACCTTTTGGTCAAGC	1079
Q _y	1021	ATGGTGCTGTGTHAAATGCAATGCAATTTGGGCAATTCATCTCTTTCTATGAGGACAGCTT	1080
D _b	1080	ATGGTGCTGTGTHAAATGCAATGCAATTTGGGCAATTCATCTCTCTTTCTATGAGGACAGCTT	1139
Q _y	1081	CTAAGAACAGGGTTGAAGTATGTTCTCTCTTTAAGTTATGGTGCAAGCCCCACACTGC	1140
D _b	1140	CTAAGAACAGGGTTGAAGTATGTTCTCTCTTTAAGTTATGGTGCAAGCCCCACACTGC	1199
Q _y	1141	TCAAATGTCACAATAAAAGTGCTATAGACTTGGCTCCCAACACACAGTAAAAGAAAAGAT	1200
D _b	1200	TCAAATGTCACAATAAAAGTGCTATAGACTTGGCTCCCAACACACAGTAAAAGAAAAGAT	1259
Q _y	1201	TAGCATATGAATTTAAAGGCCACTCGTTGTGCGAAGCTGCAAGAGAGCTGATGTTACTC	1260
D _b	1260	TAGCATATGAATTTAAAGGCCACTCGTTGTGCGAAGCTGCAAGAGAGCTGATGTTACTC	1319

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Db	1380	CAGCATTGCATTGTGCTGCTGCATCTCCATATCCCAAAAGAAAGCAAAATATGTGAACTGT	1439
Qy	1381	TGCTAAGAAAAGGAGCAAAACATCAATGAAAGACTAAAGAAATTTCTTGACTCTCTGCACG	1440
Db	1440	TGCTAAGAAAAGGAGCAAAACATCAATGAAAGACTAAAGAAATTTCTTGACTCTCTGCACG	1499
Qy	1441	TGGCATCTGAAAAGCTCATAAATGATGTTGTTGGAAGTAGTGTGGAACAATGAAGCAAAAG	1500
Db	1500	TGGCATCTGAAAAGCTCATAAATGATGTTGTTGGAAGTAGTGTGGAACAATGAAGCAAAAG	1559
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Db	1560	TTAATGCTCTGGATTAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTGTGGTCATC	1619
Qy	1561	TACAAACCTGCCCCCTACTCCTCAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGG	1620
Db	1620	TACAAACCTGCCCCCTACTCCTCAGCTATGGGTGTGATCCTAACATTATATCCCTTCAGG	1679
Qy	1621	GCTTTACTGCTTTACAGATGGGAAATGAAAAATGTACAGCAACTCTCTCAAGAGGGTATCT	1680
Db	1680	GCTTTACTGCTTTACAGATGGGAAATGAAAAATGTACAGCAACTCTCTCAAGAGGGTATCT	1739
Qy	1681	CATTAGGTAAATCAGAGGCGACAGACAATGCTGTGAAAGCTGCAAGGCTGGAGATGTGCG	1740
Db	1740	CATTAGGTAAATCAGAGGCGACAGACAATGCTGTGAAAGCTGCAAGGCTGGAGATGTGCG	1799
Qy	1741	AAACTGTAAAAAATCTGTACTGTTTCAGAGTCTCAACTGCACAGACATTGAAAGGCGCTC	1800
Db	1800	AAACTGTAAAAAATCTGTACTGTTTCAGAGTCTCAACTGCACAGACATTGAAAGGCGCTC	1859
Qy	1801	AGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGC	1860
Db	1860	AGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGC	1919
Qy	1861	TACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGAGGCGCTTGTAACCTTTCGCAAAATG	1920
Db	1920	TACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGAGGCGCTTGTAACCTTTCGCAAAATG	1979
Qy	1921	CATGTTCTTATGCACATTATGAAAGTTGCAGAACTTCTGTGTTAAACATGGAGCAGTAGTTA	1980
Db	1980	CATGTTCTTATGCACATTATGAAAGTTGCAGAACTTCTGTGTTAAACATGGAGCAGTAGTTA	2039
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Db	2040	ATGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAATATG	2099
Qy	2041	AAATTTGCAAAATCTTCTGCTCCAGCATGGTGACAGCCCTACCAAAAAAACAAGGGATGGA	2100
Db	2100	AAATTTGCAAAATCTTCTGCTCCAGCATGGTGACAGCCCTACCAAAAAAACAAGGGATGGA	2159
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Db	2220	ATCAGCTTTGCTAGATGCTGCCAAGAAGGTTGTTTATAGCCAGAGTGAAGAAGTTGTCTT	2279
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Db	2280	CTCCTGATTAATGAAATGCCCCGATACCCAGGCGACACATTCAACCTTTTACATTTAG	2339
Qy	2281	CAGCTGGTTATATAATTTAGAGGTTGCAGAGTATTGTTTACAAACGAGGAGCTGATGTGA	2340
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RESULT 4

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US-10-199-937-134
; Sequence 134, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
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; PRIOR APPLICATION NUMBER: US/09/606,035
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; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 4992
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (876)..(4373)
US-10-199-937-134
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Query Match 99.4%; Score 3791.4; DB 7; Length 4992;
Best Local Similarity 99.8%; Pred No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 CGCGCTGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
Db 653 CGCGCTGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 712

QY 61 TGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db 713 TGGGCGGCGG-CGATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 771

QY 121 CCCTGAGCGCGCTCTCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 180
Db 772 CCCTGAGCGCGCTCTCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 831

QY 181 TCCGGTGTCTGCGCGCTGTTTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 240
Db 832 TCCGGTGTCTGCGCGCTGTTTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 891
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QY 241 GCGCGGGGGAGCGGCTTGGCGAGCGCGGGCCGAGCGCGTGGAGCGCGCGCC 300
DB 892 GCGCGCGGGGGAGCGGCTTGGCGAGCGCGGGCCGAGCGCGTGGAGCGCGCGCC 951
QY 301 GAGAGCTGTTTCGAGCGGTCGCGCAACGGGGAGCTGGAAACGAGTCAAGAGGCTGGTGAGCG 360
DB 952 GAGAGCTGTTTCGAGCGGTCGCGCAACGGGGAGCTGGAAACGAGTCAAGAGGCTGGTGAGCG 1011
QY 361 CTGAGAAAGGTGAACAGCGCGGACAGCGCGGAGGAAATCAACCGCGCTGCATCTGCGCG 420
DB 1012 CTGAGAAAGGTGAACAGCGCGGACAGCGCGGAGGAAATCAACCGCGCTGCATCTGCGCG 1071
QY 421 CAGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGATGGTGCATATGCCAAG 480
DB 1072 CAGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGATGGTGCATATGCCAAG 1131
QY 481 CACGTGATGATGGGGGCTTATCTCTTCATATGCAATGCTCTTTTGGTCAATGCTGAAG 540
DB 1132 CACGTGATGATGGGGGCTTATCTCTTCATATGCAATGCTCTTTTGGTCAATGCTGAAG 1191
QY 541 TAGTCAATCTCCTTTTGGGACATGGTGAGACCCCAATGCTCGAGATTAATGGAAATTATA 600
DB 1192 TAGTCAATCTCCTTTTGGGACATGGTGAGACCCCAATGCTCGAGATTAATGGAAATTATA 1251
QY 601 CTCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATGTTTGCATCTGCTGTTTACAGC 660
DB 1252 CTCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATGTTTGCATCTGCTGTTTACAGC 1311
QY 661 ATGGAGCTGAGCCCAACCATCGAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATC 720
DB 1312 ATGGAGCTGAGCCCAACCATCGAATACAGATGGAAGGACAGCATTTGGATTTAGCAGATC 1371
QY 721 CATCTGCCAAAGCAGTGTCTTACTGTGTAATAAGAAAGATGAATCTTTAGAAAGTGCCA 780
DB 1372 CATCTGCCAAAGCAGTGTCTTACTGTGTAATAAGAAAGATGAATCTTTAGAAAGTGCCA 1431
QY 781 GGAGTGGCAATGAAGAAATGATGGCTTACTCAGACCATTAATGTTCACTGCCAG 840
DB 1432 GGAGTGGCAATGAAGAAATGATGGCTTACTCAGACCATTAATGTTCACTGCCAG 1491
QY 841 CAAGTGATGGCAGAAAGTCAATCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGA 900
DB 1492 CAAGTGATGGCAGAAAGTCAATCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGA 1551
QY 901 TTGTACAGCTGTTACTGCAACATGGAGCTGATGCCATGCTTAAAGATAAAGGTGATCTGG 960
DB 1552 TTGTACAGCTGTTACTGCAACATGGAGCTGATGCCATGCTTAAAGATAAAGGTGATCTGG 1611
QY 961 TACCAATTACAAATGCCTGTTCTTATGGTCAATTAAGAGTAACTGAACTTTTGGTCAAGC 1020
DB 1612 TACCAATTACAAATGCCTGTTCTTATGGTCAATTAAGAGTAACTGAACTTTTGGTCAAGC 1671
QY 1021 ATGGTGCTGTGTAATGCAATGGACTTGTGGCAATTCACCTCTTCAATGAGGAGCTT 1080
DB 1672 ATGGTGCTGTGTAATGCAATGGACTTGTGGCAATTCACCTCTTCAATGAGGAGCTT 1731
QY 1081 CTAAGAAACAGGGTTGAAGTATGTTCTCTTCTTAAGTTATGGTGACAGACCCAAACACTGC 1140
DB 1732 CTAAGAAACAGGGTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGACAGACCCAAACACTGC 1791
QY 1141 TCAATTTGACAAATGAAGTGTATAGACTTGGCTCCCAACCAACAGTAAAGAAAGAT 1200
DB 1792 TCAATTTGACAAATGAAGTGTATAGACTTGGCTCCCAACCAACAGTAAAGAAAGAT 1851
QY 1201 TAGCATATGAATTTAAAGGCCACTGTTGCTGCAAGCTGACGAGAGCTGATGTTACTC 1260
DB 1852 TAGCATATGAATTTAAAGGCCACTGTTGCTGCAAGCTGACGAGAGCTGATGTTACTC 1911
QY 1261 GAATCAAAAAACATCTCTCTCTGGAAATGGTGAATTTCAAGCATCTCTCAAAACATGAAA 1320
DB 1912 GAATCAAAAAACATCTCTCTCTGGAAATGGTGAATTTCAAGCATCTCTCAAAACATGAAA 1971
QY 1321 CAGCATTCGATTCGTCTGTCATCTCCATATCCCAAGAAAGCAATATGTGAATGT 1380

DB 1972 CAGCATTCGATTCGTCTGTCATCTCCATATCCCAAGAAAGCAATATGTGAATGT 2031
QY 1381 TGCTAAGAAAAAGGAGCAAAACATCAATGAAAAAGACTAAAGAAATTTCTTGACTCCTCTGACAG 1440
DB 2032 TGCTAAGAAAAAGGAGCAAAACATCAATGAAAAAGACTAAAGAAATTTCTTGACTCCTCTGACAG 2091
QY 1441 TGGCATCTGAGAAAGCTCATATGATGTTGTAAGTAGTGGTGAACATGAAGAAAG 1500
DB 2092 TGGCATCTGAGAAAGCTCATATGATGTTGTAAGTAGTGGTGAACATGAAGAAAG 2151
QY 1501 TTAATGCTCTGATTAATCTTTGGTTCAGACTTCTCTACACAGAGCTGCATATTTGGTGCATC 1560
DB 2152 TTAATGCTCTGATTAATCTTTGGTTCAGACTTCTCTACACAGAGCTGCATATTTGGTGCATC 2211
QY 1561 TACAAACCTGCGCGCTATCCTGAGCTATGGGTGATCCTTAACATTAATCCTTCAGG 1620
DB 2212 TACAAACCTGCGCGCTATCCTGAGCTATGGGTGATCCTTAACATTAATCCTTCAGG 2271
QY 1621 GCTTTACTGCTTTACAGATGGGAAATGAAATGTAACAGAACTCTCCCAAGAGGATCT 1680
DB 2272 GCTTTACTGCTTTACAGATGGGAAATGAAATGTAACAGAACTCTCCCAAGAGGATCT 2331
QY 1681 CATTAGGTAATTCAGAGGACAGACAAATTCGTGGAAGCTGCAAAAGGCTGGAGATGTCG 1740
DB 2332 CATTAGGTAATTCAGAGGACAGACAAATTCGTGGAAGCTGCAAAAGGCTGGAGATGTCG 2391
QY 1741 AAACGTAAAAAACTGTGTAATCTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGGCTC 1800
DB 2392 AAACGTAAAAAACTGTGTAATCTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGGCTC 2451
QY 1801 AGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGC 1860
DB 2452 AGTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGC 2511
QY 1861 TACAGCATGGAGCTGATGTCATGCTTAAAGATAAAGGAGGCTTGTACCTTTGCACAATG 1920
DB 2512 TACAGCATGGAGCTGATGTCATGCTTAAAGATAAAGGAGGCTTGTACCTTTGCACAATG 2571
QY 1921 CATGTTCTTATGGACATTAATGAAGTTGCAGAACTTCTTGTAAACATGGAGCAGTAGTTA 1980
DB 2572 CATGTTCTTATGGACATTAATGAAGTTGCAGAACTTCTTGTAAACATGGAGCAGTAGTTA 2631
QY 1981 ATGTAGCTGATTTATGGAATTTTACACCTTTATCATGACGACGACAAAGGAAATATG 2040
DB 2632 ATGTAGCTGATTTATGGAATTTTACACCTTTATCATGACGACGACAAAGGAAATATG 2691
QY 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACCAAAAAAACAGGGATGGAA 2100
DB 2692 AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCCTACCAAAAAAACAGGGATGGAA 2751
QY 2101 ATACTCCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGAG 2160
DB 2752 ATACTCCTTTGGATCTTTGTTAAAGATGGAGATACAGATATTCAGATCTGCTTAGGGAG 2811
QY 2161 ATGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTT 2220
DB 2812 ATGCAGCTTTGCTAGATGCTGCCAAGAGGTTGTTTAGCCAGAGTGAAGAGTTGCTT 2871
QY 2221 CTCCTGATTAATGTAATTCGCGGATACCAAGGACAGACATTCAAACACCTTTACATTTAG 2280
DB 2872 CTCCTGATTAATGTAATTCGCGGATACCAAGGACAGACATTCAAACACCTTTACATTTAG 2931
QY 2281 CAGCTGGTTTATTAATATTTAGAAAGTTGCGAGATTAATTTGTTTACAAACAGGAGCTGATGTA 2340
DB 2932 CAGCTGGTTTATTAATATTTAGAAAGTTGCGAGATTAATTTGTTTACAAACAGGAGCTGATGTA 2991
QY 2341 ATGCCCAAGACAAAGGAGCTTATTCCTTTTACATGACAGCATCTTACGGGATGTAG 2400
DB 2992 ATGCCCAAGACAAAGGAGCTTATTCCTTTTACATGACAGCATCTTACGGGATGTAG 3051
QY 2401 ATGTAGCAGCTTACTTAATAAAGTAAATGTCATGTCTCAATGCCACGACAAATGGGCTT 2460

QY 301 GAGAGCTGTTGAGGGCTGCCGCAACGGGGACGTGGAAACAGTCAAGAGGCTGGTGAAGC 360
DB 962 GAGAGCTGTTGAGGGCTGCCGCAACGGGGACGTGGAAACAGTCAAGAGGCTGGTGAAGC 1021
QY 361 CTGAGAGGTTGAACAGCCGACACGCGCGGAGGAAATCCACCCGCTGCACTTCGCGG 420
DB 1022 CTGAGAGGTTGAACAGCCGACACGCGCGGAGGAAATCCACCCGCTGCACTTCGCGG 1081
QY 421 CAGGTTTTGGCGGAAAGAGCTAGTTGAAATATTTGCTTCAGAAATGGTGCAAAATGTTCAAG 480
DB 1082 CAGGTTTTGGCGGAAAGAGCTAGTTGAAATATTTGCTTCAGAAATGGTGCAAAATGTTCAAG 1141
QY 481 CAGTGATGATGGGGGCTTATTCCTCTTCATTAATGATGCTCTTTTGGTTCATGCTGAAG 540
DB 1142 CAGTGATGATGGGGGCTTATTCCTCTTCATTAATGATGCTCTTTTGGTTCATGCTGAAG 1201
QY 541 TAGTCAATCTCCTTTTGGGACATGGTGACAGCCCAATGCTCGAGATAATTTGGAATATTA 1261
DB 1202 TAGTCAATCTCCTTTTGGGACATGGTGACAGCCCAATGCTCGAGATAATTTGGAATATTA 1321
QY 601 CTCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATGTTTGCATTTGCTGTACAGC 660
DB 1262 CTCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATGTTTGCATTTGCTGTACAGC 1321
QY 661 ATGAGCTGAGCCCAACCATCCGAATAACAGATGGAAGGACAGCAATGGATTTAGCAGATC 720
DB 1322 ATGAGCTGAGCCCAACCATCCGAATAACAGATGGAAGGACAGCAATGGATTTAGCAGATC 1381
QY 721 CATCTGCCAAGCAGTCTTACTGGTGAATATTAAGAAAGATGAATCTTTAGAAAGTGCCA 780
DB 1382 CATCTGCCAAGCAGTCTTACTGGTGAATATTAAGAAAGATGAATCTTTAGAAAGTGCCA 1441
QY 781 GGAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACCAATTAATGTTCAACTGCCACG 840
DB 1442 GGAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACCAATTAATGTTCAACTGCCACG 1501
QY 841 CAAGTGATGGCAGAAAGTCAATCCATTAATTTGGCAGCAGAGATATAACAGAGTAAAGA 900
DB 1502 CAAGTGATGGCAGAAAGTCAATCCATTAATTTGGCAGCAGAGATATAACAGAGTAAAGA 1561
QY 901 TTGTACAGCTGTTACTCCACATGGAGCTGATGCCATGCTTAAGATAAAGGTGATCTGG 960
DB 1562 TTGTACAGCTGTTACTCCACATGGAGCTGATGCCATGCTTAAGATAAAGGTGATCTGG 1621
QY 961 TACCATTACCAATGCTGTTCTTATGGTCATTAATGAAGTAACTGAACTTTTGGTCAAGC 1020
DB 1622 TACCATTACCAATGCTGTTCTTATGGTCATTAATGAAGTAACTGAACTTTTGGTCAAGC 1681
QY 1021 ATGGTGCTGTGTTAAATGCAATGGACCTTGGGCAATTCACCTCTTCATGAGGAGCTTT 1080
DB 1682 ATGGTGCTGTGTTAAATGCAATGGACCTTGGGCAATTCACCTCTTCATGAGGAGCTTT 1741
QY 1081 CTAAAGACAGGTTGAAGTATGTTCTCTCTTAAGTTATGTGTCAGAGCCCAACCTGC 1140
DB 1742 CTAAAGACAGGTTGAAGTATGTTCTCTCTTAAGTTATGTGTCAGAGCCCAACCTGC 1801
QY 1141 TCAATTGTCAATATAAAGTGCTATAGACTTTGGCTCCCAACCAACAGTAAAGAAAGAT 1200
DB 1802 TCAATTGTCAATATAAAGTGCTATAGACTTTGGCTCCCAACCAACAGTAAAGAAAGAT 1861
QY 1201 TAGCATATGAATTTAAAGGCCACTCTGTTGTGCAAGCTGCAAGAGAGCTGATTTACTC 1260
DB 1862 TAGCATATGAATTTAAAGGCCACTCTGTTGTGCAAGCTGCAAGAGAGCTGATTTACTC 1921
QY 1261 GNATCAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTTCAACACATGAAA 1320
DB 1921 GNATCAAAAACATCTCTCTGGAATGGTGAATTTCAAGCATCTTCAACACATGAAA 1981
QY 1321 CAGCATTTGCAATTTGCTGCTGCTCATCTCCATATCCCAAAAAGAAAGCAATATGTGAAGT 1380
DB 1982 CAGCATTTGCAATTTGCTGCTGCTCATCTCCATATCCCAAAAAGAAAGCAATATGTGAAGT 2041

QY 1381 TGCTAAGAAAAGGAGCAAAACATCAATGAAGAAAGACTAAAGAAATCTTTGACTCTCTCGACG 1440
DB 2042 TGCTAAGAAAAGGAGCAAAACATCAATGAAGAAAGACTAAAGAAATCTTTGACTCTCTCGACG 2101
QY 1441 TGGCATCTCTGAGAAAGCTCATAATGATGTTGTTGAAAGTAGTGGTGAACATGAAGCAAAAG 1500
DB 2102 TGGCATCTCTGAGAAAGCTCATAATGATGTTGTTGAAAGTAGTGGTGAACATGAAGCAAAAG 2161
QY 1501 TTAAATGCTCTGAGTAATCTTTGGTGCAGACTTCTACACAGAGCTGCATATTGGTGCATC 1560
DB 2162 TTAAATGCTCTGAGTAATCTTTGGTGCAGACTTCTACACAGAGCTGCATATTGGTGCATC 2221
QY 1561 TACAAACCTGCCGCCCTACTCCTGAGCTATGGGTGTCATCTCAACATTTATATCCCTTCAGG 1620
DB 2222 TACAAACCTGCCGCCCTACTCCTGAGCTATGGGTGTCATCTCAACATTTATATCCCTTCAGG 2281
QY 1621 GCTTTACTGCTTTTACAGATGGGAAATGAAGATGTACAGCAACTCCTCCAAGAGGGTATCT 1680
DB 2282 GCTTTACTGCTTTTACAGATGGGAAATGAAGATGTACAGCAACTCCTCCAAGAGGGTATCT 2341
QY 1681 CATTAGGTAAATTCAGAGGACAGACAGCAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCG 1740
DB 2342 CATTAGGTAAATTCAGAGGACAGACAGCAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCG 2401
QY 1741 AAACCTGTAAGAAAACCTGTTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGGCTC 1800
DB 2402 AAACCTGTAAGAAAACCTGTTACTGTTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGGCTC 2461
QY 1801 AGTCTACACCACTTCATTTTGGCAGCTGGGTATTAACAGAGTGTCCGTGGTGGAAATATCTGC 1860
DB 2462 AGTCTACACCACTTCATTTTGGCAGCTGGGTATTAACAGAGTGTCCGTGGTGGAAATATCTGC 2521
QY 1861 TACAGCATGGAGCTGATGTCATGCTTAAGATTAAGAGGSCCTTGACCTTTGCAACAATG 1920
DB 2522 TACAGCATGGAGCTGATGTCATGCTTAAGATTAAGAGGSCCTTGACCTTTGCAACAATG 2581
QY 1921 CATGTTCTTATGACATTAATGAAGTTGCAGAACTCTCTGTTAAACATGGAGCAGTAGTTA 1980
DB 2582 CATGTTCTTATGACATTAATGAAGTTGCAGAACTCTCTGTTAAACATGGAGCAGTAGTTA 2641
QY 1981 ATGTAGCTGATTTATGGAAATTTACACCTTTTACATGAAGCAGCAGCAAAAAGGAAATATG 2040
DB 2642 ATGTAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAAGGAAATATG 2701
QY 2041 AAATTTGCAAACTTCTGCTCCACATGGTGCAGACCCCTACCAAAAAGGAGGATGGA 2100
DB 2702 AAATTTGCAAACTTCTGCTCCACATGGTGCAGACCCCTACCAAAAAGGAGGATGGA 2761
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QY 2161 ATGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAGTGTCTT 2220
DB 2822 ATGCAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAGTGTCTT 2881
QY 2221 CTCTGATTAATGTAATTTGCGCGATACCCAGGACAGATTCACACCTTTTACATTTAG 2280
DB 2882 CTCTGATTAATGTAATTTGCGCGATACCCAGGACAGATTCACACCTTTTACATTTAG 2941
QY 2281 CAGCTGGTATTAATTAATTTAGAAAGTTGACAGATTTTGTACACACGAGCTCATGTGA 2340
DB 2942 CAGCTGGTATTAATTAATTTAGAAAGTTGACAGATTTTGTACACACGAGGAGCTCATGTGA 3001
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DB 3002 ATGCCCAAGACAAAGGAGGACTTATTCCTTTTACATAATGACAGCATTTTACGGGCATGTAG 3061
QY 2401 ATGTAGCAGCTCTACTAATTAAGATTAATGATGTGTCATGTCACACGAGCAAAATGGGCTT 2460
DB 3062 ATGTAGCAGCTCTACTAATTAAGATTAATGATGTGTCATGTCACACGAGCAAAATGGGCTT 3121
QY 2461 TCACACCTTTTGCAAGAGCAGGCCCAAGGAGCAACACAGCTTTTGTGCTTTGTTGCTAG 2520

Db 3122 TCACACCTTTGACGAGCAGCCCAAAAGGAGCGAACACAGCTTTGTGCTTTGCTAG 3181
QY
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Db 3242 CAGCAGATGATGTACGGCTCTTCTGACAGAGCCCATGCCCATCTGCTCTGCCCTCTT 3301
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Db 3302 GTTACAGGCTCAAGTGTCAATGGTGTGAGAAGCCAGAGCCACTGCAGATGCTCTT 3361
QY 2701 CTTTCAGGCTCATCTAGCCCATCAAGCTTTCTGACGACGAGCTCTTGACAACTTATCTG 2760
Db 3362 CTTTCAGGCTCATCTAGCCCATCAAGCTTTCTGACGACGAGCTCTTGACAACTTATCTG 3421
QY 2761 GGAGTTTTTTCAGAACTGTCTTCAGTAGTTAGTTCAAGTGGAAACAGAGGTGCTTCCAGTT 2820
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QY 2821 TGGAGAAAAGAGGTTCCAGAGTAGATTTTACGATAACTCAATTCGTAAGGAATCTTG 2880
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QY 2881 GACTTTGACACCTTAATGGATATATTTGAGAGAACAGATCACTTTGGATGTATTAGTTG 2940
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QY 3001 TAAATTAAGGAGTCGAGAGACTTATCTCCGGACAAACAGGTCCTTAACCCATATTTAACTT 3060
Db 3662 TAAATTAAGGAGTCGAGAGACTTATCTCCGGACAAACAGGTCCTTAACCCATATTTAACTT 3721
QY 3061 TGAACACCTCTGGTAGTGGCAAACTTATATAGATCTGCTCTGATGATGAAGATTTC 3120
Db 3722 TGAACACCTCTGGTAGTGGCAAACTTATATAGATCTGCTCTGATGATGAAGATTTC 3781
QY 3121 AGTCTGTGGAGGAGAGATGCAAAAGTACAGATTTCGAGAGCACAGAGATGGAGTCAATGAG 3180
Db 3782 AGTCTGTGGAGGAGAGATGCAAAAGTACAGATTTCGAGAGCACAGAGATGGAGTCAATGAG 3841
QY 3181 GTTGAATCTTCAACAGATACAAATATTTCAAGATTTCAGAGGTTTGTAAACAGAAACTAT 3240
Db 3842 GTTGAATCTTCAACAGATACAAATATTTCAAGATTTCAGAGGTTTGTAAACAGAAACTAT 3901
QY 3241 GGGAAAGATACACTCACCGGAGAAAGATTTCGAGAAACACCAACCATGCCAATG 3300
Db 3902 GGGAAAGATACACTCACCGGAGAAAGATTTCGAGAAACACCAACCATGCCAATG 3961
QY 3301 AACGAATGCTATTTTCATGGTCTCTTTGTCGAATGCAATATCACAAAGCTTTGATG 3360
Db 3962 AACGAATGCTATTTTCATGGTCTCTTTGTCGAATGCAATATCACAAAGCTTTGATG 4021
QY 3361 AAAGGATCGCTACATAGGTGTATTTTGGAGCTGGCAATTTATTTGCTGAAAACTCTT 3420
Db 4022 AAAGGATCGCTACATAGGTGTATTTGAGCTGGCAATTTATTTGCTGAAAACTCTT 4081
QY 3421 CCAAAAGCAATCAATATGATGAAATTTGAGAGGATCTGGGTGTCCAGTTTCAAAAG 3480
Db 4082 CCAAAAGCAATCAATATGATGAAATTTGAGAGGATCTGGGTGTCCAGTTTCAAAAG 4141
QY 3481 ACAGATCTTGTATATTTGCCACAGGAGCTCTTTTGGCGGTAACTTGGAAAGT 3540
Db 4142 ACAGATCTTGTATATTTGCCACAGGAGCTCTTTTGGCGGTAACTTGGAAAGT 4201
QY 3541 CTTTCTCGAGTTCAAGTCAATGAAATGGCAATTTCTCTCCAGTTCATCACTCAGTCA 3600

Db 4202 CTTTCTCGAGTTCAAGTCAATGAAATGGCAATTTCTCTCCAGTTCATCACTCAGTCA 4261
QY 3601 CTGGTAGGCCAGTCTAAATGGCCCTAGCATTTAGCTGAATATGTTATTTACAGAGGAGAAC 3660
Db 4262 CTGGTAGGCCAGTCTAAATGGCCCTAGCATTTAGCTGAATATGTTATTTACAGAGGAGAAC 4321
QY 3661 AGGCTTATCTCTGAGTATTTAAATTTACTTACAGATTATGAGGCTGAAGGTATGGTCTGATG 3720
Db 4322 AGGCTTATCTCTGAGTATTTAAATTTACTTACAGATTATGAGGCTGAAGGTATGGTCTGATG 4381
QY 3721 GATAAATAGTTATTTTAAAGAACTAAATTTCCACTGAACCTAAATATCATCAAGCAGCAGTG 3780
Db 4382 GATAAATAGTTATTTTAAAGAACTAAATTTCCACTGAACCTAAATATCATCAAGCAGCAGTG 4441
QY 3781 GCCTCTAGCTTTTACTCTCTTTGCTGAAAAAAA 3813
Db 4442 GCCTCTAGCTTTTACTCTCTTTGCTGAAAAAAA 4474

RESULT 6
US-10-898-653-5
; Sequence 5, Application US/10898653
; Publication No. US20050143370A1
; GENERAL INFORMATION:
; APPLICANT: Helleday et al
; TITLE OF INVENTION: Therapeutic Compounds
; FILE REFERENCE: J660-046
; CURRENT APPLICATION NUMBER: US/10/898,653
; CURRENT FILING DATE: 2004-07-23
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 5
; LENGTH: 6189
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-898-653-5

Query Match 99.4%; Score 3791.4; DB 10; Length 6189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3806; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 CGCGCTGCTCCG 60
Db 157 CGCGCTGCTCCG 216
QY 61 TGGCG 120
Db 217 TGGCGCGCGG-CCATGGGACTCGCGCGGATCCGGTGACAGAGGAGCCAAAGCGCGCGCG 275
QY 121 CCCTGAGCGCGCTTCTCCG 180
Db 276 CCCTGAGCGCGCTTCTCCG 335
QY 181 TCCGCTGCTCGCGCGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 336 TCCGCTGCTCGCGCGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 395
QY 241 CG 300
Db 396 CG 455
QY 301 GAGAGCTGTTTCGAGCGCTGCCGCAACGGGAGCTGGAAACGAGTCAAGAGGCTGGTGACGC 360
Db 456 GAGAGCTGTTTCGAGCGCTGCCGCAACGGGAGCTGGAAACGAGTCAAGAGGCTGGTGACGC 515
QY 361 CTGAGAAGTGAACAGCG 420
Db 516 CTGAGAAGTGAACAGCG 575
QY 421 CAGGTTTTGGCGGAAAGACGCTAGTTGAATATTTGCTTTCAGAAATGTTGCTTTCAGG 480
Db 576 CAGGTTTTGGCGGAAAGACGCTAGTTGAATATTTGCTTTCAGAAATGTTGCTTTCAGG 635
QY 481 CACGTGATGATGGGGCGCTTATCTCTTCATATGATGCTCTTTTGGTTCATGCTGAAG 540

Db ||||| 636 CACGTGATGATGGGGCCCTTAATCTCTTCAATATGCAATGCTCTTTTGGTCATGCTGAAG 695
Qy ||||| 541 TAGTCAATCTCTTTTGGACATGCTGAGACCCCAATGCTCGAGATAATTTGGAATTATA 600
Db ||||| 696 TAGTCAATCTCTCTTTTGGACATGCTGAGACCCCAATGCTCGAGATAATTTGGAATTATA 755
Qy ||||| 601 CTCCTCTCCATGAAGCTGCAATTAAGGAAGATTTGATGTTTGCATTTGCTGTTTACAGC 660
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Qy ||||| 661 ATGGAGCTGAGCCCAACCATCCGAATACAGATGGAAGCAGCATTTGGATTTAGCAGATC 720
Db ||||| 816 ATGGAGCTGAGCCCAACCATCCGAATACAGATGGAAGCAGCATTTGGATTTAGCAGATC 875
Qy ||||| 721 CATCTGCCAAAGCAGTCTTACTTGTGTGAATTAAGAAAGATGAATCTTTAGAAAGTGCCA 780
Db ||||| 876 CATCTGCCAAAGCAGTCTTACTTGTGTGAATTAAGAAAGATGAATCTTTAGAAAGTGCCA 935
Qy ||||| 781 GGAGTGGCAATGAAGAAATAATGATGGCTCTACTCACACCATTAATGTCAACTGCCAG 840
Db ||||| 936 GGAGTGGCAATGAAGAAATAATGATGGCTCTACTCACACCATTAATGTCAACTGCCAG 995
Qy ||||| 841 CAAGTGATGGCAGAAAGTCAATCCATTACATTTTGGCAGCAGGATATAACAGAGTAAAGA 900
Db ||||| 996 CAAGTGATGGCAGAAAGTCAATCCATTACATTTTGGCAGCAGGATATAACAGAGTAAAGA 1055
Qy ||||| 901 TTGTACAGCTGTACTGCAACATGAGAGTGTATGTCATGCTTAAAGATAAAGTGATCTGG 960
Db ||||| 1056 TTGTACAGCTGTACTGCAACATGAGAGTGTATGTCATGCTTAAAGATAAAGTGATCTGG 1115
Qy ||||| 961 TACCATTAACAATGCTTCTTATGTGTCATTAATGAAGTAACTGAACTTTTGGTCAAGC 1020
Db ||||| 1116 TACCATTAACAATGCTTCTTATGTGTCATTAATGAAGTAACTGAACTTTTGGTCAAGC 1175
Qy ||||| 1021 ATGTCCTGTGTAATGCAATGAGCTTGTGCAATTCACCTCTTCTCATGAGGAGCTT 1080
Db ||||| 1176 ATGTCCTGTGTAATGCAATGAGCTTGTGCAATTCACCTCTTCTCATGAGGAGCTT 1235
Qy ||||| 1081 CTAAGAAACAGGTTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGAGACCCCAACACTGC 1140
Db ||||| 1236 CTAAGAAACAGGTTTGAAGTATGTTCTCTTCTTAAAGTTATGGTGAGACCCCAACACTGC 1295
Qy ||||| 1141 TCAATTTGCATAATTAAGTGTATAGACTTGGCTCCACACCAACAGTTAAAGAAAGAT 1200
Db ||||| 1296 TCAATTTGCATAATTAAGTGTATAGACTTGGCTCCACACCAACAGTTAAAGAAAGAT 1355
Qy ||||| 1201 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAGAAGCTGATGTTACTC 1260
Db ||||| 1356 TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCAGAGAAGCTGATGTTACTC 1415
Qy ||||| 1261 GAATCAAAAAACATCTCTCTCTGGAATTTGGTGAATTTCAAGCATCTTCAAAACACATGAAA 1320
Db ||||| 1416 GAATCAAAAAACATCTCTCTCTGGAATTTGGTGAATTTCAAGCATCTTCAAAACACATGAAA 1475
Qy ||||| 1321 CAGCATTTGCATTTGCTGCTGCAATCCATATCCCAAGAAAGCAATATATGTGAATCTGT 1380
Db ||||| 1476 CAGCATTTGCATTTGCTGCTGCAATCCATATCCCAAGAAAGCAATATATGTGAATCTGT 1535
Qy ||||| 1381 TGCTTAAGAAAGGAGCAACATCAATGAAGAGCTTAAAGAAATTTTGACTCTCTGCAAG 1440
Db ||||| 1536 TGCTTAAGAAAGGAGCAACATCAATGAAGAGCTTAAAGAAATTTTGACTCTCTGCAAG 1595
Qy ||||| 1441 TGGCATCTGAGAAAGCTCATATATGATTTGTTGAAAGTAGTGGTGAAGCAATGAAGCAAAAG 1500
Db ||||| 1596 TGGCATCTGAGAAAGCTCATATATGATTTGTTGAAAGTAGTGGTGAAGCAATGAAGCAAAAG 1655
Qy ||||| 1501 TTAATGCTCTGGAATATCTTGGTCAAGCTTCTTACACAGAGCTGCATATTTGTCATC 1560
Db ||||| 1656 TTAATGCTCTGGAATATCTTGGTCAAGCTTCTTACACAGAGCTGCATATTTGTCATC 1715
Qy ||||| 1561 TACAAACCTGCGCCTACTCTGAGCTATGGGTGATCCTAAACATTAATATCCCTTCAGG 1620

Db ||||| 1716 TACAAACCTGCGCCTACTCTGAGCTATGGGTGATCCTAAACATTAATATATATCCCTTCAGG 1775
Qy ||||| 1621 GCTTTACTGCTTTTACAGATGGGAAATGAAAAATGTTACAGCAACTCTCTCCAAAGAGGATATCT 1680
Db ||||| 1776 GCTTTACTGCTTTTACAGATGGGAAATGAAAAATGTTACAGCAACTCTCTCCAAAGAGGATATCT 1835
Qy ||||| 1681 CATTAGGTAAATTCAGAGGCAGACAGACAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGTGC 1740
Db ||||| 1836 CATTAGGTAAATTCAGAGGCAGACAGACAATTTGCTGGAAGCTGCAAAAGGCTGGAGATGTGC 1895
Qy ||||| 1741 AAACCTGTAATAAACTGTGTACTGTTTCAAGTGTCAACTGCAGAGACATTTGAAGGGCGTC 1800
Db ||||| 1896 AAACCTGTAATAAACTGTGTACTGTTTCAAGTGTCAACTGCAGAGACATTTGAAGGGCGTC 1955
Qy ||||| 1801 AGTCTACACCACTTCATTTTTCAGAGCTGGGTATTAACAGAGTGTCCGTGGTGAATATCTGC 1860
Db ||||| 1956 AGTCTACACCACTTCATTTTTCAGAGCTGGGTATTAACAGAGTGTCCGTGGTGAATATCTGC 2015
Qy ||||| 1861 TACAGCATGGAGCTGATGTGCATGTCTTAAAGATAAAGAGGCGCTTGTACCTTTGCACAATG 1920
Db ||||| 2016 TACAGCATGGAGCTGATGTGCATGTCTTAAAGATAAAGAGGCGCTTGTACCTTTGCACAATG 2075
Qy ||||| 1921 CATGTTCTTTATGGACATTAATGAAGTTGCAGAACTTCTTGTAAACATGGAGCAGTAGTTA 1980
Db ||||| 2076 CATGTTCTTTATGGACATTAATGAAGTTGCAGAACTTCTTGTAAACATGGAGCAGTAGTTA 2135
Qy ||||| 1981 ATGTAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATG 2040
Db ||||| 2136 ATGTAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATG 2195
Qy ||||| 2041 AAATTTGCAAACTTCTGCTCCAGCATGGTGAGACCTTACCACCAAAAAAACAGGATGGAA 2100
Db ||||| 2196 AAATTTGCAAACTTCTGCTCCAGCATGGTGAGACCTTACCACCAAAAAAACAGGATGGAA 2255
Qy ||||| 2101 ATACTCTTTTGGATCTTGTAAAGATGGAGATACAGATATTCAGATCTGCTTTAGGGGAG 2160
Db ||||| 2256 ATACTCTTTTGGATCTTGTAAAGATGGAGATACAGATATTCAGATCTGCTTTAGGGGAG 2315
Qy ||||| 2161 ATGCAGCTTTGTAGATGCTGCCAAGAGGGTTGTTTACGAGAGTGAAGAAGTTGTCTT 2220
Db ||||| 2316 ATGCAGCTTTGTAGATGCTGCCAAGAGGGTTGTTTACGAGAGTGAAGAAGTTGTCTT 2375
Qy ||||| 2221 CTCCTGATAATGTAATTCGCCGATACCAAGGAGACATTCAACACCTTTTACATTTAG 2280
Db ||||| 2376 CTCCTGATAATGTAATTCGCCGATACCAAGGAGACATTCAACACCTTTTACATTTAG 2435
Qy ||||| 2281 CAGCTGGTTTATTAATTAATTTAGAAAGTTGAGAGTATTTGTTTAAACACGGAGCTGATGA 2340
Db ||||| 2436 CAGCTGGTTTATTAATTAATTTAGAAAGTTGAGAGTATTTGTTTAAACACGGAGCTGATGA 2495
Qy ||||| 2341 ATGCCCAAGACAAAGGAGGACTTTTCCCTTTACATAATGAGAGCATCTTACGGGAGTGA 2400
Db ||||| 2496 ATGCCCAAGACAAAGGAGGACTTTTCCCTTTACATAATGAGAGCATCTTACGGGAGTGA 2555
Qy ||||| 2401 ATGTAGCAGCTCTACTTAATAAAGTATAATGCTCAATGCCAGCAGCAAAATGGGCTT 2460
Db ||||| 2556 ATGTAGCAGCTCTACTTAATAAAGTATAATGCTCAATGCCAGCAGCAAAATGGGCTT 2615
Qy ||||| 2461 TCACACCTTTTGACGAAGCAGACCCAAAAGGGAGCAACACAGCTTTTGTGCTAG 2520
Db ||||| 2616 TCACACCTTTTGACGAAGCAGACCCAAAAGGGAGCAACACAGCTTTTGTGCTAG 2675
Qy ||||| 2521 CCCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGACAAACACCTTTTAGTTAGTTT 2580
Db ||||| 2676 CCCATGGAGCTGACCCGACTCTTTAAATAATCAGGAAGGACAAACACCTTTTAGTTAGTTT 2735
Qy ||||| 2581 CAGCGGATGATGTACAGCGCTCTTCTGACAGCAGCCATGCCCATCTGCTCTGCCCTCTT 2640
Db ||||| 2736 CAGCGAGATGATGTACAGCGCTCTTCTGACAGCAGCCATGCCCATCTGCTCTGCCCTCTT 2795
Qy ||||| 2641 GTTACAAAGCTTCAAGTGTCTCAATGGTGTGAGAAAGCCAGGAGCCACTGACAGATGCTCTCT 2700
Db ||||| 2796 GTTACAAAGCTTCAAGTGTCTCAATGGTGTGAGAAAGCCAGGAGCCACTGACAGATGCTCTCT 2855

Qy	3781	GCCTCTACGTTTACTCCTTTGCTGAAAAAAA 3813
Db	3936	GCCTCTACGTTTACTCCTTTGCTGAAAAAAA 3968
RESULT 7		
US-09-849-602-11		
; Sequence 11, Application US/09849602		
; Publication No. US20030165834A1		
; GENERAL INFORMATION:		
; APPLICANT: Scanlan, Matthew J.		
; APPLICANT: Old, Lloyd J.		
; APPLICANT: Stockert, Elisabeth		
; APPLICANT: Chen, Yao-Tseung		
; TITLE OF INVENTION: Colon Cancer Antigen Panel		
; FILE REFERENCE: L0461/7105(JRV)		
; CURRENT APPLICATION NUMBER: US/09/849,602		
; CURRENT FILING DATE: 2001-05-04		
; NUMBER OF SEQ ID NOS: 30		
; SOFTWARE: PatentIn version 3.0		
; SEQ ID NO 11		
; LENGTH: 6018		
; TYPE: DNA		
; ORGANISM: Homo sapien		
US-09-849-602-11		
Query Match 99.3%; Score 3788.4; DB 3; Length 6018;		
Best Local Similarity 99.8%; Pred. No. 0;		
Matches 3803; Conservative 0; Mismatches 6; Indels 1; Gaps 1;		
Qy	4	GCTGCTCCGCCCGCGCGGGGACGCCGGGGGACGGAGCCACGAGGGGCGCGCTGG 63
Db	1	GCTGCTCCGCCCGCGGGGACGCCGGGGGACGGAGCCACGAGGGGCGCGCTGG 60
Qy	64	GCGGGCCATGGACTGCGCCGATCCGCTGACAGCAGGAGCCAGCGCCCGGGCCC 123
Db	61	GCGCGG-CCATGGGACTGCGCCCGGATCCGCTGACAGCAGGAGCCAGCGCCCGGGCCC 119
Qy	124	TGAGCGCGTCTTCTCGGGGGGCGCTGCCCTCTCTGCTCGCGGGGCCCGGGGCTCTGTGCTCC 183
Db	120	TGAGCGGGTCTTCTCGGGGGGCGCTGCCCTCTCTGCTCGCGGGGCCCGGGGCTCTGTGCTCC 179
Qy	184	GTTTGTGCGCGCTGTTGCTGGCTGTGGCGCGCCAGGATCATGTGCGGTGCGCGCTGGC 243
Db	180	GTTTGTGCGCGCTGTTGCTGGCTGTGGCGCGCCAGGATCATGTGCGGTGCGCGCTGGC 239
Qy	244	CCGCGGGGAGCGGCTTGGCCAGCGCCCGCGCCGAGGCGCTGGAGCCCGGCCCGCCGAG 303
Db	240	CCGCGGGGAGCGGCTTGGCCAGCGCCCGCGCCGAGGCGCTGGAGCCCGGCCCGCCGAG 299
Qy	304	AGCTGTTTCGAGGCGTGCCGCAACGGGACGTGGAAACGAGTCAAGAGGCTTGGTGAACGCTG 363
Db	300	AGCTGTTTCGAGGCGTGCCGCAACGGGACGTGGAAACGAGTCAAGAGGCTTGGTGAACGCTG 359
Qy	364	AGAAGGTGAACAGCCGCGACACCGCGGGCAGGAAATCCACCCGCTGCATTTGCGCCGAG 423
Db	360	AGAAGGTGAACAGCCGCGACACCGCGGGCAGGAAATCCACCCGCTGCATTTGCGCCGAG 419
Qy	424	GTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCGAATGGTGCAAATGTCCAAGCAC 483
Db	420	GTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCGAATGGTGCAAATGTCCAAGCAC 479
Qy	484	GTGATGATGGGGCCTTATTCTCTTCATATGCATGCTCTTTTGGTTCATGCTGAAGTAG 543
Db	480	GTGATGATGGGGCCTTATTCTCTTCATATGCATGCTCTTTTGGTTCATGCTGAAGTAG 539
Qy	544	TCAATCTCTTTTGCACATGTCGACAGCCCAATGCTCGAGATAATTGGAATTATCTC 603
Db	540	TCAATCTCTTTTGCACATGTCGACAGCCCAATGCTCGAGATAATTGGAATTATCTC 599
Qy	604	CTCTCCATGAAGCTGCAATTAAGAAAGATGATGTTTCATGTGCTGCTTACAGCATG 663
Db	600	CTCTCATGAAGCTGCAATTAAGAAAGATGATGTTTCATGTGCTGCTTACAGCATG 659

QY	664	GAGCTGAGCCCAACCATCCGAATATACAGATGAGGACAGCACTTGGATTAGCAGATCCAT	723
Db	660	GAGCTGAGCCCAACCATCCGAATATACAGATGAGGACAGCACTTGGATTAGCAGATCCAT	719
QY	724	CTGCCAAGCAGTGTCTACTGGTGAATATAAGAAAGATGAACCTTTAGAAAGTGCACAGA	783
Db	720	CTGCCAAGCAGTGTCTACTGGTGAATATAAGAAAGATGAACCTTTAGAAAGTGCACAGA	779
QY	784	GTGGCAATGAAGAAATAATGATGGCTCTACTCACACCAATTAATAATGCAACTGCCACGAA	843
Db	780	GTGGCAATGAAGAAATAATGATGGCTCTACTCACACCAATTAATAATGCAACTGCCACGAA	839
QY	844	GTGATGCGAGAAAGTCAACTCCATTAACATTTGGCAGCAGGATATAACAGATGAAGATTG	903
Db	840	GTGATGCGAGAAAGTCAACTCCATTAACATTTGGCAGCAGGATATAACAGATGAAGATTG	899
QY	904	TACAGCTGTACTCGCAACATGGAGCTGATGTCATCTAAAGATAAAGTGATCTGGTAC	963
Db	900	TACAGCTGTACTCGCAACATGGAGCTGATGTCATCTAAAGATAAAGTGATCTGGTAC	959
QY	964	CATTACACAATGCCCTGTCTTATGGTCAATTAAGAGTAACCTTTTGGTCAAGCATG	1023
Db	960	CATTACACAATGCCCTGTCTTATGGTCAATTAAGAGTAACCTTTTGGTCAAGCATG	1019
QY	1024	GTGCTGTGTAATGCAATGCACTGGAGCTGTGGCAATTCACCTCTTCATGAGGAGCTTCTA	1083
Db	1020	GTGCTGTGTAATGCAATGCACTGGAGCTGTGGCAATTCACCTCTTCATGAGGAGCTTCTA	1079
QY	1084	AGAACAGGGTTGAAGTAGTGTCTCTCTCTTAAGTTATGGTGCAGACCCAAACACTGCTCA	1143
Db	1080	AGAACAGGGTTGAAGTAGTGTCTCTCTCTTAAGTTATGGTGCAGACCCAAACACTGCTCA	1139
QY	1144	ATTGTCAATPAANAAGTGTCTATAGACTTGGTCCACACCAAGTAAAGAAAGATTAG	1203
Db	1140	ATTGTCAATPAANAAGTGTCTATAGACTTGGTCCACACCAAGTAAAGAAAGATTAG	1199
QY	1204	CATATGAATTTAAAGGCCACTCGTGTGCGAAGCTGCAAGTGCACGAGAGCTGATTTCTGAA	1263
Db	1200	CATATGAATTTAAAGGCCACTCGTGTGCGAAGCTGCAAGTGCACGAGAGCTGATTTCTGAA	1259
QY	1264	TCAAAAACATCTCTCTCGGAATGGTGAATTTCAAGCATCCTCAAAACACATGAACAG	1323
Db	1260	TCAAAAACATCTCTCTCGGAATGGTGAATTTCAAGCATCCTCAAAACACATGAACAG	1319
QY	1324	CATTGCAATTTGCTGCTGCTCATCTCCATATCCCAAGAAAGCAAAATATGTAACCTGTTGC	1383
Db	1320	CATTGCAATTTGCTGCTGCTCATCTCCATATCCCAAGAAAGCAAAATATGTAACCTGTTGC	1379
QY	1384	TAAGAAAGGAGCAACATCAATGAAGAGCTAAAGAAATTTCTGACTCTCTGCAAGTGG	1443
Db	1380	TAAGAAAGGAGCAACATCAATGAAGAGCTAAAGAAATTTCTGACTCTCTGCAAGTGG	1439
QY	1444	CATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGTTA	1503
Db	1440	CATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGTTA	1499
QY	1504	ATGCTCTGGATAAATCTTGGTGCAGACTTCTCTACACAGAGCTGCAATTTGGTCACTTAC	1563
Db	1500	ATGCTCTGGATAAATCTTGGTGCAGACTTCTCTACACAGAGCTGCAATTTGGTCACTTAC	1559
QY	1564	AAACCTGCGGCTACTCTGAGCTATGGGTGTGATCTTAAACATTTATATATCCCTTCAGGCT	1623
Db	1560	AAACCTGCGGCTACTCTGAGCTATGGGTGTGATCTTAAACATTTATATATCCCTTCAGGCT	1619
QY	1624	TTACTGCTTTACAGATGGGAATGAAGATGACAGCAACTCTCCAGAGGATCTCAT	1683
Db	1620	TTACTGCTTTACAGATGGGAATGAAGATGACAGCAACTCTCCAGAGGATCTCAT	1679
QY	1684	TAGTAATTCAGAGGACAGACAAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCGAAA	1743
Db	1680	TAGTAATTCAGAGGACAGACAAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCGAAA	1739

QY	1744	CTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCAGT	1803
Db	1740	CTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGTCAGT	1799
QY	1804	CTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGATATATCTGTAC	1863
Db	1800	CTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGGATATATCTGTAC	1859
QY	1864	AGCATGGAGCTGATGTGCATGTCTAAAGATAAAGGAGGCTTTGTACCTTTGCACAATGCAT	1923
Db	1860	AGCATGGAGCTGATGTGCATGTCTAAAGATAAAGGAGGCTTTGTACCTTTGCACAATGCAT	1919
QY	1924	GTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTCTTAAACATGAGCAGTAGTTAATG	1983
Db	1920	GTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTCTTAAACATGAGCAGTAGTTAATG	1979
QY	1984	TAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAAAATATGAAA	2043
Db	1980	TAGCTGATTTATGGAAATTTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAAAATATGAAA	2039
QY	2044	TTTGTCAAACTTCTGTCTCAGCATGTGTGAGACCTTACCAAAAAAAGGATGGAAATA	2103
Db	2040	TTTGTCAAACTTCTGTCTCAGCATGTGTGAGACCTTACCAAAAAAAGGATGGAAATA	2099
QY	2104	CTCCTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGAGATG	2163
Db	2100	CTCCTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGAGATG	2159
QY	2164	CAGCTTTGTAGATGTGCAAGAAAGGGTGTGTTTAGCCAGAGTGAAGAGTGTCTTCTTC	2223
Db	2160	CAGCTTTGTAGATGTGCAAGAAAGGGTGTGTTTAGCCAGAGTGAAGAGTGTCTTCTTC	2219
QY	2224	CTGATAATGTAATTTAGAAAGTGCAGAGTGTGTTTACCAAGCAGACATTTACATTTAGCAG	2283
Db	2220	CTGATAATGTAATTTAGAAAGTGCAGAGTGTGTTTACCAAGCAGACATTTACATTTAGCAG	2279
QY	2284	CTGGTTATAATTAATTTAGAAAGTGCAGAGTGTGTTTACCAAGCAGAGTGTGTAATG	2343
Db	2280	CTGGTTATAATTAATTTAGAAAGTGCAGAGTGTGTTTACCAAGCAGAGTGTGTAATG	2339
QY	2344	CCCAAGACAAAGGAGGACTTATTTCTTTTACATAATGACAGCATCTTACGGGCATGTAGATG	2403
Db	2340	CCCAAGACAAAGGAGGACTTATTTCTTTTACATAATGACAGCATCTTACGGGCATGTAGATG	2399
QY	2404	TAGCAGCTCTACTAATAAAGTATAATGATGTGTAATGCGCAGGACAAATGGGCTTTCA	2463
Db	2400	TAGCAGCTCTACTAATAAAGTATAATGATGTGTAATGCGCAGGACAAATGGGCTTTCA	2459
QY	2464	CACCTTTGCACGAGCAGCCCAAAAGGGGACGACAGCTTTGTGCTTTGTGCTAGCCCC	2523
Db	2460	CACCTTTGCACGAGCAGCCCAAAAGGGGACGACAGCTTTGTGCTTTGTGCTAGCCCC	2519
QY	2524	ATGGAGCTGACCCGACTCTTAAATAATCAGAAAGGACAAACACCTTTAGATTTAGTTTCAG	2583
Db	2520	ATGGAGCTGACCCGACTCTTAAATAATCAGAAAGGACAAACACCTTTAGATTTAGTTTCAG	2579
QY	2584	CGGATGATGTGAGCGCTCTTCTGACAGCAGCATGCCCCCATCTGCTGCCCCCTTTGTT	2643
Db	2580	CAGATGATGTGAGCGCTCTTCTGACAGCAGCATGCCCCCATCTGCTGCCCCCTTTGTT	2639
QY	2644	ACAGCCTCAAGTGTCTCAATGGTGTGAGAAAGCCAGAGGCCACTGCGAGATGCTCTCTTT	2703
Db	2640	ACAGCCTCAAGTGTCTCAATGGTGTGAGAAAGCCAGAGGCCACTGCGAGATGCTCTCTTT	2699
QY	2704	CAGGTCCCATCTAGCCCATCAAGCCTTTCTGACAGCAGCAGTCTTGACAACTTATCTGGGA	2763
Db	2700	CAGGTCCCATCTAGCCCATCAAGCCTTTCTGACAGCAGCAGTCTTGACAACTTATCTGGGA	2759
QY	2764	GTTTTTCAGAACTGTCTTCAGTAGTGTAGTTCAAGTGGAAACAGAGGCTGCTTCAGTTGG	2823
Db	2760	GTTTTTCAGAACTGTCTTCAGTAGTGTAGTTCAAGTGGAAACAGAGGCTGCTTCAGTTGG	2819
QY	2824	AGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATTAACCTCAATTCGTAAGGAATCTTGGAC	2883

Db 2820 AGAAAAAGGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTGAAGAACTCTGGAC 2879
QY 2884 TTGAGCACCTTAATGGATATATTTGAGAGAAACAGATCACTTTGGATGTATTAGTTGAGA 2943
Db 2880 TTGAGCACCTTAATGGATATATTTGAGAGAAACAGATCACTTTGGATGTATTAGTTGAGA 2939
QY 2944 TGGGGCAACAGGAGCTGAAGGAGATTGGAATCAATGCTTTATGGACATAGGCACAACTAA 3003
Db 2940 TGGGGCAACAGGAGCTGAAGGAGATTGGAATCAATGCTTTATGGACATAGGCACAACTAA 2999
QY 3004 TTAAGGAGTCGAGAGACTTAATCTCCGGAACAAGGCTTTAAACCATATTTAACTTTGA 3063
Db 3000 TTAAGGAGTCGAGAGACTTAATCTCCGGAACAAGGCTTTAAACCATATTTAACTTTGA 3059
QY 3064 ACACCTCTGGTAGTGAAACAATCTTATAGATCTGCTCTCATATGAAGATTTTCAGT 3123
Db 3060 ACACCTCTGGTAGTGAAACAATCTTATAGATCTGCTCTCATATGAAGATTTTCAGT 3119
QY 3124 CTGTGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGATGGAGTCAATGAGGTG 3183
Db 3120 CTGTGAGGAAGAGATGCAAAAGTACAGTTTCGAGAGCACAGATGGAGTCAATGAGGTG 3179
QY 3184 GAATCTTCAACAGATACAAATATTTCTCAAGATTCAGAAGGTTTGTAAACAGAAACTATGGG 3243
Db 3180 GAATCTTCAACAGATACAAATATTTCTCAAGATTCAGAAGGTTTGTAAACAGAAACTATGGG 3239
QY 3244 AAAGATACACTCACCGGAAAGAAAGATTTCTGAAGAAACACAAACCATGCAATGAAC 3303
Db 3240 AAAGATACACTCACCGGAAAGAAAGATTTCTGAAGAAACACAAACCATGCAATGAAC 3299
QY 3304 GAATGCTATTTCATGGTCTCTCTTTGTGAATGCAATTTATCACAAGAGCTTTTGATGAA 3363
Db 3300 GAATGCTATTTCATGGTCTCTCTTTGTGAATGCAATTTATCACAAGAGCTTTTGATGAA 3359
QY 3364 GGCATGCGTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTGCTGAAACTCTTTCCA 3423
Db 3360 GGCATGCGTACATAGGTGGTATGTTTGGAGCTGGCAATTTATTTGCTGAAACTCTTTCCA 3419
QY 3424 AAAGCAATCAATATGATATGAAATTTGAGGAGGTACTGGGTGTCAGTTTCAAAAGACA 3483
Db 3420 AAAGCAATCAATATGATATGAAATTTGAGGAGGTACTGGGTGTCAGTTTCAAAAGACA 3479
QY 3484 GATCTTGTATACATTTGCCACAGCAGCTGCTCTTTTGCAGGTAACCTTTGGGAAAGTCTT 3543
Db 3480 GATCTTGTATACATTTGCCACAGCAGCTGCTCTTTTGCAGGTAACCTTTGGGAAAGTCTT 3539
QY 3544 TCCTCAGTTTCAAGTCAATGAAATGGCAATTTCTCTCCAGGTCAATCACTCAGTCACTG 3603
Db 3540 TCCTCAGTTTCAAGTCAATGAAATGGCAATTTCTCTCCAGGTCAATCACTCAGTCACTG 3599
QY 3604 FTAGGCCAGTGTAAATGGCCTAGCATTTAGCTGAATATGTTATTTACAGAGAGAACAGG 3663
Db 3600 FTAGGCCAGTGTAAATGGCCTAGCATTTAGCTGAATATGTTATTTACAGAGAGAACAGG 3659
QY 3664 CTTATCCTGAGTATTTAATTAATCTACAGATTTAGGCTCAAGGTATGGTTCGATGGAT 3723
Db 3660 CTTATCCTGAGTATTTAATTAATCTACAGATTTAGGCTCAAGGTATGGTTCGATGGAT 3719
QY 3724 AAATAGTATTTTAAAGAACTAAATTCACATGAACCTTAAATCATCAAGGAGAGTGGCC 3783
Db 3720 AAATAGTATTTTAAAGAACTAAATTCACATGAACCTTAAATCATCAAGGAGAGTGGCC 3779
QY 3784 TCTAGCTTTTACTCTCTTGTGCTGAAAAAAA 3813
Db 3780 TCTAGCTTTTACTCTCTTGTGCTGAAAAAAA 3809

RESULT 8

US-10-302-172-556
; Sequence 556, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Dmanac, Radoje T.
TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids and
FILE REFERENCE: 803 1CNCp
CURRENT APPLICATION NUMBER: US/10/302,172
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/225,251
PRIOR FILING DATE: 2002-08-20 PCT US02/05095
PRIOR APPLICATION NUMBER: PCT US02/05095
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 09/799,451
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 950
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 556
LENGTH: 5075
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (253)..(3750)
US-10-302-172-556

Query Match

Best Local Similarity 98.8%; Score 3770.8; DB 8; Length 5075;
Matches 3800; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 1 CGCGCTGCTCCGCCCG 60
Db 29 CGCGCTGCTCCGCCCG 88
QY 61 TGGGCG 120
Db 89 TGGGCGCGCG - CCATGGGACCTGCGCGCGGATCCGGTGTACAGCAGGAGGCCAAGCGCGCGCG 147
QY 121 CCCTGAGCGCGCTTCTCCG 179
Db 148 CCCTGAGCGCGCTTCTCCG 207
QY 180 CTCGGTTGCTGGCGCTGTTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 239
Db 208 CTCGGTTGCTGGCGCTGTTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 267
QY 240 TGGCG 299
Db 268 TGGCG 327
QY 300 CGAGAGCTGTTTCGAGGCGTCCGCAACCGGGGACGTTGGAAACGAGTCAAGAGGCTGTTGAG 359
Db 328 CGAGAGCTGTTTCGAGGCGTCCGCAACCGGGGACGTTGGAAACGAGTCAAGAGGCTGTTGAG 387
QY 360 CCTGAGAGGTGAACAGCG 419
Db 388 CCTGAGAGGTGAACAGCG 447
QY 420 GCAGGTTTGGCGCGGAAAGACGTTGTAATTTTGTTCAGAAATGTTGTCAGAAATGTTCCAA 479
Db 448 GCAGGTTTGGCGCGGAAAGACGTTGTAATTTTGTTCAGAAATGTTGTCAGAAATGTTCCAA 507
QY 480 GCAGTGAATGATGGGCGCTTATTCCTCTTCATATGATGCTCTTTTGGTTCATGCTGAA 539
Db 508 GCAGTGAATGATGGGCGCTTATTCCTCTTCATATGATGCTCTTTTGGTTCATGCTGAA 567
QY 540 GTAGTCAATCTCTTTTTCGACATGGTGCACACCCCAATGCTCCGAGATAATTTGGAATTAT 599
Db 568 GTAGTCAATCTCTTTTTCGACATGGTGCACACCCCAATGCTCCGAGATAATTTGGAATTAT 627
QY 600 ACTCCTCTCCATGAAGCTGCAATTTAAAGAAAGATTTGATGTTGCAATTTGCTGTTACAG 659
Db 628 ACTCCTCTCCATGAAGCTGCAATTTAAAGAAAGATTTGATGTTGCAATTTGCTGTTACAG 687

QY 660 CATGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTTAGCAGAT 719
DB 688 CATGGAGCTGAGCCAAACCATCCGAAATACAGATGGAAGGACAGCATTTGGATTTTAGCAGAT 747
QY 720 CCATCTGCCAAAGCAGTCTTACTGTTGTAATATGAAGAGATGAACCTCTTAGAAGTGCC 779
DB 748 CCATCTGCCAAAGCAGTCTTACTTGGTGAATATGAAGAGATGAACCTCTTAGAAGTGCC 807
QY 780 AGGAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACATTTAAATGTCAATGCCAC 839
DB 808 AGGAGTGGCAATGAAGAAAAAATGATGGCTCTACTCACACATTTAAATGTCAATGCCAC 867
QY 840 GCAAGTGATGGCAGAAAGTCAATCCATTACATTTGGCAGCAGAGATATAACAGAGTAAAG 899
DB 868 GCAAGTGATGGCAGAAAGTCAATCCATTACATTTGGCAGCAGAGATATAACAGAGTAAAG 927
QY 900 ATTCTGACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTAAAGATAAAGGTGATCTG 959
DB 928 ATTCTGACAGCTGTTACTGCAACATGGAGCTGATGTCATGCTAAAGATAAAGGTGATCTG 987
QY 960 GTACCATTTACAAATGCCCTGTTCTTATGGTCATTATGAAGTAACTGAACTTTTGGTCAAG 1019
DB 988 GTACCATTTACAAATGCCCTGTTCTTATGGTCATTATGAAGTAACTGAACTTTTGGTCAAG 1047
QY 1020 CATGGTGCCTGTGAATGAATGGAATGGAATTTGAGTGAATTTCACTCCTCTTCATGAGGACCT 1079
DB 1048 CATGGTGCCTGTGAATGGAATGGAATTTGAGTGAATTTCACTCCTCTTCATGAGGACCT 1107
QY 1080 TCTAAGAACAGGTTGAAGTATGTTCTCTCTTAAAGTATGTTGACAGACCAACACTG 1139
DB 1108 TCTAAGAACAGGTTGAAGTATGTTCTCTCTTAAAGTATGTTGACAGACCAACACTG 1167
QY 1140 CTCAATTTGTCAATATAAGTGTATAGACTTTGGCTCCACACACACAGTTAAAGAAAGA 1199
DB 1168 CTCAATTTGTCAATATAAGTGTATAGACTTTGGCTCCACACACACAGTTAAAGAAAGA 1227
QY 1200 TTAGCATATGAATTTAAAGGCACTCGTGTGCTGCAAGCTGCAAGAGAGCTGATGTTACT 1259
DB 1228 TTAGCATATGAATTTAAAGGCACTCGTGTGCTGCAAGCTGCAAGAGAGCTGATGTTACT 1287
QY 1260 CGAATCAAAAACATCTCTCTGGAATGTTGAATTTCAAGCATCTTCAACACATGAA 1319
DB 1288 CGAATCAAAAACATCTCTCTGGAATGTTGAATTTCAAGCATCTTCAACACATGAA 1347
QY 1320 ACAGCATTTGCAATTTGTGCTGCTGCAATCTCCATATCCAAAAGAAAGCAATATGTGAAC 1379
DB 1348 ACAGCATTTGCAATTTGTGCTGCTGCAATCTCCATATCCAAAAGAAAGCAATATGTGAAC 1407
QY 1380 TTGCTAAGAAAAGGAGCAAAACATCAATGAAAAGACTAAAGAAATTTCTGACTCTCTGCAC 1439
DB 1408 TTGCTAAGAAAAGGAGCAAAACATCAATGAAAAGACTAAAGAAATTTCTGACTCTCTGCAC 1467
QY 1440 GTGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAAAGCAAG 1499
DB 1468 GTGGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAAAGCAAG 1527
QY 1500 GTTAATGCTCTGGAATAATCTTGGTCAGACTCTCTACACAGAGCTGCATATTTGGTGCAT 1559
DB 1528 GTTAATGCTCTGGAATAATCTTGGTCAGACTCTCTACACAGAGCTGCATATTTGGTGCAT 1587
QY 1560 CTACAAACCTCGCGCTACTCTCTGAGCTATGAGGTGATGCTTAAACATTTATATCCCTTACG 1619
DB 1588 CTACAAACCTCGCGCTACTCTCTGAGCTATGAGGTGATGCTTAAACATTTATATCCCTTACG 1647
QY 1620 GGCTTTACTGCTTTTACAGATGGGAATGAAATGTACAGCACTCTCTCAAGAGGATATC 1679
DB 1648 GGCTTTACTGCTTTTACAGATGGGAATGAAATGTACAGCACTCTCTCAAGAGGATATC 1707
QY 1680 TCATTTAGTAAATTCAGAGGACAGACAAATTTGCTGGAAGCTGCAAGGCTGGAGATGTC 1739
DB 1708 TCATTTAGTAAATTCAGAGGACAGACAAATTTGCTGGAAGCTGCAAGGCTGGAGATGTC 1767
QY 1740 GAACTGTAAAAAATACTGTGTACTGTTCCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGT 1799

DB 1768 GAACTGTAAAAAATACTGTGTACTGTTCCAGAGTGTCAACTGCAGAGACATTTGAAGGGCGT 1827
QY 1800 CAGTCTACACCACCTTCATTTTTCAGCTGGGTATAACAGAGTGTCCGTGTGGTAATCTG 1859
DB 1828 CAGTCTACACCACCTTCATTTTTCAGCTGGGTATAACAGAGTGTCCGTGTGGTAATCTG 1887
QY 1860 CTACAGCATGAGCTGATGTGCATGCTAAAGATAAGGAGGCTTTGTACCTTTGCACAAT 1919
DB 1888 CTACAGCATGAGCTGATGTGCATGCTAAAGATAAGGAGGCTTTGTACCTTTTGCACAAT 1947
QY 1920 GCATCTCTTTATGGACATTTATGAAGTTGCAGAACTCTTGTGTTAAAAATCATGGAGCAGTAGTT 1979
DB 1948 GCATCTCTTTATGGACATTTATGAAGTTGCAGAACTCTTGTGTTAAAAATCATGGAGCAGTAGTT 2007
QY 1980 AATGTAGCTGATTTATGGAATTTTACACTTTTACATGAAGCAGCAGCAAAAGGAAATAT 2039
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DB 2068 GAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCAGAAAAAACAGGGATGGA 2127
QY 2100 AATACTCTCTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAAGATCTGCTTTAGGGGA 2159
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QY 2220 TCTCTGATTAATGTAATTTGCCGATATCCCAAGGCAGACATTTCAACCTTTTACATTTA 2279
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DB 2308 GCAGCTGTTTAAATAATTTAGAAAGTTGCAGAGTATTTGTTTCAACAACGGAGCTGATGTG 2367
QY 2340 AATGCCCAAGCAAAAGGAGGACTTTATTCCTTTACATAATGCGAGCATCTTACGGGCATGTA 2399
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DB 2788 GGGAGTTTTTCAAGACTGCTTTCAGTAGTTAGTTCAAGTGGAAACAGAGGCTGCTTCAGT 2847
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Db 2848 TTGGAGAAAAAGAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAAGGAATCTT 2907
Qy
Db 2880 GGACTTGAGCACCTAATGATATATTCAGAGAGACAGATCACCTTTGGATGATTAAGTT 2939
Db 2908 GGACTTGAGCACCTAATGATATATTCAGAGAGACAGATCACCTTTGGATGATTAAGTT 2967
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Qy 3000 CTAATTAAGGAGTGCAGAGACTTATCCCGACAAACAGGCTTTAAACCCATATTTAACT 3059
Db 3028 CTAATTAAGGAGTGCAGAGACTTATCCCGACAAACAGGCTTTAAACCCATATTTAACT 3087
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Db 3088 TTGAACACTCTGGTAGTGAACAATCTTATAGATCTGCTCCTGATGATAAAGAGTTT 3147
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Db 3148 CAGTCTGTGGAGGAAGATGCAAAAGTACAGTTTCGAGAGCAGAGATGGAGGTCATGCA 3207
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Db 3208 GGTGAATCTTCAACAGATACAAATTTCTCAAGATTCAGAGTTGTAAACAAGAACTA 3267
Qy 3240 TGGGAAGATACACTCACCGGAGAAAGAGTTTCTGAAGAAACCAACCAATGCCAAT 3299
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Qy 3300 GAACGAATGCTATTTTCATGGGCTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTTGAT 3359
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Qy 3360 GAAAGGCATCGGTACATAGGTGATGTTTGGAGCTGGCATTTATTTTGTGAAACTCT 3419
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Db 3508 GACAGATCTTGTATATTTGGCAGAGGAGTCTCTTTTGGCGGTAACCTTTGGGAAAG 3567
Qy 3540 TCTTTTCGCAATTCAGTGAATGAAATGGCAGATTTCTCTCCAGGTCATCACTCAGTC 3599
Db 3568 TCTTTTCGCAATTCAGTGAATGAAATGGCAGATTTCTCTCCAGGTCATCACTCAGTC 3627
Qy 3600 ACTGGTAGGCCAGTGAATGGCCCTAGCATTTAGCTGAATATGTTTATTCAGAGGAGAA 3659
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Db 3748 GGATAAATAGTTATTTAAGAACTAATTTCACTGAACCTTAATTAATTAATTAATTAATTAAT 3807
Qy 3780 GGCCTCTACGTTTACTCTTTTGTGTAAGAAAAA 3813
Db 3808 GGCCTCTACGTTTACTCTTTTGTGTAAGAAAAA 3841

RESULT 9

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; LENGTH: 4127
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3508)
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (3509)..(4127)
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Query Match 94.2%; Score 3595.8; DB 7; Length 4127;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3597; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 215 GGCCAGGATCATGTCGGTGCCTGCGCGGGGAGCGGCTTGCAGAGCGCGC 274
Db 1 GGCCAGGATCATGTCGGTGCCTGCGCGGGGAGCGGCTTGCAGAGCGCGC 60
Qy 275 GGCCAGGCGTGCAGCGCGCGCGCGCGAGCTTTCGAGGCGTCCGCAACGGGAGCT 334
Db 61 GGCCAGGCGTGCAGCGCGCGCGCGCGAGCTTTCGAGGCGTCCGCAACGGGAGCT 120
Qy 335 GGAACGAGTCAAGAGGCTGGTGCCTGAGAGGTGAACAGCCGCGACACCGCGGGCAG 394
Db 121 GGAACGAGTCAAGAGGCTGGTGCCTGAGAGGTGAACAGCCGCGACACCGCGGGCAG 180
Qy 395 GAAATCCACCCCGCTGCATTCGCCGCGAGGTTTTGGCGGAAAGACGTTAGTGAATATT 454
Db 181 GAAATCCACCCCGCTGCATTCGCCGCGAGGTTTTGGCGGAAAGACGTTAGTGAATATT 240
Qy 455 GCTTCAGATGGTCAAAATGTCCAAGCACGTCATGATGGGGGCTTATTCCTTCATAA 514
Db 241 GCTTCAGATGGTCAAAATGTCCAAGCACGTCATGATGGGGGCTTATTCCTTCATAA 300
Qy 515 TGCATGCTCTTTTGGTGCATGCTGAAGTAGTCAATCTCTCTTTGCGACATGTCGAGACCC 574
Db 301 TGCATGCTCTTTTGGTGCATGCTGAAGTAGTCAATCTCTCTTTGCGACATGTCGAGACCC 360
Qy 575 CAATGCTCGAGATAATTTGGAATTATCTCTCTCCATGAAGCTCAATTTAAAGGAAAGAT 634
Db 361 CAATGCTCGAGATAATTTGGAATTATCTCTCTCCATGAAGCTCAATTTAAAGGAAAGAT 420
Qy 635 TGATGTTTGCATTTGCTGTTTACAGATGGAGCTGAGCCCAACCATCCGAAATACAGATGG 694
Db 421 TGATGTTTGCATTTGCTGTTTACAGATGGAGCTGAGCCCAACCATCCGAAATACAGATGG 480
Qy 695 AAGGACAGCATTTGATTTAGCAGATCCATCTGCCAAAGCAGTGTCTTCTGGTGAATATAA 754
Db 481 AAGGACAGCATTTGATTTAGCAGATCCATCTGCCAAAGCAGTGTCTTCTGGTGAATATAA 540
Qy 755 GAAAGATGAACCTCTTAGAAAGTGCAGAGTGGCAATGAAGAAAAATGATGGCTCTACT 814
Db 541 GAAAGATGAACCTCTTAGAAAGTGCAGAGTGGCAATGAAGAAAAATGATGGCTCTACT 600
Qy 815 CACACCATTAATGTCATTCGCGACGCAAGTGTGCGAGAAAGTCAACTCCATTACATTT 874
Db 601 CACACCATTAATGTCATTCGCGACGCAAGTGTGCGAGAAAGTCAACTCCATTACATTT 660

Qy	875	GGCAGCAGGATATACAGAGTAAAGATTGTACAGCTGTTTACTGCACCAATCGAGCGCTGATGT	934
Db	661	GGCAGCAGGATATACAGAGTAAAGATTGTACAGCTGTTTACTGCACCAATCGAGCGCTGATGT	720
Qy	935	CCATGCTAAAGATAAAGAGTGATCTGGTACCATATACAAATGCCTGTTCTTATGGTCAATTA	994
Db	721	CCATGCTAAAGATAAAGAGTGATCTGGTACCATATACAAATGCCTGTTCTTATGGTCAATTA	780
Qy	995	TGAAGTAACTGAACTTTTGGTCAAGCATGGTGCCTGTGTAAATGCAATGGACCTTGTGGCA	1054
Db	781	TGAAGTAACTGAACTTTTGGTCAAGCATGGTGCCTGTGTAAATGCAATGGACCTTGTGGCA	840
Qy	1055	ATTCACTCCTCTTCATGAGGCAGCTTCTAAGAACAGGGTGAAGTAGTGTCTCTCTCTCT	1114
Db	841	ATTCACTCCTCTTCATGAGGCAGCTTCTAAGAACAGGGTGAAGTAGTGTCTCTCTCTCT	900
Qy	1115	AAAGTTATGGTGCAGACCCACACTGCTCAATTTGTCACAAATAAAGTCTATAGACTTGGC	1174
Db	901	AAAGTTATGGTGCAGACCCACACTGCTCAATTTGTCACAAATAAAGTCTATAGACTTGGC	960
Qy	1175	TCCACACCAACAGTTAAAGAAAGATTAGCATATGAATTTAAAGGCCACCTCGTTGCTGCA	1234
Db	961	TCCACACCAACAGTTAAAGAAAGATTAGCATATGAATTTAAAGGCCACCTCGTTGCTGCA	1020
Qy	1235	AGCTGCAGAGAAAGCTGATGTTACTCGAATCAAAAAACATCTCTCTGGAATATGGTGAA	1294
Db	1021	AGCTGCAGAGAAAGCTGATGTTACTCGAATCAAAAAACATCTCTCTGGAATATGGTGAA	1080
Qy	1295	TTTTCAAGCATCCTCAAAACACATGAAACAGCATTTGCATTTGGTCTGCTGCATCTCCATATCC	1354
Db	1081	TTTTCAAGCATCCTCAAAACACATGAAACAGCATTTGCATTTGGTCTGCTGCATCTCCATATCC	1140
Qy	1355	CAAAAGAAAGCAAAATATGTGAACTGTTGCTTAAGAAAAAGGAGCAAAACATCAATGAAAAAGAC	1414
Db	1141	CAAAAGAAAGCAAAATATGTGAACTGTTGCTTAAGAAAAAGGAGCAAAACATCAATGAAAAAGAC	1200
Qy	1415	TAAAGAAATCTTGACTCCTCTGCACGTGGCATCTGAGAAAGCTCATTAATGATGTTGTGA	1474
Db	1201	TAAAGAAATCTTGACTCCTCTGCACGTGGCATCTGAGAAAGCTCATTAATGATGTTGTGA	1260
Qy	1475	AGTAGTGGTGAACATGACCAAGGTTAATGCTCTGGATAAATCTTGGTCAGACTTCTCT	1534
Db	1261	AGTAGTGGTGAACATGACCAAGGTTAATGCTCTGGATAAATCTTGGTCAGACTTCTCT	1320
Qy	1535	ACACAGAGCTGCATATTTGTGGTCACTACAAAACCTGCGCGCTACTCCTGAGCTATGGGTG	1594
Db	1321	ACACAGAGCTGCATATTTGTGGTCACTACAAAACCTGCGCGCTACTCCTGAGCTATGGGTG	1380
Qy	1595	TGATCTTAAACATTAATATCCCTTTCAGGCTTTACTGCTTTACAGATGGGAAATGAAAAATGT	1654
Db	1381	TGATCTTAAACATTAATATCCCTTTCAGGCTTTACTGCTTTACAGATGGGAAATGAAAAATGT	1440
Qy	1655	ACAGCAACTCCTCCAAGAGGGTATCTCATTAGGTAATTCAGAGGCACACAGACNAATGCT	1714
Db	1441	ACAGCAACTCCTCCAAGAGGGTATCTCATTAGGTAATTCAGAGGCACACAGACNAATGCT	1500
Qy	1715	GGAGCTGCAAAAGGCTGGAGATGCGAAACCTGTAAAAAAAACCTGTGTACTGTTCAAGAGTGT	1774
Db	1501	GGAGCTGCAAAAGGCTGGAGATGCGAAACCTGTAAAAAAAACCTGTGTACTGTTCAAGAGTGT	1560
Qy	1775	CAACTGCAGAGACATTAAGAGGGCTCAGTCTACACCACTTCATTTTGCAGCTGGGTATAA	1834
Db	1561	CAACTGCAGAGACATTAAGAGGGCTCAGTCTACACCACTTCATTTTGCAGCTGGGTATAA	1620
Qy	1835	CAGAGTGTCCGTGGTGAATATCTGCTACAGCATGGAGCTGATGTGATGCTAAAGATAA	1894
Db	1621	CAGAGTGTCCGTGGTGAATATCTGCTACAGCATGGAGCTGATGTGATGCTAAAGATAA	1680
Qy	1895	AGGAGGCTTGTACTCTTTGCAACATGATGTTCTTATGGACATTTATGAAGTTGCGAGAACT	1954
Db	1681	AGGAGGCTTGTACTCTTTGCAACATGATGTTCTTATGGACATTTATGAAGTTGCGAGAACT	1740
Qy	1955	TCCTGTTTAAACATGGAGCAGTAGTTAAATGTAGTCTGATTTATGGAAATTTTACACCTTTTACA	2014

Db	1741		TCCTGTTAAACATGGAGCAGTAGTTAATGTAGCTGAATTTATGGAAATTTTACACCTTTTACA	1800
Qy	2015		TGAAGCAGCAGCAAAAAGGAAAAATATGAAATTTTGCAAACTTCTGCTCCAGCATGGTGCAGA	2074
Db	1801		TGAAGCAGCAGCAAAAAGGAAAAATATGAAATTTTGCAAACTTCTGCTCCAGCATGGTGCAGA	1860
Qy	2075		CCCTACCAAAAAAACAAGGATGGAAATACTCTCTTTGGATCTTTGTTTAAAGATGGAGATAC	2134
Db	1861		CCCTACCAAAAAAACAAGGATGGAAATACTCTCTTTGGATCTTTGTTTAAAGATGGAGATAC	1920
Qy	2135		AGATATTCAGATCTCTTTAGGGGAGATGCAGCTTTGTAGATGCTGCCAAGAGAGGTTG	2194
Db	1921		AGATATTCAGATCTCTTTAGGGGAGATGCAGCTTTGTAGATGCTGCCAAGAGAGGTTG	1980
Qy	2195		TTTGGCCAGAGTCAAGAAGTTGCTTCTCTGTGATAATGTAAATTTGCCGGGATACCCCAAGG	2254
Db	1981		TTTGGCCAGAGTCAAGAAGTTGCTTCTCTGTGATAATGTAAATTTGCCGGGATACCCCAAGG	2040
Qy	2255		CAGACATTCACACCTTTTACATTTAGCAGCTGGTTATTAATAATTTAGAAAGTTGCACAGTA	2314
Db	2041		CAGACATTCACACCTTTTACATTTAGCAGCTGGTTATTAATAATTTAGAAAGTTGCACAGTA	2100
Qy	2315		TTTGTTTACACACGGAGCTGATGTAATGCCCAAGCAAGAGGAGCTTATTTCCTTTTACA	2374
Db	2101		TTTGTTTACACACGGAGCTGATGTAATGCCCAAGCAAGAGGAGCTTATTTCCTTTTACA	2160
Qy	2375		TAAATGCAGCATCTTACGGGCATCTAGATGTAGCAGCTCTACTAATAAGATATAATGCATG	2434
Db	2161		TAAATGCAGCATCTTACGGGCATCTAGATGTAGCAGCTCTACTAATAAGATATAATGCATG	2220
Qy	2435		TGTCAATGGCCACGACAAATGGGCTTTTCAACCTTTGCCAAGCAGCCCAAGAGGACG	2494
Db	2221		TGTCAATGGCCACGACAAATGGGCTTTTCAACCTTTGCCAAGCAGCCCAAGAGGACG	2280
Qy	2495		AACACAGCTTTGTGCTTTGTGTTAGTTTTCAGCGGATGATGTCAAGGCTCTCTCTGACAGCAGC	2554
Db	2281		AACACAGCTTTGTGCTTTGTGTTAGTTTTCAGCGGATGATGTCAAGGCTCTCTCTGACAGCAGC	2340
Qy	2555		AGGACAAACACCTTTTAGATTTTGTGTTTTCAGCGGATGATGTCAAGGCTCTCTCTGACAGCAGC	2614
Db	2341		AGGACAAACACCTTTTAGATTTTGTGTTTTCAGCGGATGATGTCAAGGCTCTCTCTGACAGCAGC	2400
Qy	2615		CATGCCCCCATCTGCTCTGCCCTCTTTGTTTCAAGCCTCAAGTGCTCAATGGTGTGAGAAG	2674
Db	2401		CATGCCCCCATCTGCTCTGCCCTCTTTGTTTCAAGCCTCAAGTGCTCAATGGTGTGAGAAG	2460
Qy	2675		CCAGGAGCCACTGACAGATGCTCTCTCTCAGTGCTCATCTAGGCCATCAAGCCCTTTCTGC	2734
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Qy	2735		AGCCAGAGTCTTGAACAACCTTATCTGGAGTTTTCAGAACTCTCTCTCAGTAGTAGTTTC	2794
Db	2521		AGCCAGAGTCTTGAACAACCTTATCTGGAGTTTTCAGAACTCTCTCTCAGTAGTAGTTTC	2580
Qy	2795		AAGTGGAAACAGAGGGTCTTCCAGTTTGGAGAAAAAGGAGTTTCCAGGAGTAGATTTTAG	2854
Db	2581		AAGTGGAAACAGAGGGTCTTCCAGTTTGGAGAAAAAGGAGTTTCCAGGAGTAGATTTTAG	2640
Qy	2855		CATAACTCAATTCGTAAGGAATCTTGACCTTGAGCACCCTAATGGATATATTTTCAGAGAGA	2914
Db	2641		CATAACTCAATTCGTAAGGAATCTTGAGCTTGAGCACCCTAATGGATATATTTTCAGAGAGA	2700
Qy	2915		ACAGATCACCTTTGGATGTATTTAGTTGAGATGGGGCAACAAGGAGCTCAAGGAGATTTCGAAT	2974
Db	2701		ACAGATCACCTTTGGATGTATTTAGTTGAGATGGGGCAACAAGGAGCTCAAGGAGATTTCGAAT	2760
Qy	2975		CAATGCTTATGGACATAGGCACAAACTAATTAAGAGGATCGAGAGACTTATCTCCGGACA	3034
Db	2761		CAATGCTTATGGACATAGGCACAAACTAATTAAGAGGATCGAGAGACTTATCTCCGGACA	2820
Qy	3035		ACAAGGCTTTAAACCCATATTTTAACTTTTGAACACCTCTGGTAGTGGAAACAATTTCTTATAGA	3094

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1021 GAAGCTGATGTTACTCGAATCAAAAAATCATCTCTCTCTGGAATGGTGAATTTCAAGCAT 1080
1305 CCTCAACACATGAACAGAGATGCAATGTTGCTGCTGCATCTCCATATCCCAAGAAAG 1364
1081 CCTCAACACATGAACAGAGATGCAATGTTGCTGCTGCATCTCCATATCCCAAGAAAG 1140
1365 CAATATGTGAATGTTGCTAAGAAAAAGGAGCAAAACATCAATGAAAAAGCTTAAAGAAATTC 1424
1141 CAATATGTGAATGTTGCTAAGAAAAAGGAGCAAAACATCAATGAAAAAGCTTAAAGAAATTC 1200
1425 TTGACTCTCTGACGCTGGGATCTGAGAAAGCTCATATGAATGTTGTTGAAGTAGTGGTG 1484
1201 TTGACTCTCTGACGCTGGGATCTGAGAAAGCTCATATGAATGTTGTTGAAGTAGTGGTG 1260
1485 AAACATGAACAAAGGTTAATGCTCTGGATAATCTTGGTCAGACTCTCTACACAGAGCT 1544
1261 AAACATGAACAAAGGTTAATGCTCTGGATAATCTTGGTCAGACTCTCTACACAGAGCT 1320
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1605 ATTATATCCCTTCAGGGCTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTC 1664
1381 ATTATATCCCTTCAGGGCTTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAACTC 1440
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1725 AAGGCTCGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCGAGA 1784
1501 AAGGCTCGAGATGTCGAAACTGTAAAAAACTGTGTACTGTTCAGAGTGTCAACTGCGAGA 1560
1785 GACATGAAGGGCTCAGTCTACACCACTTCAATTTTGAGCTGGGTATAACAGAGTGTCC 1844
1561 GACATGAAGGGCTCAGTCTACACCACTTCAATTTTGAGCTGGGTATAACAGAGTGTCC 1620
1845 GTGGTGGNAATCTGCTACAGCATGGAGCTGATGTCATGCTAAAGATAAAGGAGGCTTT 1904
1621 GTGGTGGNAATCTGCTACAGCATGGAGCTGATGTCATGCTAAAGATAAAGGAGGCTTT 1680
1905 GTACCTTTTGCAAAATGCAATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTTGTTAAA 1964
1681 GTACCTTTTGCAAAATGCAATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTTGTTAAA 1740
1965 CATGGAGCAGTAGTAAATGCTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCA 2024
1741 CATGGAGCAGTAGTAAATGCTAGCTGATTTATGGAAATTTTACACCTTTACATGAAGCAGCA 1800
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1801 GCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCCAGCATGTGCAGACCTTACCAGAA 1860
2085 AAAAAACAGGGATGGAATATCTCTTTGGATCTTGTAAAGATGGAGATACAGATATTTCAA 2144
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2145 GATCTGCTTAGGGAGATGCAAGCTTTGCTAGATGCTGCCAAGAAAGGGTGTGTTAGCCAGA 2204
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2205 GTGAAGAAAGTGTCTCTCTGATAATGTAATTTGCCGCGATACCCAGGCGAGACATTTCA 2264
1981 GTGAAGAAAGTGTCTCTCTGATAATGTAATTTGCCGCGATACCCAGGCGAGACATTTCA 2040
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2385 TCTTACGGGCGATGTAGATGTAGCAGCTCTACTAATAAAGTATATATGATGTGTCAATGCC 2444
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2581 GAGGGTCTTCCAGTTTGGAGAAAAAGGAGGTTCCAGAGATAGATTTTAGCATTAATCTCAA 2640
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2701 TTGTAATGTTAGTTGAGATGGGGCACAAGGAGCTGAAGGAGATTTGGAATCAATGCTTAT 2760
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Qy 3585 GGTTCATCACTCAGTCACTGGTAGGCCAGCTGTAATATGAGCTAGCAATAGCTGAATATGTT 3644
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Db 3541 CATCAAGCAGCAGTGGCTCTACGTTTACTCCTTTGCTGAAAAAAA 3589

RESULT 11
US-10-199-937-1
; Sequence 1, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(3508)
US-10-199-937-1

Query Match 91.8%; Score 3504.8; DB 7; Length 3508;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3506; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 275 GGCAGGCGGTGGAGCGCGCGCGCGAGAGCTGTTTCGAGGCGTGC CGCAACGGGAGCGT 334
Db 61 GGCAGGCGGTGGAGCGCGCGCGCGAGAGCTGTTTCGAGGCGTGC CGCAACGGGAGCGT 120

Qy 335 GGAACGAGTCAAGAGGCTGGTGAACGCTGAGAGGTGAACAGCGCGGAGCGGAG 394
Db 121 GGAACGAGTCAAGAGGCTGGTGAACGCTGAGAGGTGAACAGCGCGGAGCGGAG 180

Qy 395 GAAATCCACCCGCTGCACTTCGCGCGAGGTTTGGCGGGAAGAGCGTAGTTGAATATTT 454
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Qy 515 TGCACTGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCCTTTTGGACATGTTGCGAGACC 574
Db 301 TGCACTGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCCTTTTGGACATGTTGCGAGACC 360
Qy 575 CAATGCTCGAGATTAATTTGGAATATATATCTCTCTCCATGAGCTGCAATTAAGGAAAGAT 634
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Db 721 CCATGCTAAAGATAAAGTGTATCTGGTACCAATTAACAATGCTGTTCTTATGGTCATTA 780
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Db 1681 AGGAGGCTTTGTACCTTTGCACAATGCATGTTCTTATGGCACTPATGAAGTTCGAGAACT 1740
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RESULT 12

US-10-616-101-1

; Sequence 1, Application US/10616101

; Publication No. US20050074825A1

; GENERAL INFORMATION:

; APPLICANT: Luo, Ying

; APPLICANT: Chan, Eva

; APPLICANT: Xu, Xiang

; APPLICANT: Huang, Betty

; APPLICANT: Ossovskaya, Valeria

; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods

; FILE REFERENCE: RIGL-010CIP3

; CURRENT APPLICATION NUMBER: US/10/616,101

; CURRENT FILING DATE: 2003-07-08

; PRIOR APPLICATION NUMBER: US 09/843,159

; PRIOR FILING DATE: 2001-04-25

; PRIOR APPLICATION NUMBER: US 09/696,668

; PRIOR FILING DATE: 2000-10-25

; PRIOR APPLICATION NUMBER: US 09/427,154

; PRIOR FILING DATE: 1999-10-25

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 3797

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-616-101-1

Query Match 88.9%; Score 3393.4; DB 10; Length 3797;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 422 AGGTTTGGCGGAAGACGTAGTTGAATATTTGCTTCAGAAATGTCGCAAGC 481
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Db 1243 AATCAAAAAACATCTCTCTGGAATATGTTCAAGCATCTCCTCAAAACACATGAAC 1302
Qy 1322 AGCATTCATTTGCTGCTGCTCATCTCCATATCCCAAAAGAAAGCAATATGTAACATGTT 1381
Db 1303 AGCATTCATTTGCTGCTGCTCATCTCCATATCCCAAAAGAAAGCAATATGTAACATGTT 1362
Qy 1382 GCTAAGAAAAGGAGCAAAACATCAATGAAGAGCTTAAAGAAATCTTGACTCTCTGCAGGT 1441
Db 1363 GCTAAGAAAAGGAGCAAAACATCAATGAAGAGCTTAAAGAAATCTTGACTCTCTGCAGGT 1422
Qy 1442 GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAAAGGT 1501
Db 1423 GGCATCTGAGAAAGCTCATATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAAAGGT 1482
Qy 1502 TAATGCTCTGAGTAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTCATCT 1561
Db 1483 TAATGCTCTGAGTAATCTTGGTCAGACTTCTCTACACAGAGCTGCATATTTGTCATCT 1542
Qy 1562 ACAAACCTGCGCCTACTCTGAGCTATGGTGTGATCTTAAACATTTATATCCCTTCAGGG 1621
Db 1543 ACAAACCTGCGCCTACTCTGAGCTATGGTGTGATCTTAAACATTTATATCCCTTCAGGG 1602
Qy 1622 CTTTACTGCTTTACAGATGGAAATGAATGTACAGCACTCTCCTCAAGAGGCTATCTC 1681
Db 1603 CTTTACTGCTTTACAGATGGAAATGAATGTACAGCACTCTCCTCAAGAGGCTATCTC 1662
Qy 1682 ATTAGGTAATTCAGAGGCGACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCGA 1741
Db 1663 ATTAGGTAATTCAGAGGCGACAGACAATTTGCTGGAAGCTGCAAGGCTGGAGATGTCGA 1722
Qy 1742 AACTGTAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGTCAGAGACATTTGAAGGCGCTCA 1801
Db 1723 AACTGTAAAAAACTGTGTACTGTTTCAGAGTGTCAACTGTCAGAGACATTTGAAGGCGCTCA 1782
Qy 1802 GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT 1861
Db 1783 GTCTACACCACTTCATTTTGCAGCTGGGTATAACAGAGTGTCCGTGGTGAATATCTGCT 1842
Qy 1862 ACAGCATGGAGCTCATGTGATGCTTAAAGATAAAGAGGCGCTTGTACCTTTGCAAAATGC 1921
Db 1843 ACAGCATGGAGCTCATGTGATGCTTAAAGATAAAGAGGCGCTTGTACCTTTGCAAAATGC 1902
Qy 1922 ATGTTCTTATGACATTTATGAAGTTGAGAACTTTCTGTTTAAACATGAGGAGTAGTTAA 1981
Db 1903 ATGTTCTTATGACATTTATGAAGTTGAGAACTTTCTGTTTAAACATGAGGAGTAGTTAA 1962
Qy 1982 TGTAGCTGATTTATGGAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2041
Db 1963 TGTAGCTGATTTATGGAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGA 2022
Qy 2042 AATTGCAAACTTCTGCTCCAGCATGGTGCAGACCTTACCACAAAAAACAAGGATGGAAA 2101

Qy	121	CCCTGAGCGCGTCTTCTCCGGGGGGCCTCGCCCTCTGCTCGCGGGGC	CGGGGCTCCTGCG	180
Db	194	CCCTGAGCGCGTCTTCTCCGGGGGGCCTCGCCCTCTGCTCGCGGGGC	CGGGGCTCCTGCG	253
Qy	181	TCGGTTGCTGGCGCGCTGTTGCTGTGCGGGGGCCAGGATCATGT	CGGGTCCGCGCT	240
Db	254	TCGGTTGCTGGCGCGCTGTTGCTGTGCGGGGGCCAGGATCATGT	CGGGTCCGCGCT	313
Qy	241	GGCGGGGGGGGAGCGGCGTGGCGAGCGCGGGGGCGGGCGTGGAGCG	CGCGCGCGCC	300
Db	314	GGCGGGGGGGGGAGCGGCGTGGCGAGCGCGGGGGCGGGCGTGGAGCG	CGCGCGCGCC	373
Qy	301	GAGAGCTGTTTCGAGCGCTGCGCAACGGGGACGTGGAAACGAGTCAAGAG	CGTGGTGACGC	360
Db	374	GAAACCTGTTTCGAGCGTGGCGCAACGGGGACGTGGAAACGAGTCAAGAG	CGTGGTGACGC	433
Qy	361	CTGAGAAAGGTGAACAGCGCGGACACGGCGGGCAGGAAATCCACCCCGCTGCAC	TTGCGCG	420
Db	434	CTGARAAGGTGAACAGCGCGGACACNGCGGGCAGGAAATCCACCCCGCTGCAC	TTGCGCG	493
Qy	421	CAGGTTTTGGCGGAAAGACGTAGTTGAATATTTGCTTCAGAAATGGTGC	CAATGTC	480
Db	494	CANGTTTTGGCGGAAAGACCTAANTTAAATATTTGCTTCANNAATGGTGC	CAATGTC	553
Qy	481	CACGTGATGATGGGGGCTTATTCCTCTTCATATGATGCTCTTTTGGTGCATG	CTCAAG	540
Db	554	CACGTGATGATGGGGGCTTATTCCTCTTCATATGATGCTCTTTTGGTGCATG	CTCAAG	613
Qy	541	TAGTCAATCTCTTTTGGCATGGTGCAGACCCCAATGCTCGAGATAATTTGGA	ATTATA	600
Db	614	NTATCNATCTCTTTTGCNACATNGTCANAMCCCAATGCTCGAGATAATTTGGA	ATTATA	673
Qy	601	CTCCTCTCCATGAAGCTGCAAATTAAGAAAGATTTGATTTTGATTTGCTG	TTTACAGC	660
Db	674	CTCCTCNATGAAGCTGCAAATTAAGAAAGATTTGANNTTGCAATTTGCTG	TTTACAGC	733
Qy	661	ATGAGCTGAGCCCAACCATCCGAATACAGATGAAGCAGCAGTTCGATTTAG	CAGATC	720
Db	734	ATGAGCTGAGCCCAACCATCCGAATACAGATGAAGCAGCAGTTCGATTTAG	CAGATC	793
Qy	721	CATCTGCCAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACCTTTAGA	AAAGTGCCA	780
Db	794	CATCTGCCAAGCAGTGCTTACTGGTGAATATAAGAAAGATGAACCTTTAGA	AAAGTGCCA	853
Qy	781	GGAGTGGCAATGAAGAAATAATGATGGCTCTACTCACACCATTTAAATGT	CACTGCCACG	840
Db	854	GGAGTGGCAATGAAGAAATAATGATGGCTCTACTCACACCATTTAAATGT	CACTGCCACG	913
Qy	841	CAAGTGATGGCAGAAAGTCAACTCCATTTACATTTGGCAGCAGGATATAACAG	AGTAAAGA	900
Db	914	CAAGTGATGGCAGAAAGTCAACTCCATTTACATTTGGCAGCAGGATATAACAG	AGTAAAGA	973
Qy	901	TTGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGTCTAAAGATAAAG	GTGATCTGG	960
Db	974	TTGTACAGCTGTTACTGCAACATGGAGCTGATGTCCATGTCTAAAGATAAAG	GTGATCTGG	1033
Qy	961	TACCATTTACAATAGCCCTGTTCTTATGGTCAATTAAGTAAGTAACTGA	ACTTTTGGTCAAGC	1020
Db	1034	TACCATTTACAATAGCCCTGTTCTTATGGTCAATTAAGTAAGTAACTGA	ACTTTTGGTCAAGC	1093
Qy	1021	ATGGTGCTGTGTAATAGCAATGCACTTGGGCAATTCACCTCTTTCATGAG	CGACGCTT	1080
Db	1094	ATGGTGCTGTGTAATAGCAATGCACTTGGGCAATTCACCTCTTTCATGAG	CGACGCTT	1153
Qy	1081	CTAAGAACAGGGTTGAAGTATGTTCTCTTCTTTAAAGTTATGGTGCAGAC	CCCACTGCG	1140
Db	1154	CTAAGAACAGGGTTGAAGTATGTTCTCTTCTTTAAAGTTATGGTGCAGAC	CCCACTGCG	1213
Qy	1141	TCAATTTGCACAAATAAAGTGCTATAGACTTTGGTTCACACACCAAGT	TTAAAGAAAGAT	1200
Db	1214	TCAATTTGCACAAATAAAGTGCTATAGACTTTGGTTCACACACCAAGT	TTAAAGAAAGAT	1273

1201	Qy	TAGCATATGAATTTAAAGGCCACTCTCTTGTGTCAAGACTGCA	CGAAGAGCTGATGTTACTCTC	1261
1274	Db	TAGCATATGAATTTAAAGGCCACTCTCTGTCTGCAAGCTGCA	GAGAAGCTGATGTTACTCTC	1333
1261	Qy	GAATCAAAAACAATCTCTCTCTGGAATCGGTGAATTTCAAG	CAATCTCTCAAAACATGAAA	1320
1334	Db	GAATCAAAAACAATCTCTCTCTGGAATCGGTGAATTTCAAG	CAATCTCTCAAAACATGAAA	1393
1321	Qy	CAGCATTTGCATTTGTCTGTCTGTCATCTCCATATCCCAAA	AGAAAGCAAAATATGTGAACTGT	1380
1394	Db	CAGCATTTGCATTTGTCTGTCTGTCATCTCCATATCCCAAA	AGAAAGCAAAATATGTGAACTGT	1453
1381	Qy	TGCTAAAGAAAGGAGCAAAACATCAATGAAAGACTAAAGAA	TTCTTTGACTCTCTCTGCACG	1440
1454	Db	TGCTAAAGAAAGGAGCAAAACATCAATGAAAGACTAAAGAA	TTCTTTGACTCTCTCTGCACG	1513
1441	Qy	TGCGATCTGAGAAAGCTCATATGATGTTGTTGAAAGTAGT	GGTGAACAATGAAGCAAAAGG	1500
1514	Db	TGCGATCTGAGAAAGCTCATATGATGTTGTTGAAAGTAGT	GGTGAACAATGAAGCAAAAGG	1573
1501	Qy	TTAATGCTCTGGGATAATCTTGGTGCAGACTTCTCTACA	CAGAGCTGCATATTTGGTGCATC	1560
1574	Db	TTAATGCTCTGGGATAATCTTGGTGCAGACTTCTCTACA	CAGAGCTGCATATTTGGTGCATC	1633
1561	Qy	TACAAACCTGCCCTACTCTCTGAGCTATGGGTGTGATCCT	AAATATATCCCTTCAGG	1620
1634	Db	TACAAACCTGCCCTACTCTCTGAGCTATGGGTGTGATCCT	AAATATATCCCTTCAGG	1693
1621	Qy	GCCTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAA	CTCCTTCCAAGAGGTTATCT	1680
1694	Db	GCCTTACTGCTTTACAGATGGGAAATGAAATGTACAGCAA	CTCCTTCCAAGAGGTTATCT	1753
1681	Qy	CATTAGGTAATTCAGAGGCGACAGACAATTTGCTGGAAG	CTGCAAAAGGCTGGAGATGTCTG	1740
1754	Db	CATTAGGTAATTCAGAGGCGACAGACAATTTGCTGGAAG	CTGCAAAAGGCTGGAGATGTCTG	1813
1741	Qy	AAACTGTAAAAAATCTGTGTACTGTTTACAGAGTCTCAACT	TCAGAGACATTTGAAGGCGCTC	1800
1814	Db	AAACTGTAAAAAATCTGTGTACTGTTTACAGAGTCTCAACT	TCAGAGACATTTGAAGGCGCTC	1873
1801	Qy	AGTCTACACACTTTCATTTTTCAGCTGGGTATAACAGAGT	GTCCGTGGTGGAAATATCTGC	1860
1874	Db	AGTCTACACACTTTCATTTTTCAGCTGGGTATAACAGAGT	GTCCGTGGTGGAAATATCTGC	1933
1861	Qy	TACAGCATGAGCTGATGTGCATGCTAAAGATAAAGAGGCC	TTTGTACCTTTTCCACAATG	1920
1934	Db	TACAGCATGAGCTGATGTGCATGCTAAAGATAAAGAGGCC	TTTGTACCTTTTCCACAATG	1993
1921	Qy	CATGTTCTTTATGCACATTTATGAAGTTTGCAGAACTTCT	TGTTTAAACATGGAGCAGTAGTTA	1980
1994	Db	CATGTTNTTATGACATTTATGAAGTTTGCAGAACTTCTT	TGTTTAAACATGGAGCAGTAGTTA	2053
1981	Qy	ATGTAGCTGATTTATGGAAATTTTACACCTTTTACATGA	AGCAGCAGCAAAAGGAAAATATG	2040
2054	Db	ATGTAGCTGATTTATGGAAATTTTACACCTTTTACATGA	AGCAGCAGCAAAAGGAAAATATG	2113
2041	Qy	AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCTAC	CAAAAAAACAAGGAGTGGAA	2100
2114	Db	AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCTAC	CAAAAAAACAAGGAGTGGAA	2173
2101	Qy	ATACTCTCTTTGGATCTTGTTTAAAGATGGAGATACAGAT	ATTCAAGATCTGCTTTAGGGGAG	2160
2174	Db	ANATTCTNTTTGGATCTTGTTTAAAGATGGAGATACAGAT	ATTCAAGATNTGCTTTAGGGGAG	2233
2161	Qy	ATGCAGCTTTTGTCTGATGCTGCCAAGAGGGTTTGTAGCC	AGAGTGAAGAGTTGTCTTT	2220
2234	Db	ATGCAGCTTTTGTCTGATGCTGCCAAGAGGGTTTGTAGCC	AGAGTGAAGAGTTGTCTTT	2293
2221	Qy	CTCCTGATGATGTAAATTTGCCGGATACCCAAGCAGACATT	CCAACCTTTTACATTTAG	2280
2294	Db	TTCTGTGATGATGTAAATTTGCCGGATACCCAAGCAGACATT	CCAACCTTTTACATTTAG	2353
2281	Qy	CAGCTGGTTATATAATTTAGAAAGTTGCGAGATGTTTGT	TTTACAAACAGCGAGCTGATGTA	2340

Db 181 CGAATAACAGATGGAAGGACAGCAATGGATTTAGCAGATCCATCTGCCAAAGCAGTGCTT 240
Qy 741 ACTGGTGAATATAGAAGATGAACCTCTTAGAAGTGCAGGAGTGCCAAATGAAGAAAA 800
Db 241 ACTGGTGAATATAGAAGATGAACCTCTTAGAAGTGCAGGAGTGCCAAATGAAGAAAA 300
Qy 801 ATGATGGCTCTACTCACACCACTTAATATGTCNACTGCCACCAAGTGTATGCGAAGTCA 860
Db 301 ATGATGGCTCTACTCACACCACTTAATATGTCNACTGCCACCAAGTGTATGCGAAGTCA 360
Qy 861 ACTCCATTAATTTGGCAGCAGAGATATAACAGAGTAAAGATTTGACAGCTGTTACTGCAA 920
Db 361 ACTCCATTAATTTGGCAGCAGAGATATAACAGAGTAAAGATTTGACAGCTGTTACTGCAA 420
Qy 921 CATGGAGCTGATGTCATGCTAAAGATPAAAGGTGATCTGTGACCATPACAAATGCGCTGT 980
Db 421 CATGGAGCTGATGTCATGCTAAAGATPAAAGGTGATCTGTGACCATPACAAATGCGCTGT 480
Qy 981 TCTTATGGTCATTTATGAAGTAACTGAACCTTTGGTCAAGCATGGTGCCTGTGTAAATGCA 1040
Db 481 TCTTATGGTCATTTATGAAGTAACTGAACCTTTGGTCAAGCATGGTGCCTGTGTAAATGCA 540
Qy 1041 ATGGACTTGTGGCAATTCACCTCTCTCATGAGCAGCTTCTAAGAACAGGGTTGAAGTA 1100
Db 541 ATGGACTTGTGGCAATTCACCTCTCTCATGAGCAGCTTCTAAGAACAGGGTTGAAGTA 600
Qy 1101 TGTTCCTCTCTTCTTAACTTATGTTGTCAGACCCCAACACTGCTCAATGTGTCACAATAAAGT 1160
Db 601 TGTTCCTCTCTTCTTAACTTATGTTGTCAGACCCCAACACTGCTCAATGTGTAAAGT 660
Qy 1161 GCTATAGACTTGGCTCCCAACACACAGCTTAAAGAAAGATTAGCATATGAATTTAAAGGC 1220
Db 661 GCTATAGACTTGGCTCCCAACACACAGCTTAAAGAAAGATTAGCATATGAATTTAAAGGC 720
Qy 1221 CACTCTGTTGTCAGCTGACAGAGAGCTGATGTTACTCGAATCAAAAAACATCTCTCT 1280
Db 721 CACTCTGTTGTCAGCTGACAGAGAGCTGATGTTACTCGAATCAAAAAACATCTCTCT 780
Qy 1281 CTGGAATGTGTGAATTTCAAGCATCTTCAACACATGAAGAACAGCATTTGCTGTGCT 1340
Db 781 CTGGAATGTGTGAATTTCAAGCATCTTCAACACATGAAGAACAGCATTTGCTGTGCT 840
Qy 1341 GCATCTCATATCCAAAAGAAAGCAATATGTGAACCTGTCTAAGAAAAGGAGCAAC 1400
Db 841 GCATCTCATATCCAAAAGAAAGCAATATGTGAACCTGTCTAAGAAAAGGAGCAAC 900
Qy 1401 ATCAATGAAAAGACTAAGAAATCTTGACTCTCTGCACGTGGCATCTGAGAAAGCTCAT 1460
Db 901 ATCAATGAAAAGACTAAGAAATCTTGACTCTCTGCACGTGGCATCTGAGAAAGCTCAT 960
Qy 1461 AATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGTTAATGCTCTGGATAATCTTT 1520
Db 961 AATGATGTTGTTGAAGTAGTGGTGAACATGAAGCAAGGTTAATGCTCTGGATAATCTTT 1020
Qy 1521 GGTCAAGATCTCTACACAGAGCTGCATATGTGGTCACTACAAAGCTCGCGCTACTC 1580
Db 1021 GGTCAAGATCTCTACACAGAGCTGCATATGTGGTCACTACAAAGCTCGCGCTACTC 1080
Qy 1581 CTGAGCTATGGGTGTGATCTTAACATTTATATCCCTTCAGGGCTTTACTGCTTTACAGATG 1640
Db 1081 CTGAGCTATGGGTGTGATCTTAACATTTATATCCCTTCAGGGCTTTACTGCTTTACAGATG 1140
Qy 1641 GGAATGAAATGTPACAGCAACTCTCTCCAGAGGGTATCTCATTAGGTAAATTCAGAGGCA 1700
Db 1141 GGAATGAAATGTPACAGCAACTCTCTCCAGAGGGTATCTCATTAGGTAAATTCAGAGGCA 1200
Qy 1701 GACAGCAATTTGCTGGAAGCTGCNAAGGCTGGAGATGTGCNAAGCTGTAANAAGCTGTGT 1760
Db 1201 GACAGCAATTTGCTGGAAGCTGCNAAGGCTGGAGATGTGCNAAGCTGTAANAAGCTGTGT 1260
Qy 1761 ACTGTTCAAGAGTGTCAACTGCAGAGACATTTGAAGGGGTGAGTCTACACCACTTCATTTT 1820
Db 1261 ACTGTTCAAGAGTGTCAACTGCAGAGACATTTGAAGGGGTGAGTCTACACCACTTCATTTT 1320

Qy 1821 GCAGCTGGGTATTAACAGAGTGTCCGTGGTGAATATCTGCTACAGCATGAGCTGATGTG 1880
Db 1321 GCAGCTGGGTATTAACAGAGTGTCCGTGGTGAATATCTGCTACAGCATGAGCTGATGTG 1380
Qy 1881 CATGCTAAAGATAAAGAGGAGCCCTTGTACCTTTGCCAACAATGATGTTCTTATGACATTA 1940
Db 1381 CATGCTAAAGATAAAGAGGAGCCCTTGTACCTTTGCCAACAATGATGTTCTTACAGCATTA 1440
Qy 1941 GAAAGTTGCAGAACTCTTCTTTAAACATGGAGCAGTAGTTAATAGTAGCTGATTTATGAAA 2000
Db 1441 GAAAGTTGCAGAACTCTTCTTTAAACATGGAGCAGTAGTTAATAGTAGCTGATTTATGAAA 1500
Qy 2001 TTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTC 2060
Db 1501 TTTACACCTTTACATGAAGCAGCAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTC 1560
Qy 2061 CAGCATGGTGCAGACCTTACCAAAAAAACAAGGATGGAATATCTCCTTTGGATCTTGT 2120
Db 1561 CAGCATGGTGCAGACCTTACCAAAAAAACAAGGATGGAATATCTCCTTTGGATCTTGT 1620
Qy 2121 AAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGAGATGCAGCTTTGCTAGATGCT 2180
Db 1621 AAAGATGGAGATACAGATATTTCAAGATCTGCTTAGGGAGATGCAGCTTTGCTAGATGCT 1680
Qy 2181 GCCAAGAGGGTGTGTAGCCAGAGTGAAGAGTGTCTCTCTCTGATATGTAATGCTC 2240
Db 1681 GCCAAGAGGGTGTGTAGCCAGAGTGAAGAGTGTCTCTCTCTGATATGTAATGCTC 1740
Qy 2241 CGCGATACCCCAAGGAGACATTCACACCTTTACATTTAGCAGCTGGTATATAATTTA 2300
Db 1741 CGCGATACCCCAAGGAGACATTCACACCTTTACATTTAGCAGCTGGTATATAATTTA 1800
Qy 2301 GAAAGTTGCAGAGTATTTGTTTACAAACGAGAGCTGATGTGAATGCCCAAGCAAAAGGAGGA 2360
Db 1801 GAAAGTTGCAGAGTATTTGTTTACAAACGAGAGCTGATGTGAATGCCCAAGCAAAAGGAGGA 1860
Qy 2361 CTTATTTCTTTACATATGAGCATCTTAGCGGCATGTAGATGTAGCAGCTCTACTAATA 2420
Db 1861 CTTATTTCTTTACATATGAGCATCTTAGCGGCATGTAGATGTAGCAGCTCTACTAATA 1920
Qy 2421 AAGTATAATGTCATGTCTAATGCCAGACAAATGGCTTTTACACCTTTGCACGAAAGCA 2480
Db 1921 AAGTATAATGTCATCTCTAATGCCAGACAAATGGCTTTTACACCTTTGCACGAAAGCA 1980
Qy 2481 GCCCAAAAGGAGCGAAACACAGCTTTGTGTGCTAGCCCATGGAGCTGACCCGACT 2540
Db 1981 GCCCAAAAGGAGCGAAACACAGCTTTGTGTGCTAGCCCATGGAGCTGACCCGACT 2040
Qy 2541 CTTAAAAATCAGGAAGGACAAACACCTTTTATAGTTTTCAGGGATGATGTCAGCGCT 2600
Db 2041 CTTAAAAATCAGGAAGGACAAACACCTTTTATAGTTTTCAGCGATGATGTCAGCGCT 2100
Qy 2601 CTTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTCTTGTTCACAGCCCTCAAGTGCTC 2660
Db 2101 CTTCTGACAGCAGCCATGCCCCCATCTGCTCTGCCCTCTTGTTCACAGCCCTCAAGTGCTC 2160
Qy 2661 AATGAGTGTGAAGAGCCCGAGGAGCCACTGCAAGTGTCTCTCTCTCAGTCCATCTAGGCCA 2720
Db 2161 AATGAGTGTGAAGAGCCCGAGGAGCCACTGCAAGTGTCTCTCTCTCAGTCCATCTAGGCCA 2220
Qy 2721 TCAAGCCCTTTCTGAGCCAGCAGTCTTGACAACTTATCTGGGAGTTTTTTCAGACTGCT 2780
Db 2221 TCAAGCCCTTTCTGAGCCAGCAGTCTTGACAACTTATCTGGGAGTTTTTTCAGACTGCT 2280
Qy 2781 TCAGTAGTTAGTTCAAGTGGAAACAGAGGGTGTCTTCCAGTTTGGAGAAAAGAGGAGTTCCA 2840
Db 2281 TCAGTAGTTAGTTCAAGTGGAAACAGAGGGTGTCTTCCAGTTTGGAGAAAAGAGGAGTTCCA 2340
Qy 2841 GGAGTAGATTTTACGATPACTCAATTCGTAAGGAATCTTGAGACTTTGAGCACTTAATGGAT 2900
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Db 2207 TTGTTAAACATGAGCAGTAGTAAATGATAGTAGTGAATTTATGGAATTTTACACCTTTTACATG 2266
Qy 2017 AAGCAGCAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCAGCATGCTGAGACC 2076
Db 2267 AAGCAGCAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCAGCATGCTGAGACC 2326
Qy 2077 CTACCAAAAAACAGGGATGAAATPACTCTTTTGGATCTTGTAAAGATGGAGATACAG 2136
Db 2327 CTACCAAAAAACAGGGATGAAATPACTCTTTTGGATCTTGTAAAGATGGAGATACAG 2386
Qy 2137 ATATTCAAGATCTGTTAGGGAGATGCACTTTGCTAGATGCTGCCAAGAGGTTGTT 2196
Db 2387 ATATTCAAGATGTTAGGGAGATGCACTTTGCTAGATGCTGCCAAGAGGTTGTT 2446
Qy 2197 TAGCCAGAGTGAAGAGTTGTTCTTCTGATAATGTAATTTGCCGCGATACCCCAAGGCA 2256
Db 2447 TAGCCAGAGTGAAGAGTTTNTTCTTGATTAATGTAATTTGCCGCGATACCCCAAGGCA 2506
Qy 2257 GACATTCACACCTTTTACATTTAGCAGCT- - - - -GGTTATAATAATTTAGAGTTGCAG 2310
Db 2507 GACATTCACACCTTTTACATTTAGCAGGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2566
Qy 2311 AGTATTTGTTACACACGAGCTGATGTAATGCCCAAGACAGAGGACCTTATTCCTT 2370
Db 2567 NNN 2626
Qy 2371 TACATAATGTCAGCATCTTACGGGCATGTAGTAGCAGCTCTACTAATAAGATATAATG 2430
Db 2627 NNN 2686
Qy 2431 CATGTGTCAAATGCCAGCAAAATGGGCTTTTACACACTTTTGCAAGAGCAGCCCAAGG 2490
Db 2687 NNN 2746
Qy 2491 GACGAACACAGCTTTGTGCTTTGTTGCTAGCCATGGAGCTGACCCGACTCTTAAAAATC 2550
Db 2747 NNN 2806
Qy 2551 AGGAAGGACAAACACTTTAGATTTAGTTTACGCGATGATGTACGCGCTCTTCTGACAG 2610
Db 2807 NNN 2866
Qy 2611 CAGCCATGCCCATCTGCTGCGCTCTTGTGTACAAGCCTCAAGTGTCTCAATGGTGTGA 2670
Db 2867 CAGCCATGCCCATCTGCTGCGCTCTTGTGTACAAGCCTCAAGTGTCTCAATGGTGTGA 2926
Qy 2671 GAAGCCAGGAGCCACTGCGAGATGCTCTCTTTCAGGTCCTACTAGCCCATCAAGCCTTT 2730
Db 2927 GAAGCCAGGAGCCACTGCGAGATGCTCTCTTTCAGGTCCTACTAGCCCATCAAGCCTTT 2986
Qy 2731 CTGCGAGCCAGCAGCTTTCACACTTATCTGGAGTTTTCAGAACTGTCTTCAGTAGTTA 2790
Db 2987 CTGCGAGCCAGCAGCTTTCACACTTATCTGGAGTTTTCAGAACTGTCTTCAGTAGTTA 3046
Qy 2791 GTTCAAGTGAACAGAGGCTGCTCCAGTTTTCAGGAAAGAGGCTTCCAGAGTAGATT 2850
Db 3047 GTTCAAGTGAACAGAGGCTGCTCCAGTTTTCAGGAAAGAGGCTTCCAGAGTAGATT 3106
Qy 2851 TTAGCATAACTCAATTCGTAAGGAATCTTGGACTTTCAGCCTTAATGGATATATTTGAGA 2910
Db 3107 TTAGCATAACTCAATTCGTAAGGAATCTTGGACTTTCAGCCTTAATGGATATATTTGAGA 3166
Qy 2911 GAGAACAGATCACTTTGGATGTATTAGTTGAGATGGGCAAGAGCTGAAGGAGATTG 2970
Db 3167 GAGAACAGATCACTTTGGATGTATTAGTTGAGATGGGCAAGAGCTGAAGGAGATTG 3226
Qy 2971 GAATCAATGCTTATGACATAGGCAAACTAATTAAGAGGCTGAGAGACTTATCTCCG 3030
Db 3227 GWATCAATGCTTATGACATAGGCAAACTAATTAAGAGGCTGAGAGACTTATCTCCG 3286
Qy 3031 GACAAACAGGCTTAAACCATATTTAACTTTGAACACCTCTGGTAGTGGAACTTTCTTA 3090
Db 3287 GACAAACAGGCTTAAACCATATTTAACTTTGAACACCTCTGGTAGTGGAACTTTCTTA 3346

Qy 3091 TAGATCTCTCTCCTGATGATTAAGAGTTTCACTCTGTGGAGAAAGAGATGCAAAAGTACAG 3150
Db 3347 TAGATCTCTCTCCTGATGATTAAGAGTTTCACTCTGTGGAGAAAGAGATGCAAAAGTACAG 3406
Qy 3151 TTCGAGAGCAGAGATGGAGGTCATGAGGTGGAATCTTCAACAGATACAAATTTCTCA 3210
Db 3407 TTCGAGAGCAGAGATGGAGGTCATGAGGTGGAATCTTCAACAGATACAAATTTCTCA 3466
Qy 3211 AGATTTCAGAGGTTTGTAAACAAGAAACTATG- - - - -GGAAGAT 3249
Db 3467 AGATTTCAGAGGTTTGTAAACANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3526
Qy 3250 ACATCTCACCGGAGAAAGAGTTTCTGAAGAAAACCAACCATGCCCCTGAACGAATGC 3309
Db 3527 ACATCTCACCGGAGAAAGAGTTTCTGAAGAAAACCAACCATGCCCCTGAACGAATGC 3586
Qy 3310 TATTTCATGGGTCTCTTTTGTGGAATGCAATATTCACAAAAGGCTTGTATGAAAGCATG 3369
Db 3587 TATTTCATGGGTCTCTTTTGTGGAATGCAATATTCACAAAAGGCTTGTATGAAAGCATG 3646
Qy 3370 CGTACATAGTGGTATGTTTGGAGCTGCAATTTATTTTGTGAAACCTTCTCCAAAGCA 3429
Db 3647 CGTACATAGTGGTATGTTTGGAGCTGCAATTTATTTTGTGAAACCTTCTCCAAAGCA 3706
Qy 3430 ATCAATATGATATGGAATTTGGAGAGGTAATGCGGTGTCCAGTTTCAAAAGACAGATCTT 3489
Db 3707 ATCAATATGATATGGAATTTGGAGAGGTAATGCGGTGTCCAGTTTCAAAAGACAGATCTT 3766
Qy 3490 GTTACATTTGCCACAGGAGCTGCTCTTTTCCGGGTAACTTGGGAAAGTCTTTCTGTC 3549
Db 3767 GTTACATTTGCCACAGGAGCTGCTCTTTTCCGGGTAACTTGGGAAAGTCTTTCTGTC 3826
Qy 3550 AGTTTCAGTGCATGAAATGGACATTTCTCTCCAGGTCATCAGTCACTGCTGAGG 3609
Db 3827 AGTTTCAGTGCATGAAATGGACATTTCTCTCCAGGTCATCAGTCACTGCTGAGG 3886
Qy 3610 CCAGTGTAAATGGCTAGCATTTAGCTGAATATGTTATTTTACAGAGGAGAACAGGCTTATC 3669
Db 3887 CCAGTGTAAATGGCTAGCATTTAGCTGAATATGTTATTTTACAGAGGAGAACAGGCTTATC 3946
Qy 3670 CTGAGTATTTAATTACTTTACAGATTTAGAGGCTGAAGGTTATGTCGATGATATAATAG 3729
Db 3947 CTGAGTATTTAATTACTTTACAGATTTAGAGGCTGAAGGTTATGTCGATGATATAATAG 4006
Qy 3730 TTATTTTAAAGAACTTAATTTCCACTGAACCTTAATCATCAAGCAGCAGTGGCTCTAGG 3789
Db 4007 TTATTTTAAAGAACTTAATTTCCACTGAACCTTAATCATCAAGCAGCAGTGGCTCTAGG 4066
Qy 3790 TTTTACTCTTTTGTGAAAAAAA 3813
Db 4067 TTTTACTCTTTTGTGAAAAAAA 4090

Search completed: December 18, 2006, 21:40:51
Job time : 3883.64 secs

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QY 61 TGGCGCGGCCATGGGACTGCGCGCGGATCCGGTGAACAGAGGAGCCAAAGCGGCCCGGG 120
DB 217 TGGCGCGCGG-CCATGGGACTGCGCGCGATCCGGTGAACAGAGGAGCCAAAGCGGCCCGGG 275
QY 121 CCCTGAGCGGCTCTCTCCGGGGGGCTCGCCCTCTCTGCTCGGGGGCGCGGGCTCTCTGC 180
DB 276 CCCTGAGCGGCTCTCTCCGGGGGGCTCTCGCCCTCTCTGCTCGGGGGCGCGGGCTCTCTGC 335
QY 181 TCCGGTTGCTGGCGCTCTGCTGCTGTGGCGGCGGCCAGGATCATGTCGGGTGCGCGCT 240
DB 336 TCCGGTTGCTGGCGCTCTGCTGCTGTGGCGGCGGCCAGGATCATGTCGGGTGCGCGCT 395
QY 241 GCGCGCGGGGAGCGGCTCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 300
DB 396 GCGCGCGGGGAGCGGCTCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 455
QY 301 GAGAGCTGTTGAGGCGTCCGCAACGGGAGCTGGAAACGAGTCAAGAGGCTGGTGACGC 360
DB 456 GAGAGCTGTTGAGGCGTCCGCAACGGGAGCTGGAAACGAGTCAAGAGGCTGGTGACGC 515
QY 361 CTGAGAGGTTGAACAGCGCGGACACGCGCGGCGGAGAAATCCACCCGCTGCACCTTCGCG 420
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QY 421 CAGGTTTGGCGGAAAGAGCGTAGTTGAATATTTGCTTCAGAAATGGTGAATGTCCAAG 480
DB 576 CAGGTTTGGCGGAAAGAGCGTAGTTGAATATTTGCTTCAGAAATGGTGAATGTCCAAG 635
QY 481 CAGCTGATGATGGGGCTTATTCCTCTTCATATGATGCTCTTTTGGTTCATGCTCAAG 540
DB 636 CAGCTGATGATGGGGCTTATTCCTCTTCATATGATGCTCTTTTGGTTCATGCTCAAG 695
QY 541 TAGTCAATCTCTTTTCGACATGGTCAGACCCCAATGCTCGAGATAATTTGGAATTA 600
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QY 601 CTCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATTTGCAATTTGCTGTTCAGC 660
DB 756 CTCCTCTCCATGAAGCTGCAATTAAGGAAAGATTGATTTGCAATTTGCTGTTCAGC 815
QY 661 ATGGAGCTGAGCCAAACCATCCGAATACAGATGAAGGACAGCAATTCGATTTAGCAGATC 720
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QY 781 GGAGTGGCAATGAAGAAATAATGATGCTCTACTCAGACCAATTAATGTCNACTGCCACG 840
DB 936 GGAGTGGCAATGAAGAAATAATGATGCTCTACTCAGACCAATTAATGTCNACTGCCACG 995
QY 841 CAAGTGTGGCAGAAAGTCAACTCCATTAATTTGGCAGCAGGATATAACAGAGTAAGA 900
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DB 1116 TACCATTACCAATGCTGTCTTATGGTCATTAATGAAGTAACTGAATCTTTTGGTCAAGC 1175
QY 1021 ATGGTGCCTGTGTAATGCAATGACTTGTGGCAATTCACCTCTCTTCATGAGGACGCTT 1080
DB 1176 ATGGTGCCTGTGTAATGCAATGACTTGTGGCAATTCACCTCTCTTCATGAGGACGCTT 1235
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DB 1776 GCTTTACTGCTTTACAGATGGGAAAATGAATAATGTACAGCAACTCTCTCAAGAGGATATCT 1835
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QY 1741 AAACCTGTAAAAAACCTGTGTACTGTTTCAGAGTGTCAAATGTCAGAGACATTTGAAGGGGCTC 1800
DB 1896 AAACCTGTAAAAAACCTGTGTACTGTTTCAGAGTGTCAAATGTCAGAGACATTTGAAGGGGCTC 1955
QY 1801 AGTCTACACACTTCAATTTTGACGCTGGGTATAACAGAGTGTCCGTTGGGAATATCTGC 1860
DB 1956 AGTCTACACACTTCAATTTTGACGCTGGGTATAACAGAGTGTCCGTTGGGAATATCTGC 2015
QY 1861 TACAGCATGAGCTGATGTGCATGCTTAAAGATAAAGGAGGCTTGTACCTTTGACCAATG 1920
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DB 2076 CATGTTCTTTATGGACATTAATGAAGTTGCAGAACTTCTTTGTTAAACATGGAGCAGTAGTTA 2135
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QY 2161 ATGAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAGTGTCTT 2220
DB 2316 ATGAGCTTTGCTAGATGCTGCCAAGAGGGTGTGTTTAGCCAGAGTGAAGAGTGTCTT 2375
QY 2221 CTCTGTATAATGTAAATTTGCGCGGATACCCCAAGGACAGCATTCACACCTTTTACATTTAG 2280

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Db 3576 CCAAAAGCAATCAATATGTATATGGAATTTGAGAGGAGTACTGGGTGTCCAGTTCAAAAG 3635
Qy 3481 ACAGATCTTGTACATTTGCGACAGGAGCTGCTCTTTTGGCGGTAACCTTTGGGAAAGT 3540
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Qy 3601 CTGTAGGCCCAGTGTAAATGGCCCTAGCATTTAGCTGAATATGTTTATACAGAGGAGAAC 3660
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Qy 3661 AGGCTTATCTTCAGTATTTAAATTTACTTACCAGATTTATGAGGCTGAAGGTATGTCGATG 3720
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RESULT 2

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; Sequence 23602, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIORITY FILING DATE: 2005-11-03
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; PRIORITY FILING DATE: EP 04105507.0
; PRIORITY FILING DATE: 2004-11-03
; PRIORITY FILING DATE: EP 04105485.9
; PRIORITY FILING DATE: 2004-11-03
; PRIORITY FILING DATE: EP 04105484.2
; PRIORITY FILING DATE: 2004-11-03
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; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 23602
; LENGTH: 3815
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23602

Query Match 97.6%; Score 3724.8; DB 8; Length 3815;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 3726; Conservative		0; Mismatches	2; Indels	0; Gaps	0
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Qy	146	CCTCGCCCTCCTGCTCGCGGGGCGGGGCTCTGCTCCCGTTGCTGGCGCTGTGTGCTGGC	205		
Db	61	CCTCGCCCTCCTGCTCGCGGGGCGGGGCTCTGCTCCCGTTGCTGGCGCTGTGTGCTGGC	120		
Qy	206	TGTGGCGGGCGCAGGATCATGTTCGGGTGCGCGCTGCGCGCGGGGGAGCGCCCTGCCG	265		
Db	121	TGTGGCGGGCGCAGGATCATGTTCGGGTGCGCGCTGCGCGCGGGGGAGCGCCCTGCCG	180		
Qy	266	GAGCGCGCGCGCAGGCGCGGTGAGCGCGCGCCGACAGAGCTGTTCAGAGCGTGC CGCAA	325		
Db	181	GAGCGCGCGCGCAGGCGCGGTGAGCGCGCGCCGCGAGCTGTTCAGAGCGTGC CGCAA	240		
Qy	326	CGGGGACGTGGAAACGAGTCAAGAGGCTGTGTGACGCTTGAGAAAGTGAAACGCGCACAC	385		
Db	241	CGGGGACGTGGAAACGAGTCAAGAGGCTGTGTGACGCTTGAGAAAGTGAAACGCGCACAC	300		
Qy	386	GGCGGGCAGAAATCCACCCGCTGCACCTTCGCGCGCAGGTTTTGGCGGGAAAGACGTAGT	445		
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Qy	446	TGAATATTTCTTTCAGAACTGGTCAAAATGTC CAAGCACGTGATGATGGGGGCTTTATTC	505		
Db	361	TGAATATTTCTTTCAGAACTGGTGGAAATGTC CAAGCACGTGATGATGGGGGCTTTATTC	420		
Qy	506	TCTTCATAATGTCATGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCCTTTTGGCAGATGG	565		
Db	421	TCCTTCATAATGTCATGCTCTTTTGGTCACTGCTGAAGTAGTCAATCTCCTTTTGGCAGATGG	480		
Qy	566	TGCAGACCCCAATGCTCGAGATAATTTGGAAATATATCTCCTCTCGATGAAGCTGCAATTA	625		
Db	481	TGCAGACCCCAATGCTCGAGATAATTTGGAAATATATCTCCTCTCGATGAAGCTGCAATTA	540		
Qy	626	AGGAAGATTGATGTTTTGCAATGCTGCTGTTACAGCATGGAGCTGAGCCACCAATCCGAAA	685		
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Qy	746	TGAATATAAGAAAGATGAACCTTTAGAAAGTGCAGGAGTGGCAATGAAGAAAAATGAT	805		
Db	661	TGAATATAAGAAAGATGAACCTTTAGAAAGTGCAGGAGTGGCAATGAAGAAAAATGAT	720		
Qy	806	GGCTCTACTCACACCATTTAAATGTCACCTGCCAGCAAGTGATGGCAGAAAGTCAACTCC	865		
Db	721	GGCTCTACTCACACCATTTAAATGTCACCTGCCAGCAAGTGATGGCAGAAAGTCAACTCC	780		
Qy	866	ATTACATTTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTATTCTGCAACATGG	925		
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Qy	926	AGCTGATGCCATGCTTAAAGATAAAGGTGATCTGGTACCAATTAACAATGCCCTGTTCTTA	985		
Db	841	AGCTGATGCCATGCTTAAAGATAAAGGTGATCTGGTACCAATTAACAATGCCCTGTTCTTA	900		
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Db	901	TGCTGCAATTGAAGTAACTCAACTTTTGGTCAAGCATGGTGCCTGTGTAATGCAATGGA	960		
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Qy	1106	TCCTCTCTTAAGTTATGGTGAGACCCAAACATCTGCTCAATTTGTCAAAATGAAGTGTCTAT	1165		
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Db	1081	AGACTTGGCTCCACACCAAGTTAAAGAGATTGATCATATGAATTTAAAGGCCACTC	1140
Qy	1226	GTTGCTGCAAGCTGCACGAGAAGCTCATGTACTCGAATCAA AAAACATCTCTCTCTGGA	1285
Db	1141	GTTGCTGCAAGCTGCACGAGAAGCTCATGTACTCGAATCAA AAAACATCTCTCTCTGGA	1200
Qy	1286	AATGGTGAAATTTCAAGCATCCTCAAACA CATGAAA CAGCAATTCATTTGCTGCTGCATC	1345
Db	1201	AATGGTGAAATTTCAAGCATCCTCAAACA CATGAAA CAGCAATTCATTTGCTGCTGCATC	1260
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Db	1321	TGAAAAGACTAAAGAAATTTCTTGACTCCTCTGCACGCTGGCATCTGAGAAAGCTCATATGA	1380
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Qy	1526	GACTTCTCTACACAGAGCTGCATATTTGCTCATCTPACAAA CCTGCGCCTACTCTCTGAG	1585
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Qy	1706	ACAATTTGCTGGAAAGCTGCAAAAGGCTGGAGATGTGAAA ACTGTAAAAAAACTGTGTACTGT	1765
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Qy	1766	TCAGATGTCMACTGCAGAGACATTTGAAGGGGCTAGTCTACACC ACTTCATTTTCGAGC	1825
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Qy	1826	TGGGTATAACAGAGTGTCCGTGGTGGAAATATCTGCTACAGCATGGAGCTGATGTGCATGC	1885
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Qy	1946	TGCAGAACTCTCTGTTTAAACATGGACAGTAGTTTAATGTAGCTGATTTATGGAATTTTAC	2005
Db	1861	TGCAGAACTCTCTGTTTAAACATGGACAGTAGTTTAATGTAGCTGATTTATGGAATTTTAC	1920
Qy	2006	ACCTTTACATGAAGCAGCAGCAAAAGGAAAATATGAAA ATTTGCAAACTTCTGCTCCAGCA	2065
Db	1921	ACCTTTACATGAAGCAGCAGCAAAAGGAAAATATGAAA ATTTGCAAACTTCTGCTCCAGCA	1980
Qy	2066	TGTTGCGAGCCCTACNAAAAAAAAA CAGGATGGAATACTCCTTTGGATCTTTGTTAAGA	2125
Db	1981	TGTTGCGAGCCCTACNAAAAAAAAA CAGGATGGAATACTCCTTTGGATCTTTGTTAAGA	2040
Qy	2126	TGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGATGCAAGCTTTGCTAGATCTGCCAA	2185
Db	2041	TGGAGATACAGATATTTCAAGATCTGCTTAGGGGAGATGCAAGCTTTGCTAGATCTGCCAA	2100
Qy	2186	GAAGGGTTGTTTAGCCAGAGTGAAGAA GTTTGCTTCTCTGATAAATGTAAATTCGCCGA	2245
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 QY 2546 AAATCAGGAGCAACACCTTTAGATTTAGTTTTCAGCGGATGATGTCAGGCTCTTCT 2605
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 QY 2606 GACAGCAGCATGCCCCCATCTGCTCTGCTCTGCTTTTACAGGCTCAAGTCTCAATGG 2665
 Db 2521 GACAGCAGCATGCCCCCATCTGCTCTGCTCTGCTTTTACAGGCTCAAGTCTCAATGG 2580
 QY 2666 TGTGAGAGCCAGGAGCCATGCGAGATGCTCTCTCTTCAAGTCCATCTAGGCCCATCAAG 2725
 Db 2581 TGTGAGAGCCAGGAGCCATGCGAGATGCTCTCTCTTCAAGTCCATCTAGGCCCATCAAG 2640
 QY 2726 CCTTTCTGAGCAGCAGCTTTCACAACTTATCTGGAGTTTTCAGAACTGTCTTCAGT 2785
 Db 2641 CCTTTCTGAGCAGCAGCTTTCACAACTTATCTGGAGTTTTCAGAACTGTCTTCAGT 2700
 QY 2786 AGTTAGTTTCAAGTGAACAGAGGCTCTTCCAGTTTGGAGAAAAGGAGTTCCAGGAGT 2845
 Db 2701 AGTTAGTTTCAAGTGAACAGAGGCTCTTCCAGTTTGGAGAAAAGGAGTTCCAGGAGT 2760
 QY 2846 AGATTTTACGATTAATCTAATCTGTAAGGAATCTTGAGCTTGAGCACTTAATGATATAT 2905
 Db 2761 AGATTTTACGATTAATCTAATCTGTAAGGAATCTTGAGCTTGAGCACTTAATGATATAT 2820
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 Db 2821 TGAGAGAGACAGATCACTTTGGATGTATTAGTTGAGATGGGCAACAGGAGCTCAAGA 2880
 QY 2966 GATTCGAATCAATGCTTTATGAGCATAGGCACAACTTAATTAAGGAGTCGAGAGCTTAT 3025
 Db 2881 GATTCGAATCAATGCTTTATGAGCATAGGCACAACTTAATTAAGGAGTCGAGAGCTTAT 2940
 QY 3026 CTCGGGACAAAGGCTTTTAAACCCATATTTAACTTTGAACTCTGGTGGTGGAGCAAT 3085
 Db 2941 CTCGGGACAAAGGCTTTTAAACCCATATTTAACTTTGAACTCTGGTGGTGGAGCAAT 3000
 QY 3086 TCTTATAGATCTGCTCTGATGATTAAGAGTTTCAAGTCTGTTGGAGGAGAGATCAAG 3145
 Db 3001 TCTTATAGATCTGCTCTGATGATTAAGAGTTTCAAGTCTGTTGGAGGAGAGATCAAG 3060
 QY 3146 TACAGTTCCAGAGACAGAGATGGAGTCTATGAGTGAATCTTCAACAGATACAATAT 3205
 Db 3061 TACAGTTCCAGAGACAGAGATGGAGTCTATGAGTGAATCTTCAACAGATACAATAT 3120
 QY 3206 TCTCAAGATTTCAAGAGTTTGTAAACAGAAATCTATGGGAAAGATACACTCACCGGAGAA 3265
 Db 3121 TCTCAAGATTTCAAGAGTTTGTAAACAGAAATCTATGGGAAAGATACACTCACCGGAGAA 3180
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 Db 3181 AGAAGTTCTGAGAGAAACCAACCAATGCCAATGAAGATGCTTATTTTCATGGGTCTCC 3240
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Db 3241 TTTTGTGAATGCAATTTATCCAAAGGCTTTGATGAAAGGCATGCGTACATAGGTGGTAT 3300
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 Db 3301 GTTTGGAGCTGGCAATTTATTTTGTGTAAGAACTCTTCCAAAAGCAATCAATATGATATGG 3360
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 Db 3541 AGCATTAGCTCAATATGTTTATTACAGAGGAGAAACAGGCTTTATCTGAGTATTTAATTAC 3600
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 Db 3601 TTACCAGATTTATAGGCTGAAAGGTATGTTGATGATGATGATGATGATGATGATGATGAT 3660
 QY 3746 ATTCCACTGAACCTTAATATCAATCAAGCAGGAGGCTCTACGTTTACTCTCTTGTG 3805
 Db 3661 ATTCCACTGAACCTTAATATCAATCAAGCAGGAGGCTCTACGTTTACTCTCTTGTG 3720
 QY 3806 AAAAAAAA 3813
 Db 3721 AAAAAAAA 3728

RESULT 3
 US-11-266-748A-29428
 ; Sequence 29428, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnston, Patrick
 ; APPLICANT: Mulligan, Karl
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and
 ; TITLE OF INVENTION: Methods of Using the Same
 ; FILE REFERENCE: 55815-0102 (319189)
 ; CURRENT APPLICATION NUMBER: US/11/266.748A
 ; PRIOR FILING DATE: 2005-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105479.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105482.6
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105483.4
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105507.0
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105485.9
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105484.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: US 60/662,276
 ; PRIOR FILING DATE: 2005-03-14
 ; PRIOR APPLICATION NUMBER: US 60/700,293
 ; PRIOR FILING DATE: 2005-07-18
 ; NUMBER OF SEQ ID NOS: 483996
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 29428
 ; LENGTH: 4134
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-11-266-748A-29428

Db 2607 AAGGTGGTAAATTTCTCTTTCATTAATCGCGCATCTTATGGGCATGTTTCACATAGCGCT 2666
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 Db 2667 TTAATGATAAATAACAACAGTGTGTAATGCAAGATAAGTGGCGTCTTACTCCCTC 2726
 Qy 2472 CACGAAGCAGCCCAAAAGGAGCAACACAGCTTTTGTCTTTGCTAGCCCATGAGCT 2531
 Db 2727 CATGAAGCAGCCCAAAAGGAGGACGAGCTGTGGCCCTCTCTAGCGCATGTCGA 2786
 Qy 2532 GACCCGACTTTAAATACAGGAAGCAACACCTTTAGATTTAGTTTTCAGCGGATGAT 2591
 Db 2787 GACCCCAACCATGAAGAACAGGAAGGCGGAGCGCTCTGGATCTGGCAACAGCTCAGCAT 2846
 Qy 2592 GTACGCGCTTTCTGACAGCAGCATGCCCATCTGCTCTGCGCTCTTTGTTTACAGGCT 2651
 Db 2847 ATCAGAGCTTTGCTGATGATGCCATGCCCGGAGGCGCTTACCTACCTGTTTAAACCT 2906
 Qy 2652 CAAGTGTCTCAATGTTGTGAGAAAGCCGAGGCACTGCGAGATGCTCTCTTTGAGGTCCA 2711
 Db 2907 CAGG-----CTACTGTAGTGAGTGCCTCTCTGATCTCACCAGCA 2945
 Qy 2712 TCTAGCCCAATCAAGCTTTCTGCGCAGCAGTCTTGACAACTTATCTGGGAGTTTTCOA 2771
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 Qy 2772 GAACTGCTTCAAGTGTAGTTCAAGTGGAAAGGAGGCTTCCAGTTTGGAGAAAG 2831
 Db 3006 GAGTTGGCGGTAGGAGGAGCTTCAATGCGGGATGCGCGCGGGAACAGAAAGGAG 3065
 Qy 2832 -----GAGGTTCCAGGAGTAGATTTTAGCATAACTCAATTCGTAAAGAACTCTCGACTT 2885
 Db 3066 GAAGAGAGTTGCTGGTCTTGACATGATATCAGCCCAATTTCTAAAGAGCTTGGCCTT 3125
 Qy 2886 GAGCACCTTAATGATATATTTGAGAGAGAACAGATCACTTTGGATGTATTTAGTTGAGATG 2945
 Db 3126 GAAACCTTCCGGATATCTTTGAAACAGAACAGATTTACACTAGATGTGTGGCTGATATG 3185
 Qy 2946 GGGCACAGGAGCTCAAGAGATTGGATCAATGCTTATGGACATAGGACGACCAAACTAAT 3005
 Db 3186 GGTCAATGAAGATTGAAGAAATAGGCATCAATGATATAGGACCGGCCCAAAATTAATC 3245
 Qy 3006 AAAGAGTTCGAGAGACTTATCTCCGGAACAAGGCTTTAAACCCATATTTAACTTTGAAC 3065
 Db 3246 AAAGAGTAGAAGACTCTTAGTGGACAAAGGCAACCAATCTTTATTTGACTTTTTCAC 3305
 Qy 3066 ACCTCTGGTAGTGGAACTTTATAGATCTGTCTCTGTATGATAAGAGTTTCAGTCT 3125
 Db 3306 TGTGTTAATCAGGGAACGATTTTGTGCTGATCTTGTCTCCAGAAAGATAAAGAAATATCAGTCA 3365
 Qy 3126 GTGGAGGAGAGATGCAAGTACAGTTTCGAGAGCAGAGATGGAGGTTCATGCGGTGGA 3185
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 Qy 3306 ATGCTATTTCATGGGTCTCTTTTGTGAATGCAATTTATCCAAAGGCTTGTGATGAAGG 3365
 Db 3546 ATGTTGTTTCATGGTCTCTTTCTTCAATTAATGCAATTTATCAATAAGGGTTGTGATGAGCA 3605
 Qy 3366 CATGCTACATAGTGGTATGTTTGGAGCTGCAATTTATTTTGGCTGAAACTCTTTCCAAA 3425
 Db 3606 CATGATACATAGGAGGATGTTTGGGCGCGGATTTATTTTGTCTGAAACTCTCTCAAAA 3665
 Qy 3426 AGCAATCAATATGATATGGAATTTGGAGGAGTACTGGGTGTCAGTTTCACAAAGACAGA 3485
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Qy 3486 TCTTGTATCATTTTGCACAGGAGCTGCTCTTTTGGCCGGTAACCTTGGGAAAGTCTTTC 3545
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 Qy 3606 AGGCCAGTGTAAATGGCTAGCATTAAGTCAATATGTTTATACAGAGGAGAACAGCT 3665
 Db 3846 AGACCGAGCTCAATGGGCTGGCATATGCTGAATATGTCATCTACAGAGGAGAACAGGCA 3905
 Qy 3666 TATCTGAGTATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3708
 Db 3906 TACCAGAGTATCTTATCACTTACCAGATCATGAAGCCAGAG 3948

 RESULT 4
 US-11-266-748A-22929
 ; Sequence 22929, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnston, Patrick
 ; APPLICANT: Mulligan, Karl
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and
 ; TITLE OF INVENTION: Methods of Using the Same
 ; FILE REFERENCE: 55815-0102 (319189)
 ; CURRENT APPLICATION NUMBER: US/11/266.748A
 ; CURRENT FILING DATE: 2005-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105479.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105482.6
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105483.4
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105507.0
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105485.9
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105484.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: US 60/662,276
 ; PRIOR FILING DATE: 2005-03-14
 ; PRIOR APPLICATION NUMBER: US 60/700,293
 ; PRIOR FILING DATE: 2005-07-18
 ; NUMBER OF SEQ ID NOS: 483996
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 22929
 ; LENGTH: 8901
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-11-266-748A-22929

 Query Match 47.1%; Score 1796.4; DB 8; Length 8901;
 Best Local Similarity 72.5%; Pred. No. 0;
 Matches 2366; Conservative 0; Mismatches 871; Indels 27; Gaps 2;

 Qy 451 ATTTGCTTTCAGAAATGGTGCAATGTCCAAAGCACGATGATGGGGCCCTTATTCCTCTTC 510
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 Qy 511 ATATGCAATGCTCTTTTGGTCACTGATGAGTAGTCAATCTCTCTTCATGAGATGCTGAC 570
 Db 62 ATAATGCTGTCTTTTGGCCATGCTGAGGTGTGAGTCTGTATTGTCGAAGAGAGCTG 121
 Qy 571 ACCCAATGCTCGAGATAATTTGGAAATATATCTCTCCATGAACTGCAATTTAAAGGAA 630
 Db 122 ATCCAAATGCCAGGATTAACCTGGAACATAACCTCTGATGAAGTCTGTTTAAAGGA 181
 Qy 631 AGATTGATGTTTGCATGCTGCTGTTTACAGCATGGAGCTGAGCCCAACCAATCCGAAATACAG 690

Db 182 AGATCGATGTGTCATTTGCTGCTGCAGCAGCGAGCTGACCCAAACATTCGGAACTG 241
Qy
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Db 242 ATGGGAATCAGCCCTGGACCTGGCAGATCCTTCAGCAAAAGCTGTCTTTACAGGTTGAAT 301
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Qy 751 ATAGAAGATGACTCTTAGAAGTCCAGGAGTGCATAGAGAAATGATGGCTC 810
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Db 302 ACAAGAAAGACGAACCTCTAGAGCTCTAGGAGTGGTAATGAGAAATACTAATGGCTT 361
Qy
Qy 811 TACTCACACCAATTAATAGTCAACTGCCACGCAAGTGATGGCAGAAAGTCAACTCCATTAC 870
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Db 362 TACTGACTCTCTAAATGTGNAATTGCCATGCGAGTATGGCGNAAGTCCGACTCCTTTAC 421
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Qy 871 ATTTGGCAGCAGGATATAACAGAGTAAAGATTTGACAGCTGTTTACTGCAACATGGAGCTG 930
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Qy 931 ATGTCCATGCTAAGATAAAGGTGATCTGGTACCAATTTACACNAATGCCCTGTTCTTATGGTC 990
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Qy 991 ATATGAAGTAACAGAACTTTTGGTCAAGCATGTGCTGTGTAATGCAATGGACTTGT 1050
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Qy
Qy 1651 ATGTACAGCAACTCTCCAGAGGGTATCTCATTTAGGTAAATTCAGAGCAGCAGACAAT 1710
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Qy 1711 TGCTGGAGAGCTGCAAGGCTGGAGATGCGAAACTGTAAAAAAACTGTACTGTTCTCAGA 1770
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Db 1262 TCTTAGAGGCATCTAAGCTGGAGACTTGGAAACTGTGAGCAACTTTTGCAGCTCTCAAA 1321

Qy 1771 GTGTCAACTGCAGAGACATTTGAAGGGGTCAGTCTACACCACCTTCATTTTGCAGCTGGT 1830
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Qy 1831 ATAAACAGAGTGTCCGTGGTGGAAATATCTGTACAGCATGAGCTGATGTGCATGCTCTAAAG 1890
Db 1382 ACAACCGGTGTCTGTGTAGAGTACTGTCTACACACGGTGCAGATGTCATGCGCAAG 1441
Qy 1891 ATAAAGGAGGCTTTGATCCTTTTGCAAAATGATGTTCTTATGGACATTTATGAAGTTGCAG 1950
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Qy 2011 TACATGAAGCAGCAGCAAAAGGAAATATGAAATTTTGCAAACTTCTGCTCCAGCATGGT 2070
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Qy 2071 CAGACCTTACCAAAAAAACAAGGATGGAATACTCCTTTGGATCTTGTTTAAAGATGGAG 2130
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Qy 2131 ATACAGATTTCAAGATCTGCTTAGGGAGATGCAAGCTTTGCTAGATGCTGCCAAGAGG 2190
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Qy 2191 GTTGTTTAGCCAGAGTGAAGAGTGTCTTCTCTGATAATGTAAATTTGCCGCGATACCC 2250
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Db 1802 AGGCAGAAATTTCAACCCCTCTGCACTGGCAGCAGGCTATAATACTGGAAGTAGCTG 1861
Qy 2311 AGTATTTGTTCAACACGGAGCTGATGTGATGCCCAAGCAAAAGGAGGACTTTATTCCTT 2370
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Qy 2371 TACATATGCAAGCATTTACGGGCATGTAGATGTAGCAGCTCTACTAATAAAGATATAATG 2430
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Qy 2431 CATGTGTAATGCGACGCAAAATGGCTTTTACACCTTTTGCAGAAAGCAGCCCAAAAGG 2490
Db 1982 CGTGTGTAATGCAACAGATAAGTGGCGTTTACTCCCTCCATGAAGCAGCCCAAGAAAG 2041
Qy 2491 GACGAACACAGCTTTGTGCTTTGTGCTAGCCCATGGAGCTGACCCGACCTCTTAAAAATC 2550
Db 2042 GAAGGACGACGCTGTGGCCCTCTCTAGCGCATGGTGAGACCCCAACCATGAAGAAC 2101
Qy 2551 AGGAAGGACAAACACCTTTTAGATTTAGTTTTCAGCGATGATGTGAGCGCTCTTCTGACAG 2610
Db 2102 AGAAGGCCAGACGCTCTGGATCTGCAACAGCTGACGATATCAGAGCTTTGCTGATAG 2161
Qy 2611 CAGCCATGCCCCCATCTGCTCTGCCCTCTTGTAAAGCCTCAAGCTGCTCAATGGTGTGA 2670
Db 2162 ATGCCATGCCCCAGAGGCTTACCTACCTGTTTAAACCTCAGG----- 2206
Qy 2671 GAAGCCAGAGGCCCATGCGAGATGCTCTCTTTCAGGTCCATCTAGCCCAACAAGCCCTTT 2730
Db 2207 -----CTACTGTAGTGAAGTGCCTCTCTGATCTCACAGCATCCACCCCTCTCTGCTCT 2260
Qy 2731 CTGAGCGCAGCAGTCTTGACAACTTATCTGGAGTGTCTTTCAGAACTGTCTTTCAGTAGTTA 2790
Db 2261 CGGCTGCAGCAGCATAGACAACTCTACTGGCCCTTTTAGCAGAGTTGGCCGTAGGAGGAG 2320
Qy 2791 GTTCAAGTGGAAACAGAGGGTGTCTTCCAGTTTGGAGAAAAAG-----GAGTTTCCAGGAG 2844
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QY 3096 CTGCTCTCTGATGAT 3110
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Db 661 CTGCTCTCTGATGAT 675

RESULT 6
US-11-266-748A-311521/c
; Sequence 311521, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
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; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 311521
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-311521

Query Match 17.4%; Score 663.8; DB 8; Length 675;
Best Local Similarity 99.0%; Pred. No. 1.3e-151; Indels 0; Gaps 0;
Matches 668; Conservative 7; Mismatches 7;

QY 2436 GTCATGCCACGCAAAATGGGCTTTACACCTTTGCAGAGCAGCCCAAGGGACGA 2495
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Db 675 GTCATGCCACGCAAAATGGGCTTTACACCTTTGCAGAGCAGCCCAAGGGACGA 616

QY 2496 ACACAGCTTTGTGCTTTGTGCTAGCCCATGAGCTGACCCGACTCTTAAAAATCAGGAA 2555
| | | | | | | | | |
Db 615 ACACAGCTTTGTGCTTTGTGCTAGCCCATGAGCTGACCCGACTCTTAAAAATCAGGAA 556

QY 2556 GGACAAACACCTTTAGATTTAGTTTACAGGCTCAAGTCTCAATGGTGTGAGAGCC 2615
| | | | | | | | | |
Db 555 GGACAAACACCTTTAGATTTAGTTTACAGGCTCAAGTCTCAATGGTGTGAGAGCC 496

QY 2616 ATGCCCCCATCTGCTCTGCCCTTTGTTTACAGGCTCAAGTCTCAATGGTGTGAGAGCC 2675
| | | | | | | | | |
Db 495 ATGCCCCCATCTGCTCTGCCCTTTGTTTACAGGCTCAAGTCTCAATGGTGTGAGAGCC 436

QY 2676 CCAGAGCCATCTGACAGTCTCTCTCTTCAAGTCCATCTAGCCCATCAAGCCTTTCTGCA 2735
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Db 435 CCAGAGCCATCTGACAGTCTCTCTCTTCAAGTCCATCTAGCCCATCAAGCCTTTCTGCA 376

QY 2736 GCCAGCAGTCTTGACAACTTATCTGGAGTCTTTCAGAACTCTCTTCAGTAGTTAGTTCA 2795
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Db 375 GCCAGCAGTCTTGACAACTTATCTGGAGTCTTTCAGAACTCTCTTCAGTAGTTAGTTCA 316

QY 2796 AGTGGAAACAGAGGGTGTCTTCCAGTTTGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGC 2855
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Db 315 AGTGGAAACAGAGGGTGTCTTCCAGTTTGAGAAAAAGGAGGTTCCAGGAGTAGATTTTAGC 256
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Db 255 ATAACTCAATTCGTAAGGAATCTTGACCTTGAGCACCTAATGATATATTTGAGAGAGAA 196

QY 2916 CAGATCACCTTTGGATGCTATTAGTTGAGATGGGGCACAAGGAGCTGAAGGAGATTGGAATC 2975
| | | | | | | | | |
Db 195 CAGATCACCTTTGGATGCTATTAGTTGAGATGGGGCACAAGGAGCTGAAGGAGATTGGAATC 136

QY 2976 AATGCTTATGGACATAGGCACAACTAAATTAAGGAGTGGAGAGACTTATCTCCGGACAA 3035
| | | | | | | | | |
Db 135 AATGCTTATGGACATAGGCACAACTAAATTAAGGAGTGGAGAGACTTATCTCCGGACAA 76

QY 3036 CAAAGTCTTTAAACCATATTTAACTTTGAACACCTCTGGTAGTGAACAATTTCTATAGAT 3095
| | | | | | | | | |
Db 75 CAAAGTCTTTAAACCATATTTAACTTTGAACACCTCTGGTAGTGAACAATTTCTATAGAT 16

QY 3096 CTGCTCTCTGATGAT 3110
| | | | | | | | | |
Db 15 CTGCTCTCTGATGAT 1
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RESULT 7
US-11-266-748A-99554
; Sequence 99554, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99554
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-99554

Query Match 14.9%; Score 570; DB 8; Length 594;
Best Local Similarity 99.7%; Pred. No. 8.9e-129; Indels 2; Gaps 2;
Matches 592; Conservative 0; Mismatches 0;

QY 3213 ATTCAGAAGGTTTGTAAACAAG-AAACTATGGGAAGATACACTCACCGG-AGAAAAAGAG 3270
| | | | | | | | | |
Db 1 ATTCAGAAGGTTTGTAAACAAGAACTATGGGAAGATACACTCACCGGAAGAAAGAG 60

QY 3271 TTTCTGAAGAAACCAACCACTGCCAATGAACGAATGCTATTTCATGGGTCTCTTTTG 3330
| | | | | | | | | |
Db 61 TTTCTGAAGAAACCAACCACTGCCAATGAACGAATGCTATTTCATGGGTCTCTCTTTTG 120

QY 3331 TGAATGCAATTATCCACAAAGGCTTTGATGAAGGCATGCTACATAGGTGGTATGTTTG 3390
| | | | | | | | | |
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-189602

Query Match      14.0%; Score 535.6; DB 8; Length 929;
Best Local Similarity 74.0%; Pred. No. 2.8e-120;
Matches 679; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

QY 1707 CAATTGCTGGAAGCTGCAAGGCTGAGATGTCGAAACTGTAAAAAATCTGTGTACTGTT 1766
Db 12 CGACTCTTAGAGGCATCTAAAGCTGAGACTTGGAACTGTGAAGCAACTTTTGCAGCTCT 71
QY 1767 CAGAGTGTCACTGAGAGACATTTGAAGGGCTGAGTCTACACCACTTTCATTTGCGAGCT 1826
Db 72 CAAAATGTGAATTTAGAGACTTTAGAGGGCCGGCATTTCCACGCCCTTACACTTCGGAGCA 131
QY 1827 GGGTATAACAGAGTGTCCGTGCTGGAATATCTGCTACAGCATGGAGCTGATGTGATGCT 1886
Db 132 GGTACACACCGGTGTCTGTGTAGAGTACCTGCTACACACGGTGCCGATGTCCATGCC 191
QY 1887 AAAGATAAAGGAGGCTTGTACTTTTGCAATGCAATGTTCTTATGGACATTTATGAAGTT 1946
Db 192 AAAGACAAGGGTGGCTTGTGTGCCCCCTTCATAATGCCGTTCATATGGACACTATGAGGTG 251
QY 1947 GCAGAACTTCTTTTAAACATGAGCAGTGTATTTATGTAGCTGATTTATGGAAATTTTACA 2006
Db 252 GCTGAGCTTTTATAGTAAGGCATGGGGCTTCTGTCAATGTGGCGGACTTATGGAATTTTACC 311
QY 2007 CTTTACATGAAGCAGCAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCCAGCAT 2066
Db 312 CTTCTCCATGAAGCAGCAGCTTAAGGAAAGTATGAATTCGACGCTCTTTTAAACAT 371
QY 2067 GGTGAGAGCCCTTACCAAAAAAAGAGGATGAAATATCTCTTTGGATCTTGTAAAGAT 2126
Db 372 GGAGCAGATCCCACTTAAAGAAAGACAGAGATGAAATATACACCTTTGGATTTGGTAAAGGAA 431
QY 2127 GGAGATACAGATATTCAGATCTGCTTAGGGAGATGAGCTTTGCTAGATGCTGCCAAG 2186
Db 432 GGAGACACAGATATTCAGGACTTACTGAGAGGGGATGCTGCTTTGTTGATGCTGCCAAG 491
QY 2187 AAGGGTGTGTAGCCAGAGTGAAGAGTGTCTCTCTCTGATAATGTAAATTTGCCCGCAT 2246
Db 492 AAGGGCTGCTGCGAAGAGTGCNAGAGCTCTGTACCCAGAGATATCACTGCGAGAGAC 551
QY 2247 ACCAAGGAGACATTTCAACA CTTTACATTTAGCAGCTGGTTATTAATTTAGAAAGTT 2306
Db 552 ACCCAGGGCAGAAATTTCAACCCCTCTGCACTGCGAGCAGGCTATTAATTAACCTGGAAGTA 611
QY 2307 GCAGAGATTTGTTACACACGAGCTGATGTGATGCCCAAGACAAAGGAGGACTTATT 2366
Db 612 GCTGAATATCTTCTAGAGCATGGAGCTGATGTAAATGCCCCAGGACAAGGGTGGTTAAAT 671
QY 2367 CCTTTACATATATGCAAGCATCTTACGGGCAATGTAGATGTAGCAGCTCTACTATAAGATAT 2426
Db 672 CCTCTTCATATGCGGCATCTTATGGCATGTGTGATAGAGCGCTTTATGTATTAATATAC 731
QY 2427 AATGATGTGTCATATGCCAGCAAAATGGGCTTTTACACCTTTGCAAGAGCAGGCCAA 2486
Db 732 AACAGCTGTGTAATATGCAACAGATAAGTGGGCGTTTACTCCCTCCATGAAGCAGGCCAG 791
QY 2487 AAGGACGACACAGCTTTGTGCTTTGTTGCTTAGCCCATGGAGCTGACCCGACTCTTAA 2546
Db 792 AAAGGAAGGACGAGCTGTGCGCCCTCTCTCTAGGCGCATGGTGCAGACCCCAACCATGAAG 851
QY 2547 AATCAGGAAGGACAAACACCTTTTATGATTTTATGTTTTCAGCGGATGATGTACAGCGCTTCTCTG 2606
Db 852 AACAGGAAGGCGGACGAGCTCTGATCTGGCAACAGCTGACGATATCAGAGCTTTGCTG 911
QY 2607 ACAGCAGCCATGCCCCCA 2624
Db 912 ATAGATGCCATGCCCCCA 929
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RESULT 10
US-11-266-748A-55144
; Sequence 55144, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johneton, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55144
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-55144

Query Match      14.0%; Score 533.6; DB 8; Length 564;
Best Local Similarity 99.3%; Pred. No. 6.5e-120;
Matches 536; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3274 CTGAAGAAACCAACCAACCAATGCCAATGAACGAATGCTATTTCATGGTCTCTTTTGTGA 3333
Db 1 CTGAAGAAACCAACCAACCAATGCCAATGGAACATATGCTATTTCATGGTCTCTTTTGTGA 60
QY 3334 ATGCAATATTCACAAAGGCTTTGATGAAAGGATGCGTACATAGGTGATTTTGGAG 3393
Db 61 ATGCAATATTCACAAAGGCTTTGATGAAAGGATGCGTACATAGGTGATTTTGGAG 120
QY 3394 CTGGCATTTATTTTGTGTAAGAACTCTTCCAAAGCAATCAATATGATATGGAATTCGAG 3453
Db 121 CTGGCATTTATTTTGTGTAAGAACTCTTCCAAAGCAATCAATATGATATGGAATTCGAG 180
QY 3454 GAGGTACTGGGTGCTCCAGTTTCAAAAGACAGATCTTGTACATTTTGCACAGGCGCTGC 3513
Db 181 GAGGTACTGGGTGCTCCAGTTTCAAAAGACAGATCTTGTACATTTTGCACAGGCGCTGC 240
QY 3514 TCTTTTTCGGGTAACTCTTGGGAAAGTCTTTCTGCAAGTTTCAAGTCAATGAAATGGCAC 3573
Db 241 TCTTTTTCGGGTAACTCTTGGGAAAGTCTTTCTGCAAGTTTCAAGTCAATGAAATGGCAC 300
QY 3574 ATTCTCTCCAGTCACTCACTAGTCACTGGTAGGCCAGGTAAATGGCTAGCATTAG 3633
Db 301 ATTCTCTCCAGTCACTCACTAGTCACTGGTAGGCCAGGTAAATGGCTAGCATTAG 360
QY 3634 CTGAATATGTTTATTACAGAGGAGAAACAGGCTTTATCTGAGTATTTTAAATTTACCAGA 3693
Db 361 CTGAATATGTTTATTACAGAGGAGAAACAGGCTTTATCTGAGTATTTTAAATTTACCAGA 420
QY 3694 TTATGAGGCTGAAAGTATGGTTCGATGGAATAATAGTATTTTAAAGAAATTAATTCACCT 3753
Db 421 TTATGAGGCTGAAAGTATGGTTCGATGGAATAATAGTATTTTAAAGAAATTAATTCACCT 480
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Qy	3754	481	540
Db	GAACTTAAATCATCAAGCAGCAGTGGCTCTACGTTTTTCTCCTTTGCTGAAAAAAA	GAACTTAAATCATCAAGCAGCAGTGGCTCTACGTTTTTCTCCTTTGCTGAAAAAAA	GAACTTAAATCATCAAGCAGCAGTGGCTCTACGTTTTTCTCCTTTGCTGAAAAAAA

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RESULT 11
US-11-266-748A-217436
; Sequence 217436, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 5815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 217436
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-217436

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Query Match	14.0%;	Score 533.6;	DB 8;	Length 564;
Best Local Similarity	99.3%;	Pred. No. 6.5e-120;		
Matches 536;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
QY	3274	CTGAAGAAAACCAACCATGCGCAATCGAACGAATGCTATTTCATGGGCTCTCCTTTTGTGA	3333	
DB	1	CTGAAGAAAACCAACCATGCGCAATGCTATTTCATGGGCTCTCCTTTTGTGA	60	
QY	3334	ATGCAATTATCCAAAGGCTTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTCGGAG	3393	
DB	61	ATGCAATTATCCAAAGGCTTTTGATGAAAGGCATGCGTACATAGGTGGTATGTTTCGGAG	120	
QY	3394	CTGGCATTTATTTGCTGAAAACCTCTCCAAAGCAATCAATGTATATGGAATTCGGAG	3453	
DB	121	CTGGCATTTATTTGCTGAAAACCTCTCCAAAGCAATCAATGTATATGGAATTCGGAG	180	
QY	3454	GAGGTACTGGGTGTCCAGTTTCACAAAGACAGATCTCTGTTCATTTGCCACAGGCAGCTGC	3513	
DB	181	GAGGTACTGGGTGTCCAGTTTCACAAAGACAGATCTCTGTTCATTTGCCACAGGCAGCTGC	240	
QY	3514	TCCTTTGCCGGGTAAACCTTGGGAAAGTCTTTCCTGCAGTTTCAGTGCATGAAATGGCAC	3573	
DB	241	TCCTTTGCCGGGTAAACCTTGGGAAAGTCTTTCCTGCAGTTTCAGTGCATGAAATGGCAC	300	
QY	3574	ATTCTCTCTCAGGTGCATCACTCAGTCACTGGTAGGCCAGGTGTAATAATGGCCTAGCATTTAG	3633	
DB	301	ATTCTCTCTCAGGTGCATCACTCAGTCACTGGTAGGCCAGGTGTAATAATGGCCTAGCATTTAG	360	
QY	3634	CTGAATATGTTATTTACAGAGGAAACAGGCTTATCTCTGAGTATTTTAAATCTTTACCAGA	3693	
DB	361	CTGAATATGTTATTTACAGAGGAAACAGGCTTATCTCTGAGTATTTTAAATCTTTACCAGA	420	

3694	Qy	TTATGAGGCGCTGAAGGTATGTCGATGGATAAATAGTTATTTTAAAGAACTAATTCGACT	3753
421	Db	TTATGAGGCGCTGAAGGTATGTCGATGGATAAATAGCTATTTTAAAGAACTAATTCGACT	480
3754	Qy	GAACTTAAATCATCAAGCAGCAGTGGCGCTCTACGTTTTTACTCCTTGTGTAAGAAAAA	3813
481	Db	GAACTTAAATCATCAAGCAGCAGTGGCGCTCTACGATTACTCCTTGTGTAAGAAAAA	540

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RESULT 12
US-11-266-748A-165504/c
; Sequence 165504, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 165504
; LENGTH: 668
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (220)..(228)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-165504

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Query Match	13.5%;	Score 515.6;	DB 8;	Length 568;
Best Local Similarity	97.6%;	Pred. No. 1.7e-115;		
Matches 518;	Conservative 0;	Mismatches 13;	Indels 0;	Gaps 0;
QY	1663	TCCTCCAAGAGGGTATCTCATTTAGGTAAATTCAGAGGCACAGACAAATTCGTCGAAGCTG	1722	
Db	646	TCTCTACAAGAGGGTATCTCATTTAGGTAAATTCAGAGGCACAGACAAATTCGTCGAGCTG	587	
QY	1723	CAAAGGCTCGAGATGTCGAAAACGTGTAAAAAACTGTGTACTGTTACAGAGTGTCAACTGCA	1782	
Db	586	CAAAGGCTCGAGATGTCGAAAACGTGTAAAAAACTGTGTACTGTTACAGAGTGTCAACTGCA	527	
QY	1783	GAGACATTGAAGGGCGTCAGTCTACACACATTCATTTTCGACGCTGGGTATACAGAGTGT	1842	
Db	526	GAGACATTGAAGGGCGTCAGTCTACACACATTCATTTTCGACGCTGGGTATACAGAGTGT	467	
QY	1843	CCGTGTTGCAATATCTGCTACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCC	1902	
Db	466	CCGTGTTGCAATATCTGCTACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGGCC	407	
QY	1903	TTGTACCTTTTGCACAATGCATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTTGTTA	1962	

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Db 406 TTGTACCTTTGCACAAATGCATGTTCTTATTGACATTATGAAGTTGCAGAACTTCTTGTTA 347
QY 1963 AACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAATTTACCTTTACATGAAGCAG 2022
Db 346 AACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAATTTACACCTTTACATGAAGCAG 287
QY 2023 CAGCAAAAGGAAATATGAAATTTCAAACTTCTGCTCCAGCATGGTGCAGACCCTTACCA 2082
Db 286 CAGCCAAAGGAAATATGAAATTTGAAACTTCTGCTCCAGCATGGTGCAGACCCTTACNN 227
QY 2083 AAAAAACAGGATGGAATATCTCTTTTGGATCTTTGTTAAAGATGGAGATACAGATATTC 2142
Db 226 NNNNNNCAGGATGGAATATCTCTTTTGGATCTTTGTTAAAGATGGAGATACAGATATTC 167
QY 2143 AAGATCTGCTTAGGGAGATGCAGCTTTGCTAGATGCTGCTCCAAAGAGGTT 2193
Db 166 AAGATCTGCTTAGTGAGATGCAGCTTTGCTAGATGCTGCTCCAAAGAGGTT 116

RESULT 13
US-11-266-748A-244089
; Sequence 244089, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 244089
; LENGTH: 668
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (441)..(449)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-244089

Query Match 13.5%; Score 515.6; DB 8; Length 668;
Best Local Similarity 97.6%; Pred. No. 1.7e-115;
Matches 518; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1663 TCCTCCAGAGGGTATCTCATTAGGTAAATTCAGAGGCAGACAGACAATTCGTGGAGCTG 1722
Db 23 TCCTACAGAGGGTATCTCATTAGGTAAATTCAGAGGCAGACAGACAATTCGTGGAGCTG 82
QY 1723 CAAGGCTGGAGATGTCGAAATCTGTAATAAATACTGTGTAAGTTCAGAGTGTCAACTGCA 1782
Db 83 CAAGGCTGGAGATGTCGAAATCTGTAATAAATACTGTGTAAGTTCAGAGTGTCAACTGCA 142
QY 1783 GAGACATTGAAGGGGCTCAGTCTACACCCTTCATTTTGCAGCTGGGTATACAGAGTGT 1842
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Db 143 GAGACATTGAAGGGGCTCAGTCTACACCCCTTCATTTTGCAGCTGGGTATACAGAGTGT 202
QY 1843 CCGTGGTGAATATCTGCTACAGCATGGAGCTGATGTCATGCTAAAGATAAAGAGGCC 1902
Db 203 CCGTGGTGAATATCTGCTACAGCATGGAGCTGATGTCATGCTAAAGATAAAGAGGCC 262
QY 1903 TTGTACCTTTGCACAAATGCATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTGTTA 1962
Db 263 TTGTACCTTTGCACAAATGCATGTTCTTATGGACATTTATGAAGTTGCAGAACTTCTTGTTA 322
QY 1963 AACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAATTTACACCTTTTACATGAAGCAG 2022
Db 323 AACATGGAGCAGTAGTTAATGTAGCTGATTTATGGAATTTACACCTTTTACATGAAGCAG 382
QY 2023 CAGCAAAAGGAAATATGAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCTTACCA 2082
Db 383 CAGCCAAAGGAAATATGAAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCTTACNN 442
QY 2083 AAAAAACAGGATGGAATATCTCTTTTGGATCTTTGTTAAAGATGGAGATACAGATATTC 2142
Db 443 NNNNNNCAGGATGGAATATCTCTTTTGGATCTTTGTTAAAGATGGAGATACAGATATTC 502
QY 2143 AAGATCTGCTTAGGGAGATGCAGCTTTGCTAGATGCTGCTCCAAAGAGGTT 2193
Db 503 AAGATCTGCTTAGTGAGATGCAGCTTTGCTAGATGCTGCTCCAAAGAGGTT 553

RESULT 14
US-11-266-748A-116071
; Sequence 116071, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 116071
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-116071

Query Match 13.2%; Score 503.2; DB 8; Length 1000;
Best Local Similarity 76.2%; Pred. No. 2.3e-112;
Matches 619; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 2897 GGATATATTGAGAGAGAACAGATCATTCTTGGATGTATTGATTGAGATGGGGCACAAGGA 2956
Db 3 GGATATCTTTGAACACAGACAGATTACACTAGATGTGTTGGCTGATATGGGTATGGAAGA 62
```


Qy 3677 TTTAATTACTTACCAGATTATGAGGCCTGAAG 3708
| | | | | | | | | | | | | | | | | | | | | |
Db 218 TCTTATCACTTACCAGATCATGAGCCAGAAG 187

Search completed: December 18, 2006, 19:31:42
Job time : 762.887 secs

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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:21:00 ; Search time 139.536 Seconds
(without alignments)
3489.682 Million cell updates/sec

Title: US-10-616-101-3
Perfect score: 5585
Sequence: 1 GFGRRKDVVEYLLQNGASVQA.....AMKMAHSPGHHVSGRPSV 1065

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5585	100.0	1065	9	Ady97761 Human tan
2	5585	100.0	1083	9	Ady97770 Human tan
3	5585	100.0	1084	6	Abg73736 Tankyrase
4	5585	100.0	1100	4	Aay97748 Tankyrase
5	5585	100.0	1100	6	Abg73732 Tankyrase
6	5585	100.0	1100	6	Abg73730 Tankyrase
7	5585	100.0	1100	7	Adh69405 Human tan
8	5585	100.0	1100	9	Ady97766 Human tan
9	5582	99.9	1166	4	Aab66295 Human tan
10	5582	99.9	1166	5	Abp69457 Human pol
11	5582	99.9	1166	8	Adr14792 Amino aci
12	5582	99.9	1169	4	Aab66288 Human tan
13	5582	99.9	1169	4	Aab66278 Human tan
14	5582	99.9	1240	4	Aay97749 Tankyrase
15	5582	99.9	1240	6	Abg73731 Tankyrase
16	5582	99.9	1240	7	Adh69406 Human tan
17	5582	99.9	1240	9	Ady97762 Human tan
18	5582	99.9	1262	4	Aab66290 Human tan
19	5582	99.9	1287	8	Adr66429 Human pro
20	5582	99.9	1287	8	Adr66087 Human pro
21	5582	99.9	1385	4	Aab66294 Human tan
22	5579	99.9	1100	6	Abg73735 Tankyrase
23	5579	99.9	1100	9	Ady97769 Human tan

24	5566	99.7	1166	3	AAB27211	Human tan
25	5533	99.1	1166	4	AAy72589	Human tan
26	5421	97.1	1074	2	AAy05734	Human Gb
27	5017	89.8	1166	4	ABa47022	Human SA
28	4974	89.1	1083	6	AAE35352	Human col
29	4748.5	85.0	1333	3	AAB27209	Human tan
30	4740.5	84.9	1327	3	AAy44402	Human tan
31	4740.5	84.9	1327	3	AAB27212	Human tan
32	4740.5	84.9	1327	4	AAb66279	Human tan
33	4740.5	84.9	1327	5	AAU79537	Human tan
34	4740.5	84.9	1327	8	ADR14791	Amino aci
35	4675	83.7	1431	3	AAB27210	Human tan
36	4523.5	81.0	991	4	AAAB47023	Mouse SPA
37	4440.5	79.5	907	4	AAAB48574	Human bre
38	3918	70.2	784	4	AAb66285	Human tan
39	3775	67.6	756	4	AAb66286	Human tan
40	3706.5	66.4	1181	4	ABE60894	Drosophil
41	3706.5	66.4	1181	4	ABE60894	Drosophil
42	3412	61.1	802	5	AAO20512	Protein o
43	3093	55.4	949	3	AAy44404	Human tru
44	3093	55.4	949	5	AAU79539	Truncated
45	2916	52.2	583	9	ADY97768	Human tan

ALIGNMENTS

RESULT 1
ID ADY97761 standard; protein; 1065 AA.
AC ADY97761;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human tankyrase homologue isotype 1 protein SEQ ID NO:3.
XX
KW cell cycle; cancer; cytosolic; tankyrase homologue isotype 1.
XX
OS Homo sapiens.
XX
PN US2005074825-A1.
XX
PD 07-APR-2005.
XX
PF 08-JUL-2003; 2003US-00616101.
XX
PR 25-OCT-1999; 99US-00427154.
PR 25-OCT-2000; 2000US-00696668.
PR 25-APR-2001; 2001US-00843159.
XX
PA (LUOY/) LUO Y.
PA (CHAN/) CHAN E.
PA (XUXU/) XU X.
PA (HUAN/) HUANG B.
XX (OSSO/) OSSOVSKAYA V.
PI Luo Y, Chan E, Xu X, Huang B, Ossovskaya V;
XX WPI; 2005-294737/30.
DR N-PSDB; ADY97759.
XX
PT Novel recombinant polypeptide such as cell cycle protein e.g. tankyrase homolog, useful for screening its modulator.
XX
XX Claim 21; SEQ ID NO 3; 75pp; English.
CC The invention relates to a recombinant polypeptide (I) such as cell cycle protein e.g. tankyrase homologue (TaHo), comprising an amino acid sequence having 85% or more sequence identity to the 1065 amino acid sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also described: (I) diagnosing cancer, which involves determining the activity of (I) from a test sample of an individual and comparing the level with a

CC control with a control; (2) treating (M1) an individual with a cell cycle
 CC related disorder, which involves administering to the individual an
 CC inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (I),
 CC comprising a nucleic acid that hybridizes under high stringent conditions
 CC to a sequence complementary to the 3797 base pair sequence of ADY97759 or
 CC the 3816 base pair sequence of ADY97760, or a nucleic acid having 85% or
 CC more sequence identity to ADY97759 or ADY97760; (4) an expression vector
 CC (III) comprising (II) operably linked to regulatory sequences recognized
 CC by a host cell (IV) transformed with the nucleic acid; (5) a host cell
 CC specifically binds to (I); and (6) producing (I); (7) a polypeptide that
 CC specifically binds to (I); and (8) inhibiting (M2) growth of a tumor
 CC cell, involves contacting the tumor with a bioactive agent capable of
 CC inhibiting TaHo activity. (I) is useful for screening a bioactive agent
 CC capable of modulating (I), or screening for agents capable of interfering
 CC with the binding of (I) and P21. (M1) is useful for treating an
 CC individual with a cell cycle related disorder. (M2) is useful for
 CC inhibiting growth of a tumor cell by a bioactive agent e.g. antisense
 CC oligonucleotide. The present sequence represents the human tankyrase
 CC homologue isotype 1.
 XX
 SQ Sequence 1065 AA;

Query Match 100.0%; Score 5585; DB 9; Length 1065;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGKDVVEYLLQNGASVOARDGGLIPLHNACSPGHAEVNVNLLRHGADPNARDNNVYT 60
 DB 1 GFGKDVVEYLLQNGASVOARDGGLIPLHNACSPGHAEVNVNLLRHGADPNARDNNVYT 60

QY 61 PLHEAAIKGKIDVCIVLQHGAEPIRTDGTALDADPSAKAVLTGEYKDELLSAR 120
 DB 61 PLHEAAIKGKIDVCIVLQHGAEPIRTDGTALDADPSAKAVLTGEYKDELLSAR 120

QY 121 SGNEKMWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 180
 DB 121 SGNEKMWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 180

QY 181 PLHNACSYGHYEVTELLVKHGACVNMADLWQFTPLHEAASKNVRVCSLLLSYGADPTLL 240
 DB 181 PLHNACSYGHYEVTELLVKHGACVNMADLWQFTPLHEAASKNVRVCSLLLSYGADPTLL 240

QY 241 NCHNKSALDAPLPOLKERLAYEFKHSLLQAREADVTRIKKHSLEWVNFKHPQTHET 300
 DB 241 NCHNKSALDAPLPOLKERLAYEFKHSLLQAREADVTRIKKHSLEWVNFKHPQTHET 300

QY 301 ALHCAAASPYPRKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVVVKEAKV 360
 DB 301 ALHCAAASPYPRKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVVVKEAKV 360

QY 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISLQFTALQMGNEVQQLLQEGIS 420
 DB 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISLQFTALQMGNEVQQLLQEGIS 420

QY 421 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
 DB 421 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480

QY 481 QHGADVHAKDGGVLVPLHNACSYGHYEAELLVKGAVNVNADLWKFTPLHEAAAKGYE 540
 DB 481 QHGADVHAKDGGVLVPLHNACSYGHYEAELLVKGAVNVNADLWKFTPLHEAAAKGYE 540

QY 541 ICKLLLQHGADPTKKNRGNTPLDLVKDGDITDQLLRGDAALLDAAKGCLARVKLLSS 600
 DB 541 ICKLLLQHGADPTKKNRGNTPLDLVKDGDITDQLLRGDAALLDAAKGCLARVKLLSS 600

QY 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
 DB 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660

QY 661 VAALLIKYNACVNTDKWAFPLHEAAKGRQTLQCALLAHGADPTLKNQEGQTPDLVLVS 720
 DB 661 VAALLIKYNACVNTDKWAFPLHEAAKGRQTLQCALLAHGADPTLKNQEGQTPDLVLVS 720

QY 721 ADDVSALLTAAMPSPALPCYKPOVLNGVRSPGATADALSSGFPSSSLSAASLDNLG 780
 DB 721 ADDVSALLTAAMPSPALPCYKPOVLNGVRSPGATADALSSGFPSSSLSAASLDNLG 780

QY 781 SFSELSVVSSSGTSGASSLEKKEVGVDFSIQFVRNLGLEHLMDFIFEREQITLDVLE 840
 DB 781 SFSELSVVSSSGTSGASSLEKKEVGVDFSIQFVRNLGLEHLMDFIFEREQITLDVLE 840

QY 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILDLSPDDKEFQ 900
 DB 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILDLSPDDKEFQ 900

QY 901 SYVEEEMQSTVREHRDGGHAGGIFNRYNIIKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960
 DB 901 SYVEEEMQSTVREHRDGGHAGGIFNRYNIIKIQKVCNKKLWERYTHRRKEVSEENHNHANE 960

QY 961 RMLFHGSPFVNAI IHKGFDERHAYIGMEFAGIYFAENSCKSNQYVYGIGGTCGPVHKD 1020
 DB 961 RMLFHGSPFVNAI IHKGFDERHAYIGMEFAGIYFAENSCKSNQYVYGIGGTCGPVHKD 1020

QY 1021 RSCYICHRQLLCFVRTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
 DB 1021 RSCYICHRQLLCFVRTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065

RESULT 2
 ADY97770
 ID ADY97770 standard; protein; 1083 AA.
 XX ADY97770;
 AC ADY97770;
 DT 16-JUN-2005 (first entry)
 DE Human tankyrase homologue isotype 1 mutant protein SEQ ID NO:12.
 KW cell cycle; cancer; cytostatic; tankyrase homologue isotype 1; mutuin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX US2005074825-A1.
 PN 07-APR-2005.
 PD 08-JUL-2003; 2003US-00616101.
 PF 25-OCT-1999; 99US-00427154.
 PR 25-OCT-2000; 2000US-00696668.
 PR 25-APR-2001; 2001US-00843159.
 XX (LUOY/) LUO Y.
 PA (CHAN/) CHAN E.
 PA (XUX/) XU X.
 PA (HUAN/) HUANG B.
 PA (OSSO/) OSSOVSKAYA V.
 XX
 PI Luo Y, Chan E, Xu X, Huang B, Ossovskaya V;
 XX WPI; 2005-294737/30.
 DR
 XX
 PT Novel recombinant polypeptide such as cell cycle protein e.g. tankyrase
 PT homolog, useful for screening its modulator.
 XX
 XX Disclosure; SEQ ID NO 12; 75pp; English.
 PS
 CC The invention relates to a recombinant polypeptide (I) such as cell cycle
 CC protein e.g. tankyrase homologue (TaHo), comprising an amino acid
 CC sequence having 85% or more sequence identity to the 1065 amino acid
 CC sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also
 CC described: (1) diagnosing cancer, which involves determining the activity
 CC of (I) from a test sample of an individual and comparing the level with a
 CC control with a control; (2) treating (M1) an individual with a cell cycle

CC related disorder, which involves administering to the individual an
CC inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (I),
CC comprising a nucleic acid that hybridizes under high stringent conditions
CC to a sequence complementary to the 3797 base pair sequence of ADY97759 or
CC the 3816 base pair sequence of ADY97760, or a nucleic acid having 85% or
CC more sequence identity to ADY97759 or ADY97760; (4) an expression vector
CC (III) comprising (II) operably linked to regulatory sequences recognized
CC by a host cell (IV) transformed with the nucleic acid; (5) a host cell
CC comprising (II) or (III); (6) producing (I); (7) a polypeptide that
CC specifically binds to (I); and (8) inhibiting (M2) growth of a tumor
CC cell, involves contacting the tumor with a bioactive agent capable of
CC inhibiting TaHo activity. (I) is useful for screening a bioactive agent
CC capable of modulating (I), or screening for agents capable of interfering
CC with the binding of (I) and P21. (M1) is useful for treating an
CC individual with a cell cycle related disorder. (M2) is useful for
CC inhibiting growth of a tumor cell by a bioactive agent e.g. antisense
CC oligonucleotide. The present sequence represents a human tankyrase
CC homologue isotype 1 mutant protein.
XX
SQ Sequence 1083 AA;

Query Match 100.0%; Score 5585; DB 9; Length 1083;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGKDVVEYLLQNGASVOARDGGGLPLHNACSGHAEVNNLLRHGADPNARDNNYVT 60
Db 1 GFGKDVVEYLLQNGASVOARDGGGLPLHNACSGHAEVNNLLRHGADPNARDNNYVT 60

Qy 61 PLHEAAIKGIDVICVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKKDELLESAR 120
Db 61 PLHEAAIKGIDVICVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKKDELLESAR 120

Qy 121 SGNEEKWALLTPLVNCHASGRKSTPLHLAAGYNNRVIQVLLQHGADVHAKDGLV 180
Db 121 SGNEEKWALLTPLVNCHASGRKSTPLHLAAGYNNRVIQVLLQHGADVHAKDGLV 180

Qy 181 PLHNACSYGHVEVTELLVKGACVNMADLWQFTPLHEAASKNRVVCSSLISYGDPTLL 240
Db 181 PLHNACSYGHVEVTELLVKGACVNMADLWQFTPLHEAASKNRVVCSSLISYGDPTLL 240

Qy 241 NCHNKSALDAPTPOLKRLAYEFKGHSLLQAREADVTRIKKHSLEWVNFKHPQTHET 300
Db 241 NCHNKSALDAPTPOLKRLAYEFKGHSLLQAREADVTRIKKHSLEWVNFKHPQTHET 300

Qy 301 ALHCAAASPYPKRQICELLIRKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAKV 360
Db 301 ALHCAAASPYPKRQICELLIRKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAKV 360

Qy 361 NALDNLGQTSLHRAAYCGHLOQTCRLLSYGCDPNIIISQGTALQNGNENVOQLLQEGIS 420
Db 361 NALDNLGQTSLHRAAYCGHLOQTCRLLSYGCDPNIIISQGTALQNGNENVOQLLQEGIS 420

Qy 421 LGNSEADROLLEAAKAGDVETVKKLTQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 421 LGNSEADROLLEAAKAGDVETVKKLTQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480

Qy 481 QHGADVHAKDGGGLVPLHNACSYGHVEVAELLVKGAVVNVADLWKFTPLHEAAKAGKYE 540
Db 481 QHGADVHAKDGGGLVPLHNACSYGHVEVAELLVKGAVVNVADLWKFTPLHEAAKAGKYE 540

Qy 541 ICKLLOHGADPTKKNRDNTPDLVKGDDTDIQLLRGDAALLDAKKGCLARVKLLSS 600
Db 541 ICKLLOHGADPTKKNRDNTPDLVKGDDTDIQLLRGDAALLDAKKGCLARVKLLSS 600

Qy 601 PNVNCRDTQGRHSPTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 601 PNVNCRDTQGRHSPTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660

Qy 661 VAALLIKYNACVNTDKWAFPLHEAAQKGRTOQLCALLLHAGADPTLKNQEQOTPLDLVS 720
Db 661 VAALLIKYNACVNTDKWAFPLHEAAQKGRTOQLCALLLHAGADPTLKNQEQOTPLDLVS 720

721 ADDVSALLTAAMPSPALPSCYKQVNLGVRSPGATADALSSGSPSPSSLSAASSLDNLSSG 780
721 ADDVSALLTAAMPSPALPSCYKQVNLGVRSPGATADALSSGSPSPSSLSAASSLDNLSSG 780

781 SFSELSSVSSSGTEGASSLEKKEVPGVDFTQVVRNLGLEHLMDFEREQITLDVLVE 840
781 SFSELSSVSSSGTEGASSLEKKEVPGVDFTQVVRNLGLEHLMDFEREQITLDVLVE 840

841 MGHKELKEIGINAYGHRHKLKGVERLISGOOGLNPYLTLNTSGSGTILDLSPDDKEFQ 900
841 MGHKELKEIGINAYGHRHKLKGVERLISGOOGLNPYLTLNTSGSGTILDLSPDDKEFQ 900

901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQKVCNKKLWERYTHRRKEVSENNHANE 960
901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQKVCNKKLWERYTHRRKEVSENNHANE 960

961 RMLFHGSPFVNAILHKGFDERHAYIGGFMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD 1020
961 RMLFHGSPFVNAILHKGFDERHAYIGGFMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD 1020

1021 RSCYICHRQLLFCRVTLCKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
1021 RSCYICHRQLLFCRVTLCKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065

RESULT 3
ABG73736
ID ABG73736 standard; protein; 1084 AA.
XX
XX ABG73736;
XX
DT 08-APR-2003 (first entry)
XX
DE Tankyrase H isotype 1 TH-1 variant TaHo E/A dc.
XX
KW Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TH-1; TaHo;
KW cytosstatic; immunostimulant; gene therapy; vaccine; cancer; tumour;
KW cell cycle related disorder; poly ADP-ribose polymerase; PARP.
XX
OS Synthetic.

Key Location/Qualifiers
FT Region 1..22 /label= Ankyrin_repeat_1
FT Region 24..55 /label= Ankyrin_repeat_2
FT Region 57..87 /label= Ankyrin_repeat_3
FT Region 89..113 /label= Ankyrin_repeat_4
FT Region 115..139 /label= Ankyrin_repeat_5
FT Misc-difference 127 /note= "TH1 start"
FT Region 147..176 /label= Ankyrin_repeat_6
FT Region 178..208 /label= Ankyrin_repeat_7
FT Region 210..241 /label= Ankyrin_repeat_8
FT Region 243..281 /label= Ankyrin_repeat_9
FT Region 283..332 /label= Ankyrin_repeat_10
FT Region 334..365 /label= Ankyrin_repeat_11
FT Region 367..398 /label= Ankyrin_repeat_12
FT Region 400..424 /label= Ankyrin_repeat_13
FT Region 426..458 /label= Ankyrin_repeat_14
FT Region 460..491 /label= Ankyrin_repeat_14

FT Region /label= Ankyrin_repeat_15 493..524

FT Region /label= Ankyrin_repeat_16 526..557

FT Region /label= Ankyrin_repeat_17 559..594

FT Region /label= Ankyrin_repeat_18 596..644

FT Region /label= Ankyrin_repeat_19 646..677

FT Region /label= Ankyrin_repeat_20 679..710

FT Region /label= Ankyrin_repeat_21 712..755

FT Region /label= Ankyrin_repeat_22 757..793

FT Region /label= Ankyrin_repeat_23 797..845

FT Domain /label= SAM_domain 855..869

FT Region /note= "Unidentified region" 956..1084

FT Domain /label= PARP_domain 1072

FT Misc-difference /note= "This residue is mutated from Glu (wild type, see ABG3732) to Ala"

FT XX

FN WO200286170-A1.

PD 31-OCT-2002.

XX 25-APR-2002; 2002WO-US013185.

FF 25-APR-2001; 2001US-00843159.

PR (RIGE-) RIGEL PHARM INC.

PA

PI Luo Y, Chan E, Xu X, Huang B, Oseovskaya V;

XX WPI; 2003-093158/08.

DR

XX New recombinant nucleic acid encoding a cell cycle protein, useful for diagnosing and treating a cell cycle related disorder, e.g. cancer.

PT Disclosure; Fig 16A-C; 90pp; English.

PS

XX This invention describes a novel recombinant nucleic acid encoding the cell cycle protein TaHo, a tankyrase H isoform. The products of the invention have cytostatic and immunostimulant activity and can be used for gene therapy and in vaccines. The cell cycle protein TaHo and the nucleic acid encoding the protein are useful for diagnosing and treating a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a tumour cell. The methods are useful for screening for a bioactive agent capable of binding to a cell cycle protein tankyrase H, or a bioactive agent capable of modulating a cell cycle protein tankyrase H or PARP (poly ADP-ribose polymerase) activity. The antibodies are useful for inducing an immune response against the cell cycle proteins. This sequence represents the tankyrase H isoform 1, TaHo E/A dC, which contains a Glu to Ala mutation and has a truncated C-terminal containing a 2 amino acid insertion described in the disclosure of the invention

XX Sequence 1084 AA;

QQ Query Match 100.0%; Score 5585; DB 6; Length 1084;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGKDVVEYLLQNGASVQARDGGGLPLHNACSFGEHAEVNNLLRHGADPNARDNNWT 60

DB 1 GFGKDVVEYLLQNGASVQARDGGGLPLHNACSFGEHAEVNNLLRHGADPNARDNNWT 60

Qy 61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGR TALDLADPSAKAVLTGKYKDELLESAR 120

Db 61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGR TALDLADPSAKAVLTGKYKDELLESAR 120

Qy 121 SNESEKMMALLTPLNVNCHASGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 180

Db 121 SNESEKMMALLTPLNVNCHASGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 180

Qy 181 PLHNACSYGHYEVTLLVKGACVNMADLWQFTPLHEAAAKNRVEVCSSLSSGADPTLL 240

Db 181 PLHNACSYGHYEVTLLVKGACVNMADLWQFTPLHEAAAKNRVEVCSSLSSGADPTLL 240

Qy 241 NCHNSAIDLAPTQPKERLAYEFKGHSLLOAREADVTRI KKHLSLEMYNFKHPQTHET 300

Db 241 NCHNSAIDLAPTQPKERLAYEFKGHSLLOAREADVTRI KKHLSLEMYNFKHPQTHET 300

Qy 301 ALHCAAAAPYPRKQICELLRLKGANINEKTEFLPLHVASEKAHNDVVVVVVKHEAKV 360

Db 301 ALHCAAAAPYPRKQICELLRLKGANINEKTEFLPLHVASEKAHNDVVVVVVKHEAKV 360

Qy 361 NALDNLGOTSLHRAAYCGHLQTCRLLLSYGCDDNII SLOGFTALQMGNEVQQLQEGIS 420

Db 361 NALDNLGOTSLHRAAYCGHLQTCRLLLSYGCDDNII SLOGFTALQMGNEVQQLQEGIS 420

Qy 421 LGNSEADROLLEAAKAGDVETVKKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVVVEYLL 480

Db 421 LGNSEADROLLEAAKAGDVETVKKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVVVEYLL 480

Qy 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKGAGVNVNADLWKFTPLHEAAAKKYE 540

Db 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKGAGVNVNADLWKFTPLHEAAAKKYE 540

Qy 541 ICKLLLOHGADPTKKNRDNTPLDLVKDGDTDIDLLRGDAALLDAKKGCLARVKLSS 600

Db 541 ICKLLLOHGADPTKKNRDNTPLDLVKDGDTDIDLLRGDAALLDAKKGCLARVKLSS 600

Qy 601 PDNVNCRDTQGRHSTPLHLAAGYNNEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660

Db 601 PDNVNCRDTQGRHSTPLHLAAGYNNEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660

Qy 661 VAALLIKYNACVNAATDKWAFPLHEAAQKGTQLCALLAHGADPTLKNOEGQTPLDLVS 720

Db 661 VAALLIKYNACVNAATDKWAFPLHEAAQKGTQLCALLAHGADPTLKNOEGQTPLDLVS 720

Qy 721 ADDVSALLTAAMPSPSALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLG 780

Db 721 ADDVSALLTAAMPSPSALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLG 780

Qy 781 SFSELSVVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDVLE 840

Db 781 SFSELSVVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDVLE 840

Qy 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQQGLNPYLTINTSGSGTILIDLSPDDKEFQ 900

Db 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQQGLNPYLTINTSGSGTILIDLSPDDKEFQ 900

Qy 901 SVEEEMQSTVRHRDGGHAGGIFNRVNIILKIOKVCNKLWERYTHRRKEYSEENHNHANE 960

Db 901 SVEEEMQSTVRHRDGGHAGGIFNRVNIILKIOKVCNKLWERYTHRRKEYSEENHNHANE 960

Qy 961 RMLFPGSPFNVAI IHKGFDERHAY ICGMFGAGIYFAENSSKSNQYVYGIGGGTGPVHKD 1020

Db 961 RMLFPGSPFNVAI IHKGFDERHAY ICGMFGAGIYFAENSSKSNQYVYGIGGGTGPVHKD 1020

Qy 1021 RSCYICHRQLLCFVRTVLGKSFLOFSAMKWAHSPPGHHSVTGRPSV 1065

Db 1021 RSCYICHRQLLCFVRTVLGKSFLOFSAMKWAHSPPGHHSVTGRPSV 1065

RESULT 4

AAY97748

ID AAY97748 standard; protein; 1100 AA.

XX

AC AAY97748;

XX

DT 06-AUG-2001 (first entry)
XX Tankyrase homologue isotype 1 protein sequence.
DE
XX Tankyrase homologue isotype 1; TaHo-1; TaHo-2; cell proliferation;
KW cell cycle protein; cell cycle associated disorder; cancer; gene mapping;
KW chromosome mapping; gene therapy; vaccine.
XX
OS Unidentified.
XX
XX WO200130987-A2.
XX
XX 03-MAY-2001.
XX
XX 25-OCT-2000; 2000WO-US041528.
XX
XX 25-OCT-1999; 99US-00427154.
XX
XX (RIGE-) RIGEL PHARM INC.
XX
XX Luo Y, Chan E, Xu X, Huang B;
XX
XX WPI; 2001-300503/31.
XX
XX N-PSDB; AAA91487.
XX
XX Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing
XX or preventing cell proliferation in cells, and for diagnosing, treating
XX or preventing cell cycle associated disorders such as cancer.
XX
XX Claim 22; Fig 3; 63pp; English.
XX
XX This sequence is the Tankyrase homologue isotype 1 (TaHo-1) protein of
XX the invention. The invention also relates to the TaHo-2 protein. The TaHo
XX proteins are useful for inducing or preventing cell proliferation in
XX cells, and in the study or treatment of conditions mediated by the cell
XX cycle proteins, such as to diagnose, treat or prevent cell cycle
XX associated disorders, preferably cancer. The TaHo coding sequences are
XX useful as hybridisation probes, in chromosome and gene mapping and in the
XX generation of anti-sense DNA and RNA. The coding sequences are also
XX useful for the preparation of TaHo, for generating either transgenic
XX animals or knock out animals which, in turn, are useful in a development
XX and screening of therapeutically useful agents, in gene therapy, as
XX vaccine, and for construction of hybridisation probes for mapping the
XX gene which encodes TaHo and for the genetic analysis of individuals with
XX genetic disorders. The TaHo proteins, and their coding sequences are
XX useful in screening assays
XX
SQ Sequence 1100 AA;
Query Match 100.0%; Score 5585; DB 4; Length 1100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFGRKDVVEYLLQNGASVQARDGGGLPLHNACSFGEAEVNNLLRHGADPNARDNNYT 60
DB 1 GFGRKDVVEYLLQNGASVQARDGGGLPLHNACSFGEAEVNNLLRHGADPNARDNNYT 60
QY 61 PLHEAAIKGIDVCIVLQHGAEPTIRNDGTALDADPSAKAVLTGEYKDELLESAR 120
DB 61 PLHEAAIKGIDVCIVLQHGAEPTIRNDGTALDADPSAKAVLTGEYKDELLESAR 120
QY 121 SGNEEKMALLPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAKDKGLV 180
DB 121 SGNEEKMALLPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAKDKGLV 180
QY 181 PLHNACSYGHYEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
DB 181 PLHNACSYGHYEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
QY 241 NCHNKSADLAPTPOLKERLAYEFKGHSLLOAREADVTRIKKHLSLEWVNFKHPQTHET 300
DB 241 NCHNKSADLAPTPOLKERLAYEFKGHSLLOAREADVTRIKKHLSLEWVNFKHPQTHET 300

QY 301 ALHCAAASPYPKRKQICELLRLKGANINEKTEFELTPLHVASEKAHNDVVEVVKHEAKV 360
DB 301 ALHCAAASPYPKRKQICELLRLKGANINEKTEFELTPLHVASEKAHNDVVEVVKHEAKV 360
QY 361 NALDNLGOTSLHRAAYCGHLOTCLLLSYGCDPNIIISLOGFTALQMGNEVQOLLQEGIS 420
DB 361 NALDNLGOTSLHRAAYCGHLOTCLLLSYGCDPNIIISLOGFTALQMGNEVQOLLQEGIS 420
QY 421 LGNSEADROLLEAAKAGDVETVKKICTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
DB 421 LGNSEADROLLEAAKAGDVETVKKICTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
QY 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKGAVVNVADLWKFTPLHEAAAKGYE 540
DB 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKGAVVNVADLWKFTPLHEAAAKGYE 540
QY 541 ICKLLLOHGADPTKKNRDGNTPDLVKDGDTDIQLLGRDAALLDAAKKGCLARVKLLSS 600
DB 541 ICKLLLOHGADPTKKNRDGNTPDLVKDGDTDIQLLGRDAALLDAAKKGCLARVKLLSS 600
QY 601 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
DB 601 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
QY 661 VAALLIKYNACVNATDKWAFPLHEAAQKRTQLCALLAHGADPTLKNQEGOTPLDLVS 720
DB 661 VAALLIKYNACVNATDKWAFPLHEAAQKRTQLCALLAHGADPTLKNQEGOTPLDLVS 720
QY 721 ADDVSALLTAAMPFSALEPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLSG 780
DB 721 ADDVSALLTAAMPFSALEPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLSG 780
QY 781 SFSSELSSVSSSGTEGASSLEKKEVPGVDFSIPTFVRNLGLEHLMDFEREQITLDLVE 840
DB 781 SFSSELSSVSSSGTEGASSLEKKEVPGVDFSIPTFVRNLGLEHLMDFEREQITLDLVE 840
QY 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLNTSGSGTILDLSPDDKEFQ 900
DB 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLNTSGSGTILDLSPDDKEFQ 900
QY 901 SVEEEMQSTVEHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
DB 901 SVEEEMQSTVEHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
QY 961 RMLFHGSPFVNAILHKGFDERHAYIGGMFGAGIYPAENSSKSNQVYGGTGCPCVHKD 1020
DB 961 RMLFHGSPFVNAILHKGFDERHAYIGGMFGAGIYPAENSSKSNQVYGGTGCPCVHKD 1020
QY 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV 1065
DB 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV 1065
RESULT 5
ABG73732
ID ABG73732 standard; protein; 1100 AA.
XX
AC ABG73732;
XX
XX 08-APR-2003 (first entry)
XX
XX Tankyrase H isotype 1 TH-1.
XX
XX Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TH-1; TaHo;
KW cytosstatic; immunostimulant; gene therapy; vaccine; cancer; tumour;
KW cell cycle related disorder; poly ADP-ribose polymerase; PARP.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FT Region 1. 22
FT /label= Ankyrin_repeat_1
FT Region 24. 55

FT /label= Ankyrin_repeat_2
FT 57. .87
FT /label= Ankyrin_repeat_3
FT 89. .113
FT /label= Ankyrin_repeat_4
FT 115. .139
FT /label= Ankyrin_repeat_5
FT 127
FT Misc-difference
FT /note= "TH1 start"
FT 147. .176
FT /label= Ankyrin_repeat_6
FT 178. .208
FT /label= Ankyrin_repeat_7
FT 210. .241
FT /label= Ankyrin_repeat_8
FT 243. .281
FT /label= Ankyrin_repeat_9
FT 283. .332
FT /label= Ankyrin_repeat_10
FT 334. .365
FT /label= Ankyrin_repeat_11
FT 367. .398
FT /label= Ankyrin_repeat_12
FT 400. .424
FT /label= Ankyrin_repeat_13
FT 426. .458
FT /label= Ankyrin_repeat_14
FT 460. .491
FT /label= Ankyrin_repeat_15
FT 493. .524
FT /label= Ankyrin_repeat_16
FT 526. .557
FT /label= Ankyrin_repeat_17
FT 559. .594
FT /label= Ankyrin_repeat_18
FT 596. .644
FT /label= Ankyrin_repeat_19
FT 646. .677
FT /label= Ankyrin_repeat_20
FT 679. .710
FT /label= Ankyrin_repeat_21
FT 712. .755
FT /label= Ankyrin_repeat_22
FT 757. .793
FT /label= Ankyrin_repeat_23
FT 797. .845
FT /label= SAM_domain
FT 855. .869
FT /note= "Unidentified region"
FT 956. .1094
FT /label= PARP_domain
FT
PN WO200286170-A1.
PD 31-OCT-2002.
PF 25-APR-2002; 2002WO-US013185.
PR 25-APR-2001; 2001US-00843159.
PA (RIGE-) RIGEL PHARM INC.
XX
XX Luo Y, Chan E, Xu X, Huang B, Ossovskaaya V;
XX WPI; 2003-093158/08.
XX
XX New recombinant nucleic acid encoding a cell cycle protein, useful for
XX diagnosing and treating a cell cycle related disorder, e.g. cancer.
XX
XX Disclosure; Fig 16A-C; 90pp; English.
XX
XX This invention describes a novel recombinant nucleic acid encoding the
XX cell cycle protein TaHo, a tankyrase H isoform. The products of the

CC invention have cytostatic and immunostimulant activity and can be used
CC for gene therapy and in vaccines. The cell cycle protein TaHo and the
CC nucleic acid encoding the protein are useful for diagnosing and treating
CC a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a
CC tumour cell. The methods are useful for screening for a bioactive agent
CC capable of binding to a cell cycle protein tankyrase H, or a bioactive
CC agent capable of modulating a cell cycle protein tankyrase H or PARP
CC (poly ADP-ribose polymerase) activity. The antibodies are useful for
CC inducing an immune response against the cell cycle proteins. This
CC sequence represents tankyrase H isoform 1, TH-1, described in the
CC disclosure of the invention
XX
XX Sequence 1100 AA;

	Query Match	100.0%;	Score 5585;	DB 6;	Length 1100;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1065;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GFGRKDVVEYLLQNGASVQARDGGGLPLHNACSFQAEVNVNLLRRHGADPNARDNNYTT	60		
DB	1	GFGRKDVVEYLLQNGASVQARDGGGLPLHNACSFQAEVNVNLLRRHGADPNARDNNYTT	60		
QY	61	PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRALTADPSAKAVLTGEYKDELESAR	120		
DB	61	PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRALTADPSAKAVLTGEYKDELESAR	120		
QY	121	SGNEEKOMALLTPLNVNCHASGRKSTPLHLAAGYNRVKIVQLLQHGADYHAKDKGDLV	180		
DB	121	SGNEEKOMALLTPLNVNCHASGRKSTPLHLAAGYNRVKIVQLLQHGADYHAKDKGDLV	180		
QY	181	PLHNACSYGHEVTELLVKHGACVNAWDLWQFTPLHEAASKNRVEVCSLLSYGADPTLL	240		
DB	181	PLHNACSYGHEVTELLVKHGACVNAWDLWQFTPLHEAASKNRVEVCSLLSYGADPTLL	240		
QY	241	NCHNSAIDLAPTPOLKERLAYEFKGHSLLQAAREADVTRIKKHSLEWMVNFKHPQTHET	300		
DB	241	NCHNSAIDLAPTPOLKERLAYEFKGHSLLQAAREADVTRIKKHSLEWMVNFKHPQTHET	300		
QY	301	ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPHVASEKAHNDVVEVVVKHEAKV	360		
DB	301	ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPHVASEKAHNDVVEVVVKHEAKV	360		
QY	361	NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDDNIIISLQGTALOMGNENVQQLQSGIS	420		
DB	361	NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDDNIIISLQGTALOMGNENVQQLQSGIS	420		
QY	421	LGNSEADROLLEAAKAGDVETVKKLCITVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL	480		
DB	421	LGNSEADROLLEAAKAGDVETVKKLCITVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL	480		
QY	481	QHGADYHAKDKGGLVPLHNACSYGHEVAEALLVKHGAVNVNADLWKFTPLHEAAKGYE	540		
DB	481	QHGADYHAKDKGGLVPLHNACSYGHEVAEALLVKHGAVNVNADLWKFTPLHEAAKGYE	540		
QY	541	ICKLILLQHGADPTKKNRDGNTPLDLVKDGTDTDQLDLRGDAALLDAKKGCLARVKLSS	600		
DB	541	ICKLILLQHGADPTKKNRDGNTPLDLVKDGTDTDQLDLRGDAALLDAKKGCLARVKLSS	600		
QY	601	PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD	660		
DB	601	PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD	660		
QY	661	VAALLIKYNACVNAWKWAPTPLHEAAKQKRTQTCALLLAHGADPTTKNQGQPTPLDLVS	720		
DB	661	VAALLIKYNACVNAWKWAPTPLHEAAKQKRTQTCALLLAHGADPTTKNQGQPTPLDLVS	720		
QY	721	ADDVSALLTAAMPSPSALPCYKQVNLGVSPGATADALSSGPSSPSLSAASLDNLSG	780		
DB	721	ADDVSALLTAAMPSPSALPCYKQVNLGVSPGATADALSSGPSSPSLSAASLDNLSG	780		
QY	781	SFSELSVSVSSSGTEGASSLEKEVFGVDFSIQTFVRNLGLEHLMDFEREQITDLVIVE	840		
DB	781	SFSELSVSVSSSGTEGASSLEKEVFGVDFSIQTFVRNLGLEHLMDFEREQITDLVIVE	840		

QY 841 MGKELKEIGINAYGHRHKLKIGVERLISGOGLNPLYTLNTSGTLLIDLSPDKKEFQ 900
DB 841 MGKELKEIGINAYGHRHKLKIGVERLISGOGLNPLYTLNTSGTLLIDLSPDKKEFQ 900
QY 901 SVEEMOSTVREHRDGGHAGGIFNRYNLTKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
DB 901 SVEEMOSTVREHRDGGHAGGIFNRYNLTKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
QY 961 RMLFHGSPFVNAIITHKGFDERHAYTGMFGAGIYFAENSCKSNQVYVIGGGTGPCVHKD 1020
DB 961 RMLFHGSPFVNAIITHKGFDERHAYTGMFGAGIYFAENSCKSNQVYVIGGGTGPCVHKD 1020
QY 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065
DB 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065

RESULT 6
ABG73730
ID ABG73730 standard; protein; 1100 AA.
XX AC ABG73730;
XX DT 08-APR-2003 (first entry)
XX XX Tankyrase H isotype 1 TaHo-1 from clone TH-1.
XX KW Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-1;
XX KW TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour;
XX KW cell cycle related disorder; poly ADP-ribose polymerase; PARP.
XX OS Unidentified.
XX PN W0200286170-A1.
XX PD 31-OCT-2002.
XX PF 25-APR-2002; 2002WO-US013185.
XX PR 25-APR-2001; 2001US-00843159.
XX PA (RIGE-) RIGEL PHARM INC.
XX PI Luo Y, Chan E, Xu X, Huang B, Ossoveskaya V;
XX DR WPI; 2003-093158/08.
XX DR N-PSDB; ABQ77066.
XX PT New recombinant nucleic acid encoding a cell cycle protein, useful for
XX PT diagnosing and treating a cell cycle related disorder, e.g. cancer.
XX PS Claim 14; Fig 3; 90pp; English.
XX SS This invention describes a novel recombinant nucleic acid encoding the
CC cell cycle protein TaHo, a tankyrase H isoform. The products of the
CC invention have cytostatic and immunostimulant activity and can be used
CC for gene therapy and in vaccines. The cell cycle protein TaHo and the
CC nucleic acid encoding the protein are useful for diagnosing and treating
CC a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a
CC tumour cell. The methods are useful for screening for a bioactive agent
CC capable of binding to a cell cycle protein tankyrase H, or a bioactive
CC agent capable of modulating a cell cycle protein tankyrase H or PARP
CC (poly ADP-ribose polymerase) activity. The antibodies are useful for
CC inducing an immune response against the cell cycle proteins. This
CC sequence represents the tankyrase H isoform 1, TaHo-1, isolated from
CC clone TH-1 which is described in the disclosure of the invention
XX XX
SQ Sequence 1100 AA;

Query Match 100.0%; Score 5585; DB 6; Length 1100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGRKDVVEYLLONGASVQARDGGLIPLHNACSFHAEVNVNLLLRHGADPNARDNNYT 60
DB 1 GFGRKDVVEYLLONGASVQARDGGLIPLHNACSFHAEVNVNLLLRHGADPNARDNNYT 60
QY 61 PLHAAI1KGKIDVICIVILQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 120
DB 61 PLHAAI1KGKIDVICIVILQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 120
QY 121 SGNEKEMWALLTPLNVNCHASDGRKSTPLHLAAGVNRVKI1VOLLQHGADVHAKDGLV 180
DB 121 SGNEKEMWALLTPLNVNCHASDGRKSTPLHLAAGVNRVKI1VOLLQHGADVHAKDGLV 180
QY 181 PLHNACSYGHEVTELLVKGACVNMADLMQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
DB 181 PLHNACSYGHEVTELLVKGACVNMADLMQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
QY 241 NCHNSAIDLAPTQLKERLAYEFKSHSLLOQAAREADVTRI1KGLHLSLEMVNFKHPQTHET 300
DB 241 NCHNSAIDLAPTQLKERLAYEFKSHSLLOQAAREADVTRI1KGLHLSLEMVNFKHPQTHET 300
QY 301 ALHCAASPYPRKQICELLIRKGANINEKTEFLTPLVASEKAHNDVVEVVKHEAKV 360
DB 301 ALHCAASPYPRKQICELLIRKGANINEKTEFLTPLVASEKAHNDVVEVVKHEAKV 360
QY 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNI1ISLQGFALTALQMGNEVQQLIQEGIS 420
DB 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNI1ISLQGFALTALQMGNEVQQLIQEGIS 420
QY 421 LGNSEADRLLEAAKAGDVETVKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
DB 421 LGNSEADRLLEAAKAGDVETVKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
QY 481 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGAVNVNADLWKFTPLHEAAKGYE 540
DB 481 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGAVNVNADLWKFTPLHEAAKGYE 540
QY 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDI1QDLLRGDAALLDAKKGCLARVKLSS 600
DB 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDI1QDLLRGDAALLDAKKGCLARVKLSS 600
QY 601 PDVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
DB 601 PDVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
QY 661 VAALLIKYNACVNATDKWAFPLHEAAKGTQ1CALLLAHAGADPTLKNQSGQTPDLVLS 720
DB 661 VAALLIKYNACVNATDKWAFPLHEAAKGTQ1CALLLAHAGADPTLKNQSGQTPDLVLS 720
QY 721 ADDVSALLTAAMPPSALPCYKQVINGVRSPGATADALS6SPSSPSLSAASSLDNL5G 780
DB 721 ADDVSALLTAAMPPSALPCYKQVINGVRSPGATADALS6SPSSPSLSAASSLDNL5G 780
QY 781 SFSLSLWSSSGTEGASSLEKKEVPVDFSI1QFVRNLGLEHLMDFEREQITLIDLVE 840
DB 781 SFSLSLWSSSGTEGASSLEKKEVPVDFSI1QFVRNLGLEHLMDFEREQITLIDLVE 840
QY 841 MGKELKEIGINAYGHRHKLKIGVERLISGOGLNPLYTLNTSGTLLIDLSPDKKEFQ 900
DB 841 MGKELKEIGINAYGHRHKLKIGVERLISGOGLNPLYTLNTSGTLLIDLSPDKKEFQ 900
QY 901 SVEEMOSTVREHRDGGHAGGIFNRYNLTKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
DB 901 SVEEMOSTVREHRDGGHAGGIFNRYNLTKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
QY 961 RMLFHGSPFVNAIITHKGFDERHAYTGMFGAGIYFAENSCKSNQVYVIGGGTGPCVHKD 1020
DB 961 RMLFHGSPFVNAIITHKGFDERHAYTGMFGAGIYFAENSCKSNQVYVIGGGTGPCVHKD 1020
QY 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065
DB 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065

25-OCT-2000; 2000US-00696668.
25-APR-2001; 2001US-00843159.
(LUOY/) LUO Y.
(CHAN/) CHAN E.
(XUXX/) XU X.
(HUAN/) HUANG B.
(OSSO/) OSSOVSKAYA V.
Luo Y, Chan E, Xu X, Huang B, Ossovsckaya V;
WPI; 2005-294737/30.
Novel recombinant polypeptide such as cell cycle protein e.g. tankyrase
homolog, useful for screening its modulator.
Disclosure; SEQ ID NO 8; 75pp; English.
The invention relates to a recombinant polypeptide (I) such as cell cycle
protein e.g. tankyrase homologue (TaHo), comprising an amino acid
sequence having 85% or more sequence identity to the 1065 amino acid
sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also
described: (1) diagnosing cancer, which involves determining the activity
of (I) from a test sample of an individual and comparing the level with a
control with a control; (2) treating (M1) an individual with a cell cycle
related disorder, which involves administering to the individual an
inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (I),
comprising a nucleic acid that hybridizes under high stringent conditions
to a sequence complementary to the 3797 base pair sequence of ADY97759 or
the 3816 base pair sequence of ADY97760, or a nucleic acid having 85% or
more sequence identity to ADY97759 or ADY97760; (4) an expression vector
(III) comprising (II) operably linked to regulatory sequences recognized
by a host cell (IV) transformed with the nucleic acid; (5) a host cell
comprising (II) or (III); (6) producing (I); (7) a polypeptide that
specifically binds to (I); and (8) inhibiting (M2) growth of a tumor
cell, involves contacting the tumor with a bioactive agent capable of
inhibiting TaHo activity. (I) is useful for screening a bioactive agent
capable of modulating (I), or screening for agents capable of interfering
with the binding of (I) and P21. (M1) is useful for treating an
individual with a cell cycle related disorder. (M2) is useful for
inhibiting growth of a tumor cell by a bioactive agent e.g. antisense
oligonucleotide. The present sequence represents the human tankyrase
homologue isotype 1.
Sequence 1100 AA;
Query Match 100.0%; Score 5585; DB 9; Length 1100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFGRDVEYLLONGASVOARDGGILPLHNACSFHAEVNNLLRHGADPNARDNNYNT 60
DB 1 GFGRDVEYLLONGASVOARDGGILPLHNACSFHAEVNNLLRHGADPNARDNNYNT 60
QY 61 PLHEAAIKGKIDVCIVLLOHGAETPIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 120
DB 61 PLHEAAIKGKIDVCIVLLOHGAETPIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 120
QY 121 SGNEEKMMALLPPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLLOHGAHVAKDKGLV 180
DB 121 SGNEEKMMALLPPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLLOHGAHVAKDKGLV 180
QY 181 PLHNACSYGHVEYTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSSLISYGADPTLL 240
DB 181 PLHNACSYGHVEYTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSSLISYGADPTLL 240
QY 241 NCHNKSADIDLAPTPOLKELAYEFKHSLLQAREADVTRIKKHSLEWVNFKHPQTHET 300
DB 241 NCHNKSADIDLAPTPOLKELAYEFKHSLLQAREADVTRIKKHSLEWVNFKHPQTHET 300
QY 301 ALHCAAASPYPKRKQICELLLRKGANINEKTEFTPLHVASEKAHNDVVEVVVHEAKV 360
DB 301 ALHCAAASPYPKRKQICELLLRKGANINEKTEFTPLHVASEKAHNDVVEVVVHEAKV 360

QY 361 NALDNLGOTSILHRAAYCGHLQTCRLLLSYGCDPNIIISLQGFALQMGNNVQQLLEQGIS 420
DB 361 NALDNLGOTSILHRAAYCGHLQTCRLLLSYGCDPNIIISLQGFALQMGNNVQQLLEQGIS 420
QY 421 LGNSEADRLLEAAKAGADVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
DB 421 LGNSEADRLLEAAKAGADVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
QY 481 OHGADVHAKDKKGLVPLHNACSYGHVEYVAEALLVKHGAVNVNADLWKFTPLHEAAAKGYE 540
DB 481 OHGADVHAKDKKGLVPLHNACSYGHVEYVAEALLVKHGAVNVNADLWKFTPLHEAAAKGYE 540
QY 541 ICKLLLOHGAADPTKKNRDGNTPLDIVKDGDDTDIQLLRGDAALLDAKKGCLARVKKLSS 600
DB 541 ICKLLLOHGAADPTKKNRDGNTPLDIVKDGDDTDIQLLRGDAALLDAKKGCLARVKKLSS 600
QY 601 PDNVNCRDTPQRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
DB 601 PDNVNCRDTPQRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
QY 661 VAAALLIKYNACVNATDKWAFPLHEAAQKGRTOCALLLAHGAADPTLKNQEGQTPDLVLS 720
DB 661 VAAALLIKYNACVNATDKWAFPLHEAAQKGRTOCALLLAHGAADPTLKNQEGQTPDLVLS 720
QY 721 ADDVSALLTAAMPSPSALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
DB 721 ADDVSALLTAAMPSPSALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
QY 781 SFSBELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFERQOITLDVLVE 840
DB 781 SFSBELSSVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFERQOITLDVLVE 840
QY 841 MGHEKELKEIGINAYCHRHKLKGVRELISGOGLNPYLTNTSGSTLIDLSPPDKKEFQ 900
DB 841 MGHEKELKEIGINAYCHRHKLKGVRELISGOGLNPYLTNTSGSTLIDLSPPDKKEFQ 900
QY 901 SVEEMOSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
DB 901 SVEEMOSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
QY 961 RMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSXSNQVYVYGGGTGCPVHKD 1020
DB 961 RMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSXSNQVYVYGGGTGCPVHKD 1020
QY 1021 RSCYICHRQLLFCRVTIGKSPLOFSAMKMAHSPGHHSVTGRPSV 1065
DB 1021 RSCYICHRQLLFCRVTIGKSPLOFSAMKMAHSPGHHSVTGRPSV 1065
RESULT 9
AAB66295
ID AAB66295 standard; protein; 1166 AA.
XX AAB66295;
XX AC AAB66295;
XX DT 05-APR-2001 (first entry)
XX DE Human tankyrase2 TANK2-SHORT SEQ ID NO: 135.
XX KW Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasia; aging;
XX KW inflammatory disorder.
XX OS Homo sapiens.
XX PN WO200100849-A1.
XX PD 04-JAN-2001.
XX PF 28-JUN-2000; 2000WO-US017827.
XX PR 29-JUN-1999; 99US-0141582P.
XX XX

PA	(ICOS-) ICOS CORP.	
XX	Christenson E, Demaggio AJ, Goldman PS, Mcelligott DU;	
PI	WPI; 2001-102896/11.	
XX	N-PSDB; AAF63953.	
DR	New tankyrase2 polypeptides, useful for treating conditions mediated by	
XX	poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,	
PT	inflammatory and autoimmune disorders.	
PT	Claim 3; Page 200-203; 242pp; English.	
XX	The present invention provides the protein and coding sequence for the	
CC	human tankyrase2 protein. This is found in two different versions,	
CC	designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-	
CC	ribosylation activity and is involved in the modification of TRF1, which	
CC	is a telomere-specific binding protein. The regulation of telomere	
CC	length, in which TRF1 has a role, is linked to ageing and cancer. The	
CC	sequences are useful in the treatment of cancers and inflammatory	
CC	disorders	
XX	Sequence 1166 AA;	
SQ	Query Match 99.9%; Score 5582; DB 4; Length 1166;	
	Best Local Similarity 99.9%; Pred. No. 0;	
	Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GFGKDVVEYLLQNGASVQARDGGLPLHNACSFHAEVNVLLRRHGADPNARDNNYIT 60	
Db	67 GFGKDVVEYLLQNGANVQARDGGLPLHNACSFHAEVNVLLRRHGADPNARDNNYIT 126	
Qy	61 PLHEAAIKGIDVICVILLOHGAETPIRTDGRALDADPSAKAVLTGEYKDELLSAR 120	
Db	127 PLHEAAIKGIDVICVILLOHGAETPIRTDGRALDADPSAKAVLTGEYKDELLSAR 186	
Qy	121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLOHGDVHAKDGLV 180	
Db	187 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLOHGDVHAKDGLV 246	
Qy	181 PLHNACSYGHEVTELLVKGACVNDLMQFTPLHEAASQNRVEVCSLLLSYGADPTLL 240	
Db	247 PLHNACSYGHEVTELLVKGACVNDLMQFTPLHEAASQNRVEVCSLLLSYGADPTLL 306	
Qy	241 NCHNKAIDLAPTQPKERLAYEFKSHLSLQAAREADVTRIKHLSLEMNFKHPQTHET 300	
Db	307 NCHNKAIDLAPTQPKERLAYEFKSHLSLQAAREADVTRIKHLSLEMNFKHPQTHET 366	
Qy	301 ALHCAASPYKPKOICELLIRKGANINEKTKFELTPLHVASEKAHNDVVEVVKHEAV 360	
Db	367 ALHCAASPYKPKOICELLIRKGANINEKTKFELTPLHVASEKAHNDVVEVVKHEAV 426	
Qy	361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIISLQGFALQMGNNVQQLQEGIS 420	
Db	427 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIISLQGFALQMGNNVQQLQEGIS 486	
Qy	421 LGNSEADRLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480	
Db	487 LGNSEADRLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 546	
Qy	481 QHGADVHAKDGLVPLHNACSYGHEVVAELLVKGAVNVNADLWKETPLHEAAKGYE 540	
Db	547 QHGADVHAKDGLVPLHNACSYGHEVVAELLVKGAVNVNADLWKETPLHEAAKGYE 606	
Qy	541 ICKLLQHGADPTKKNRDNPTPLVDKGDPTDIQDLRGDAALDAAKGGCLARVKKLSS 600	
Db	607 ICKLLQHGADPTKKNRDNPTPLVDKGDPTDIQDLRGDAALDAAKGGCLARVKKLSS 666	
Qy	601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660	
Db	667 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 726	
Qy	661 VAALLIKYNACVNATDKWAFPLHEAAQKGTQTCALLLAHAGADPTLKQEGQTPDLIVS 720	
Db	727 VAALLIKYNACVNATDKWAFPLHEAAQKGTQTCALLLAHAGADPTLKQEGQTPDLIVS 786	
Qy	721 ADDVSALLTAAMPSPSALPCYKQVNLNGVRSPGATADALSSGSPSSSLSAASSLDNLG 780	
Db	787 ADDVSALLTAAMPSPSALPCYKQVNLNGVRSPGATADALSSGSPSSSLSAASSLDNLG 846	
Qy	781 SFSELSVSSSGTEGASSLEKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDVLVE 840	
Db	847 SFSELSVSSSGTEGASSLEKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDVLVE 906	
Qy	841 MGHKELKEIGINAYGHRHKLKGVRLISGQGLNPYLTNTSGSGTILDLSPDDKEFQ 900	
Db	907 MGHKELKEIGINAYGHRHKLKGVRLISGQGLNPYLTNTSGSGTILDLSPDDKEFQ 966	
Qy	901 SVEEEMQSTVREHRDGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNANE 960	
Db	967 SVEEEMQSTVREHRDGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNANE 1026	
Qy	961 RMLFHGSPFVNALIHKGDFDERHAYIGMFGAGIYFAENSCKSNQYVYIGGGTGCPCVHKD 1020	
Db	1027 RMLFHGSPFVNALIHKGDFDERHAYIGMFGAGIYFAENSCKSNQYVYIGGGTGCPCVHKD 1086	
Qy	1021 RSCVICHROLFLCRVTLGKSFLOFSAMKMAHSPGHHSVTGRPSV 1065	
Db	1087 RSCVICHROLFLCRVTLGKSFLOFSAMKMAHSPGHHSVTGRPSV 1131	
RESULT 10		
ABP69457	standard; protein; 1166 AA.	
XX	ABP69457;	
XX	20-JAN-2003 (first entry)	
DE	Human polypeptide SEQ ID NO 1504.	
KW	Human; genome mapping; gene therapy; food supplement; virus; fungus;	
KW	cell-proliferative disorder; neurodegenerative disease; bacterial;	
KW	Parkinson's disease; Alzheimer's disease; autoimmune disease;	
KW	multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;	
KW	arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;	
KW	antiparkinsonian; antidiabetic; immunosuppressive; dermatological;	
KW	haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;	
KW	antiarthritic.	
OS	Homo sapiens.	
PN	W0200270539-A2.	
XX	12-SEP-2002.	
XX	05-MAR-2002; 2002WO-US005095.	
XX	05-MAR-2001; 2001US-00799451.	
XX	(HYSE-) HYSEQ INC.	
XX	Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;	
PI	Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;	
PI	Wehrman T, Wang J, Wang D, Drmanac RT;	
XX	WPI; 2002-759812/82.	
DR	N-PSDB; ABZ11674.	
XX	New polynucleotides comprising sequences assembled from expressed	
PT	sequence tags (ESTs), useful for treating cell-proliferative, or platelet	
PT	neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or coagulation disorders.	
XX	Claim 9; SEQ ID NO 1504; 1012pp + Sequence Listing; English.	

The invention relates to an isolated polynucleotide (1) comprising a nucleotide sequence selected from any of 948 sequences (AB211119-AB212066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP69802-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences

Query Match 99.9%; Score 5582; DB 5; Length 1166;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGKRDVVEYLLQNGASVOARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYNT 60
Db 67 GFGKRDVVEYLLQNGANYOARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYNT 126

Qy 61 PLHEAAIKGKIDVCIVLQHGAEPIRTNDGRTALDPSAKAVLTGEYKDELLESAR 120
Db 127 PLHEAAIKGKIDVCIVLQHGAEPIRTNDGRTALDPSAKAVLTGEYKDELLESAR 186

Qy 121 SGNEKMWALLTPLNVNCHASDGRKSTPLHLAAGNVRVKIQLLIQHGADVHAKDGLV 180
Db 187 SGNEKMWALLTPLNVNCHASDGRKSTPLHLAAGNVRVKIQLLIQHGADVHAKDGLV 246

Qy 181 PLHNACSYGHEVTELLVKHGACVNAMDQFTPLHEAASKNRVEVCSSLISYGADPTLL 240
Db 247 PLHNACSYGHEVTELLVKHGACVNAMDQFTPLHEAASKNRVEVCSSLISYGADPTLL 306

Qy 241 NCHNKSATDLAPTOLKRLAYEFKHSLLQAAAREADVTRIKKHLSEMVNFKHPQTHET 300
Db 307 NCHNKSATDLAPTOLKRLAYEFKHSLLQAAAREADVTRIKKHLSEMVNFKHPQTHET 366

Qy 301 ALHCAAAPYKPKQICELLRKGANINEKTEFTPLHVASERAHNDVVEVVKHEAKV 360
Db 367 ALHCAAAPYKPKQICELLRKGANINEKTEFTPLHVASERAHNDVVEVVKHEAKV 426

Qy 361 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDDPNIISLQGTALQMGNNVQQLQEGIS 420
Db 427 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDDPNIISLQGTALQMGNNVQQLQEGIS 486

Qy 421 LGNSEADRLQLEAAKAGDVETVKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 487 LGNSEADRLQLEAAKAGDVETVKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 546

Qy 481 QHGADVHAKDGLVPLHNACSYGHEVTELLVKHGACVNAMDQFTPLHEAASKNRVEVCSSLISYGADPTLL 540
Db 547 QHGADVHAKDGLVPLHNACSYGHEVTELLVKHGACVNAMDQFTPLHEAASKNRVEVCSSLISYGADPTLL 606

Qy 541 ICKLLQHGADPTCKNRDGNTPDLVQKDGDDTDIQLLRGDAALDAAKKGCLARVKLLSS 600
Db 607 ICKLLQHGADPTCKNRDGNTPDLVQKDGDDTDIQLLRGDAALDAAKKGCLARVKLLSS 666

Qy 601 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 667 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 726

Qy 661 VAALLIKYNACVNATDKWAFPLHEAAKGRTOCLCALLLAGADPTLNQSGQTPDLVLS 720
Db 727 VAALLIKYNACVNATDKWAFPLHEAAKGRTOCLCALLLAGADPTLNQSGQTPDLVLS 786

Qy 721 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSQSPSSLSAASSLDNLG 780

Db 787 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSQSPSSLSAASSLDNLG 846
Qy 781 SPSLSWSSVSSGTEGASSLEKKEVPGVDFSIITOPVRNLGLEHLMDFERQITLDVLVE 840
Db 847 SPSLSWSSVSSGTEGASSLEKKEVPGVDFSIITOPVRNLGLEHLMDFERQITLDVLVE 906
Qy 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPVLTNTSGSGTILIDLSPDDKEFQ 900
Db 907 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPVLTNTSGSGTILIDLSPDDKEFQ 966

Qy 901 SVEEMOSTVREHDDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 967 SVEEMOSTVREHDDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 1026

Qy 961 RMLFHGSPFVNAILHKGDFDERHAYIGVMFGAGIYFAENSSKSNQVYVIGGGTGCPCVHKD 1020
Db 1027 RMLFHGSPFVNAILHKGDFDERHAYIGVMFGAGIYFAENSSKSNQVYVIGGGTGCPCVHKD 1086

Qy 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1087 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1131

RESULT 11
ADRL14792
ID ADRL14792 standard; protein; 1166 AA.
XX
AC ADRL14792;
AD
DT 04-NOV-2004 (first entry)
XX
DE Amino acid sequence of human MAPCAX orthologue #24.
XX
KW adenomatous polyposis coli protein; APC; axin pathway;
XX modifier of APC and axin; MAPCAX; cancer; human.
OS Homo sapiens.
XX
PN WO2004066948-A2.
XX
PD 12-AUG-2004.
XX
PF 28-JAN-2004; 2004WO-US002338.
XX
PR 29-JAN-2003; 2003US-0443484P.
PR 11-FEB-2003; 2003US-0447358P.
PR 10-APR-2003; 2003US-0461789P.
PR 14-MAY-2003; 2003US-0470684P.
PR 19-JUN-2003; 2003US-0479650P.
XX
PA (EXEL-) EXELIXIS INC.
XX
XX Gendreau SB, Morablanco EL, Lickteig K, Zhang H;
PI WPI; 2004-580849/56.
XX N-PSDB; ADRL14766.
DR
DR
XX
XX
PT Identifying a candidate adenomatous polyposis coli protein (APC) and axin
PT pathways modulating agent for treating cancer by contacting an assay
PT system comprising a modifier of APC and axin polypeptide or nucleic acid
PT with a test agent.
PS
XX Example 1; SEQ ID NO 50; 199pp; English.
XX
XX The specification describes a method for identifying a candidate
CC adenomatous polyposis coli protein (APC) and axin pathways modulating
CC agents. The method comprises providing an assay system comprising a
CC modifier of APC and axin (MAPCAX) polypeptide or nucleic acid, contacting
CC the assay system with a test agent under conditions where, except for the
CC presence of the test agent, the system provides a reference activity, and
CC detecting a test agent-biased activity of the assay system, where a
CC difference between the test agent-biased activity and the reference
CC activity identifies the test agent as a candidate APC and axin pathways

CC	modulating agent. The method is useful in identifying a candidate									
CC	adenomatous polyposis coli protein (APC) and a pathways modulating agent,									
CC	which are useful for preparing a composition for diagnosing or treating									
CC	cancer. The present sequence represents a human orthologue of a									
CC	Caenorhabditis elegans MAPCAX polypeptide. The sequence was identified									
CC	using BLAST analysis.									
XX										
SQ	Sequence 1166 AA;									
	Query Match	99.9%;	Score 5582;	DB 8;	Length 1166;					
	Best Local Similarity	99.9%;	Pred. No. 0;							
	Matches 1064;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	1	GFGRKDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT	60							
Db	67	GFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT	126							
Qy	61	PLHEAAIKGKIDVICIVLLQHGASPTIRNTDGRALDADPSAKAVLTGEYKDELLESAR	120							
Db	127	PLHEAAIKGKIDVICIVLLQHGASPTIRNTDGRALDADPSAKAVLTGEYKDELLESAR	186							
Qy	121	SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV	180							
Db	187	SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV	246							
Qy	181	PLHNACSYGHEVTELLVKGHCACVAMDLWQFTPLHEAASKNRVEVCSSLLLSYGADPTLL	240							
Db	247	PLHNACSYGHEVTELLVKGHCACVAMDLWQFTPLHEAASKNRVEVCSSLLLSYGADPTLL	306							
Qy	241	NCHNKSAIDLAPTQPKERLAYEFKSHLSLQAAREADVTRI KKHLSLEWVNFHPOTHET	300							
Db	307	NCHNKSAIDLAPTQPKERLAYEFKSHLSLQAAREADVTRI KKHLSLEWVNFHPOTHET	366							
Qy	301	ALHCAAAAPYPRKQKICELLRLRGANINEKTKEFLTPLHVASEKAHNDVVEVVVKEAKV	360							
Db	367	ALHCAAAAPYPRKQKICELLRLRGANINEKTKEFLTPLHVASEKAHNDVVEVVVKEAKV	426							
Qy	361	NALDNLGQTSLHRAAYCGHLQTRCLLSYGCDDNIISLQFTALQNGNENVOQLLEGIS	420							
Db	427	NALDNLGQTSLHRAAYCGHLQTRCLLSYGCDDNIISLQFTALQNGNENVOQLLEGIS	486							
Qy	421	LGNSEADRLQLEAAKAGDVETVKLLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL	480							
Db	487	LGNSEADRLQLEAAKAGDVETVKLLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL	546							
Qy	481	QHGAADVHAKDKGLVPLHNACSYGHEVTELLVKGHCACVAMDLWKFPTPLHEAAAKGKYE	540							
Db	547	QHGAADVHAKDKGLVPLHNACSYGHEVTELLVKGHCACVAMDLWKFPTPLHEAAAKGKYE	606							
Qy	541	ICKLLQHGADPTKQNRDGNTPDLVKDGTDIQDLRLGDAALLDAKKGCLARVKKLSS	600							
Db	607	ICKLLQHGADPTKQNRDGNTPDLVKDGTDIQDLRLGDAALLDAKKGCLARVKKLSS	666							
Qy	601	PDNVNCRDITQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD	660							
Db	667	PDNVNCRDITQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD	726							
Qy	661	VAALLIKYNACVNAWKWFTPLHEAAKQRTQCALLAHGADPTLKNQEGQTPDLDLVS	720							
Db	727	VAALLIKYNACVNAWKWFTPLHEAAKQRTQCALLAHGADPTLKNQEGQTPDLDLVS	786							
Qy	721	ADVDVALLTAAMPSPALPSCKPQVLNVRSPGATADALSSGSPSSSSAASLNLG	780							
Db	787	ADVDVALLTAAMPSPALPSCKPQVLNVRSPGATADALSSGSPSSSSAASLNLG	846							
Qy	781	SFSELSVSSSSGTEGASSLEKEVEFGVDSITQFVRNLGLEHMDIFEREQITLDVLVE	840							
Db	847	SFSELSVSSSSGTEGASSLEKEVEFGVDSITQFVRNLGLEHMDIFEREQITLDVLVE	906							
Qy	841	MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYTLTNTSGSGTILIDLPDDKEFQ	900							
Db	907	MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYTLTNTSGSGTILIDLPDDKEFQ	966							

Qy	901	SVEEEMQSTVREHRDGGHAGGIENRYNLIKQVCNKKLWERYTHRRKEYSEENHNHANE	960							
Db	967	SVEEEMQSTVREHRDGGHAGGIENRYNLIKQVCNKKLWERYTHRRKEYSEENHNHANE	1026							
Qy	961	RMLFHGSPFFVNAIIHKGFDRHAYIGGMFGAGIYFAENSCKSNQYVYGIGGTCPCVHKD	1020							
Db	1027	RMLFHGSPFFVNAIIHKGFDRHAYIGGMFGAGIYFAENSCKSNQYVYGIGGTCPCVHKD	1086							
Qy	1021	RSYIYCHROQLFCRVTLGKSFLOFSAMKMAHSPFGHHSVTGRPSV	1065							
Db	1087	RSYIYCHROQLFCRVTLGKSFLOFSAMKMAHSPFGHHSVTGRPSV	1131							
RESULT 12										
AA	AAB66288 standard; protein; 1169 AA.									
XX	AAB66288;									
XX	05-APR-2001 (first entry)									
XX	Human tankyrase2 clone consensus protein SEQ ID NO: 101.									
XX	Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasia; aging;									
XX	inflammatory disorder.									
XX	Homo sapiens.									
XX	WC200100849-A1.									
XX	04-JAN-2001.									
XX	28-JUN-2000; 2000MO-US017827.									
XX	29-JUN-1999; 99US-0141582P.									
XX	(ICOS-) ICOS CORP.									
XX	Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;									
XX	WPI; 2001-102896/11.									
XX	N-PSDB; AAF63926.									
XX	New tankyrase2 polypeptides, useful for treating conditions mediated by									
XX	poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,									
XX	inflammatory and autoimmune disorders.									
XX	Example 1; Page 162-1665; 242pp; English.									
XX	The present invention provides the protein and coding sequence for the									
XX	human tankyrase2 protein. This is found in two different versions,									
XX	designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-									
XX	ribosylation activity and is involved in the modification of TRF1, which									
XX	is a telomere-specific binding protein. The regulation of telomere									
XX	length, in which TRF1 has a role, is linked to ageing and cancer. The									
XX	sequences are useful in the treatment of cancers and inflammatory									
XX	disorders									
SQ	Sequence 1169 AA;									
	Query Match	99.9%;	Score 5582;	DB 4;	Length 1169;					
	Best Local Similarity	99.9%;	Pred. No. 0;							
	Matches 1064;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;	
Qy	1	GFGRKDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT	60							
Db	70	GFGRKDVVEYLLQNGANVQARDGGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT	129							
Qy	61	PLHEAAIKGKIDVICIVLLQHGASPTIRNTDGRALDADPSAKAVLTGEYKDELLESAR	120							
Db	130	PLHEAAIKGKIDVICIVLLQHGASPTIRNTDGRALDADPSAKAVLTGEYKDELLESAR	189							
Qy	121	SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV	180							

Db 130 SCNEEKWALLTPLNVNCHASGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 249
Qy 181 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSSLISYGADPTLL 240
Db 250 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSSLISYGADPTLL 309
Qy 241 NCHNKSADLAPTQPKERLAYEFKGHSLLQAREADVTRIKKHLSEMVNFKHPQTHET 300
Db 310 NCHNKSADLAPTQPKERLAYEFKGHSLLQAREADVTRIKKHLSEMVNFKHPQTHET 369
Qy 301 ALHCAASPYPKRKQICELLRKGANINEKTEFPLHVASEKAHNDVVEVVKHEAKV 360
Db 370 ALHCAASPYPKRKQICELLRKGANINEKTEFPLHVASEKAHNDVVEVVKHEAKV 429
Qy 361 NALDNLGQTSLHRAAYCGHLOFCRLLSYGCDPNIIISLQGTALQMGNEVQQLQEGIS 420
Db 430 NALDNLGQTSLHRAAYCGHLOFCRLLSYGCDPNIIISLQGTALQMGNEVQQLQEGIS 489
Qy 421 LGNSEADQLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 490 LGNSEADQLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 549
Qy 481 QHGADVHAKDKGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAKGYE 540
Db 550 QHGADVHAKDKGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAKGYE 609
Qy 541 ICKLLQHGADPTKKNRGDNTPLDVKQDGTIDQLLRGDAALLDAKKGCLARVKKLSS 600
Db 610 ICKLLQHGADPTKKNRGDNTPLDVKQDGTIDQLLRGDAALLDAKKGCLARVKKLSS 669
Qy 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 670 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 729
Qy 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEQTPDLVLVS 720
Db 730 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEQTPDLVLVS 789
Qy 721 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
Db 790 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 849
Qy 781 SFSELSVVSSSGTGASLEKKEKVPVDFSTQFVRNLGLEHMDIFEREQITLDVLVE 840
Db 850 SFSELSVVSSSGTGASLEKKEKVPVDFSTQFVRNLGLEHMDIFEREQITLDVLVE 909
Qy 841 MGHKELKEIGINAYGHRHKLKGVERLISGQOGLNPYLTNTSGSGTILIDLSPDDKEFQ 900
Db 910 MGHKELKEIGINAYGHRHKLKGVERLISGQOGLNPYLTNTSGSGTILIDLSPDDKEFQ 969
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCKNKKLWERYTHRRKEVSEENINHANE 960
Db 970 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCKNKKLWERYTHRRKEVSEENINHANE 1029
Qy 961 RMLFHGSPVNAIHKGPDERHAYIGMFGAGIYFAENSSKNQVYVGGTGCPVHKD 1020
Db 1030 RMLFHGSPVNAIHKGPDERHAYIGMFGAGIYFAENSSKNQVYVGGTGCPVHKD 1089
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1090 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1134

RESULT 13

AAB66278

ID AAB66278 standard; protein; 1169 AA.

XX AC AAB66278;

XX 05-APR-2001 (first entry)

XX Human tankyrase2 related protein sequence SEQ ID NO: 2.

DE

XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasia; aging;
inflammatory disorder.
KW Homo sapiens.
OS WO200100849-A1.
PN 04-JAN-2001.
PD 28-JUN-2000; 2000WO-US017827.
PF 29-JUN-1999; 99US-0141582P.
PR (ICOS-) ICOS CORP.
PI Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
XX WPI; 2001-102896/11.
XX N-PSDB; AAF63837.
DR New tankyrase2 polypeptides, useful for treating conditions mediated by
poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
inflammatory and autoimmune disorders.
PT Disclosure; Page 109-113; 242pp; English.
PS The present invention provides the protein and coding sequence for the
human tankyrase2 protein. This is found in two different versions,
designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
ribosylation activity and is involved in the regulation of telomere
length, in which TRF1 has a role, is linked to ageing and cancer. The
sequences are useful in the treatment of cancers and inflammatory
disorders
CC
SQ Sequence 1169 AA;
Query Match 99.9%; Score 5582; DB 4; Length 1169;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFGKRDVVEYLLQNGASVQARDGGLIPLHNACSYGHEVAEYNNLLRHGADPNARDNNYT 60
Db 70 GFGKRDVVEYLLQNGANVQARDGGLIPLHNACSYGHEVAEYNNLLRHGADPNARDNNYT 129
Qy 61 PLHEAAIKGKIDVICIVLQHGAEPTIRNTDGRDLDADPSAKAVLTGEYKDELLESAR 120
Db 130 PLHEAAIKGKIDVICIVLQHGAEPTIRNTDGRDLDADPSAKAVLTGEYKDELLESAR 189
Qy 121 SGNEEKWALLTPLNVNCHASGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 180
Db 190 SGNEEKWALLTPLNVNCHASGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 249
Qy 181 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSSLISYGADPTLL 240
Db 250 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSSLISYGADPTLL 309
Qy 241 NCHNKSADLAPTQPKERLAYEFKGHSLLQAREADVTRIKKHLSEMVNFKHPQTHET 300
Db 310 NCHNKSADLAPTQPKERLAYEFKGHSLLQAREADVTRIKKHLSEMVNFKHPQTHET 369
Qy 301 ALHCAASPYPKRKQICELLRKGANINEKTEFPLHVASEKAHNDVVEVVKHEAKV 360
Db 370 ALHCAASPYPKRKQICELLRKGANINEKTEFPLHVASEKAHNDVVEVVKHEAKV 429
Qy 361 NALDNLGQTSLHRAAYCGHLOFCRLLSYGCDPNIIISLQGTALQMGNEVQQLQEGIS 420
Db 430 NALDNLGQTSLHRAAYCGHLOFCRLLSYGCDPNIIISLQGTALQMGNEVQQLQEGIS 489
Qy 421 LGNSEADQLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 490 LGNSEADQLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 549

QY 481 QHGADVHAKDKGGLVPLPHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAAAKGKYE 540
Db 550 QHGADVHAKDKGGLVPLPHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAAAKGKYE 609
QY 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQLLRGDAALLDAAKKGCLARVKKLSS 600
Db 610 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQLLRGDAALLDAAKKGCLARVKKLSS 669
QY 601 PDVNCRDTPQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 670 PDVNCRDTPQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 729
QY 661 VAALLIKYNACVNAATDKWAFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQTPLDLVS 720
Db 730 VAALLIKYNACVNAATDKWAFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQTPLDLVS 789
QY 721 ADDVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSLSAASSLONLSG 780
Db 790 ADDVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSLSAASSLONLSG 849
QY 781 SFSSELSSVSSSGTEGASSLEKKEVPGVDFSIQTQVRNLGLEHLMDFEREQITLDLVE 840
Db 850 SFSSELSSVSSSGTEGASSLEKKEVPGVDFSIQTQVRNLGLEHLMDFEREQITLDLVE 909
QY 841 MGHKELKEIGINAYGHRHKLKGVERLISGQOGLNPYLTLNTSGSTLIDLSPPDKERQ 900
Db 910 MGHKELKEIGINAYGHRHKLKGVERLISGQOGLNPYLTLNTSGSTLIDLSPPDKERQ 969
QY 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHNANE 960
Db 970 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHNANE 1029
QY 961 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSCKSNQVYIGGGTGCPVHKD 1020
Db 1030 RMLFHGSPFVNAIIHKGFDERHAYIGGMFGAGIYFAENSCKSNQVYIGGGTGCPVHKD 1089
QY 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSV 1065
Db 1090 RSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSV 1134

RESULT 14

AA197749
ID AA197749 standard; protein; 1240 AA.

AC AC
AA197749;

DT DT
06-AUG-2001 (first entry)

DE DE
Tanykrase homologue isotype 2 protein sequence.

XX XX
Tanykrase homologue isotype 2; TaHo-1; TaHo-2; cell proliferation;
KW KW
cell cycle protein; cell cycle associated disorder; cancer; gene mapping;
XX XX
chromosome mapping; gene therapy; vaccine.

OS OS
Unidentified.

FN FN
WO200130987-A2.

PD PD
03-MAY-2001.

XX XX
25-OCT-2000; 2000WO-US041528.

PF PF
25-OCT-1999; 99US-00427154.

PR PR
(RIGE-) RIGEL PHARM INC.

PA PA
Luo Y, Chan E, Xu X, Huang B;

XX XX
WPI; 2001-300503/31.

XX XX
N-PSDB; AAA91488.

PT Novel recombinant cell cycle polypeptide, tanykrase H useful for inducing
PT or preventing cell proliferation in cells, and for diagnosing, treating
PT or preventing cell cycle associated disorders such as cancer.
XX
PS Claim 22; Fig 4; 63pp; English.

XX This sequence is the Tanykrase homologue isotype 2 (TaHo-2) protein of
CC the invention. The invention also relates to the TaHo-2 protein. The TaHo
CC proteins are useful for inducing or preventing cell proliferation in
CC cells, and in the study or treatment of conditions mediated by the cell
CC cycle proteins, such as to diagnose, treat or prevent cell cycle
CC associated disorders, preferably cancer. The TaHo coding sequences are
CC useful as hybridisation probes, in chromosome and gene mapping and in the
CC generation of anti-sense DNA and RNA. The coding sequences are also
CC useful for the preparation of TaHo, for generating either transgenic
CC animals or knock out animals which, in turn, are useful in a development
CC and screening of therapeutically useful agents, in gene therapy, as
CC vaccine, and for construction of hybridisation probes for mapping the
CC gene which encodes TaHo and for the genetic analysis of individuals with
CC genetic disorders. The TaHo proteins, and their coding sequences are
CC useful in screening assays

XX Sequence 1240 AA;

Query Match 99.9%; Score 5582; DB 4; Length 1240;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1084; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGRKDVVEYLLQNGASVQARDGGIPLHNACSFHAEVNNLLRHGADPNARDNNYT 60

Db 141 GFGRKDVVEYLLQNGANVQARDGGIPLHNACSFHAEVNNLLRHGADPNARDNNYT 200

QY 61 PLHEAAIKKIDVICIVLLQHGAEPTIRNTDGRDALDPSAKAVLTGEYKDELLSAR 120

Db 201 PLHEAAIKKIDVICIVLLQHGAEPTIRNTDGRDALDPSAKAVLTGEYKDELLSAR 260

QY 121 SGNEEKWALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDKGLV 180

Db 261 SGNEEKWALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDKGLV 320

QY 181 PLHNACSYGHEVTELLVKGACVNAWDLWQFTPLHEAAASKNRVEVCSLLSYGADPTLL 240

Db 321 PLHNACSYGHEVTELLVKGACVNAWDLWQFTPLHEAAASKNRVEVCSLLSYGADPTLL 380

QY 241 NCHNSAIDLAPTPQKERLAYEFKGHSLLOAAREADVTRIKHLSLEMYNFKHPQTHET 300

Db 381 NCHNSAIDLAPTPQKERLAYEFKGHSLLOAAREADVTRIKHLSLEMYNFKHPQTHET 440

QY 301 ALHCAAASPYPKRKQICELLRRKANINEKTEFLTPLVHASEKAHNDVVVVVKEAKV 360

Db 441 ALHCAAASPYPKRKQICELLRRKANINEKTEFLTPLVHASEKAHNDVVVVVKEAKV 500

QY 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYCGDNNIISLQGFALQMGNNVQQLQEGIS 420

Db 501 NALDNLGQTSLHRAAYCGHLQTCRLLSYCGDNNIISLQGFALQMGNNVQQLQEGIS 560

QY 421 LGNSEADROLLBAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHPAAGNVRVSVYELL 480

Db 561 LGNSEADROLLBAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHPAAGNVRVSVYELL 620

QY 481 QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAAAKGKYE 540

Db 621 QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAAAKGKYE 680

QY 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQLLRGDAALLDAAKKGCLARVKKLSS 600

Db 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQLLRGDAALLDAAKKGCLARVKKLSS 740

QY 601 PDVNCRDTPQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660

Db 741 PDVNCRDTPQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 800

QY 661 VAALLIKYNACVNAATDKWAFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQTPLDLVS 720

801 VAAALLIKYNACVNTDKWFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDLVS 860
721 ADDVSALLTAAMPSPALPCYKPEQVLNGVRSFGATADALSSGSPSSLSAASSLDNLSSG 780
861 ADDVSALLTAAMPSPALPCYKPEQVLNGVRSFGATADALSSGSPSSLSAASSLDNLSSG 920
781 SFSELSVVSSSGTEGASLEKKEVPGVDFSTQFVRNLGLEHLMDFPEREQITLDLVE 840
921 SFSELSVVSSSGTEGASLEKKEVPGVDFSTQFVRNLGLEHLMDFPEREQITLDLVE 980
841 MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSTILIDLSPDKKEFQ 900
981 MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSTILIDLSPDKKEFQ 1040
901 SVEEEMQSTVREHRDGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSENNHANE 960
1041 SVEEEMQSTVREHRDGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSENNHANE 1100
961 RMLFHGSPFNVAIIHKGFDERHAYIGMFCAGIYFAENSSKNQVYVYGGTGCPCVHKD 1020
1101 RMLFHGSPFNVAIIHKGFDERHAYIGMFCAGIYFAENSSKNQVYVYGGTGCPCVHKD 1160
1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
1161 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1205

RESULT 15

ABG73731
ID ABG73731 standard; protein; 1240 AA.
AC ABG73731;
XX
XX
DT 08-APR-2003 (first entry)
DE Tankyrase H isotype 2 TaHo-2 fragment from clone K23.
KW Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-2;
KW TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour;
KW cell cycle related disorder; poly ADP-ribose polymerase; PARP.
XX
XX Unidentified.
OS
FN WO200286170-A1.
PD 31-OCT-2002.
XX
XX 25-APR-2002; 2002WO-US013185.
XX
XX 25-APR-2001; 2001US-00843159.
XX (RIGE-) RIGEL PHARM INC.
XX
XX Luo Y, Chan E, Xu X, Huang B, Ossoskaya V;
XX
XX WPI; 2003-093158/08.
DR N-PSDB; ABQ77067.

New recombinant nucleic acid encoding a cell cycle protein, useful for
diagnosing and treating a cell cycle related disorder, e.g. cancer.

Claim 14; Fig 4; 90pp; English.

This invention describes a novel recombinant nucleic acid encoding the
cell cycle protein TaHo, a tankyrase H isoform. The products of the
invention have cytostatic and immunostimulant activity and can be used
for gene therapy and in vaccines. The cell cycle protein TaHo and the
nucleic acid encoding the protein are useful for diagnosing and treating
a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a
tumour cell. The methods are useful for screening for a bioactive agent
capable of binding to a cell cycle protein tankyrase H, or a bioactive
agent capable of modulating a cell cycle protein tankyrase H or PARP

CC (poly ADP-ribose polymerase) activity. The antibodies are useful for
inducing an immune response against the cell cycle proteins. This
sequence represents the tankyrase H isoform 2, TaHo-2, isolated from
clone K23 which is described in the disclosure of the invention
XX
SQ Sequence 1240 AA;
Query Match 99.9%; Score 5582; DB 6; Length 1240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNWT 60
DB 141 GFRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNWT 200
QY 61 PLHEAAIKGKIDVCIVLLOHGAEPTRINTDGTALDPSAKAVLTGEYKDELESAR 120
DB 201 PLHEAAIKGKIDVCIVLLOHGAEPTRINTDGTALDPSAKAVLTGEYKDELESAR 260
QY 121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 180
DB 261 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQHGADVHAKDGLV 320
QY 181 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVCVSLLSYGADPTLL 240
DB 321 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVCVSLLSYGADPTLL 380
QY 241 NCHNKSALDAPTPOLKERLAYEFKSHLSLQAAAREADVTRIKKHLSELVNFKHPQTHET 300
DB 381 NCHNKSALDAPTPOLKERLAYEFKSHLSLQAAAREADVTRIKKHLSELVNFKHPQTHET 440
QY 301 ALHCAAAAPYPRKQICELLRLKGANINEKTEFTPLHVAASEKAHNDVVEVVHAEKV 360
DB 441 ALHCAAAAPYPRKQICELLRLKGANINEKTEFTPLHVAASEKAHNDVVEVVHAEKV 500
QY 361 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDDPNIIISLQGFALQWNNVQOLLQEGIS 420
DB 501 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDDPNIIISLQGFALQWNNVQOLLQEGIS 560
QY 421 LGNSADRLLEAAKAGVETVKLCITVQSVNCRDIEGRQSTPLHFAAGYNNVSVVEYLL 480
DB 561 LGNSADRLLEAAKAGVETVKLCITVQSVNCRDIEGRQSTPLHFAAGYNNVSVVEYLL 620
QY 481 OHGADVHAKDKGGLVPLHNACSYGHEVVAELLVKHGAVNNVADLWKFTPLHEAAAKGYE 540
DB 621 OHGADVHAKDKGGLVPLHNACSYGHEVVAELLVKHGAVNNVADLWKFTPLHEAAAKGYE 680
QY 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDITDIQDLRGDAALLDAKKGCLARVKLSS 600
DB 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGDITDIQDLRGDAALLDAKKGCLARVKLSS 740
QY 601 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASVGHVD 660
DB 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASVGHVD 800
QY 661 VAAALLIKYNACVNTDKWFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDLVS 720
DB 801 VAAALLIKYNACVNTDKWFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDLVS 860
QY 721 ADDVSALLTAAMPSPALPCYKPEQVLNGVRSFGATADALSSGSPSSLSAASSLDNLSSG 780
DB 861 ADDVSALLTAAMPSPALPCYKPEQVLNGVRSFGATADALSSGSPSSLSAASSLDNLSSG 920
QY 781 SFSELSVVSSSGTEGASLEKKEVPGVDFSTQFVRNLGLEHLMDFPEREQITLDLVE 840
DB 921 SFSELSVVSSSGTEGASLEKKEVPGVDFSTQFVRNLGLEHLMDFPEREQITLDLVE 980
QY 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSTILIDLSPDKKEFQ 900
DB 981 MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSTILIDLSPDKKEFQ 1040
QY 901 SVEEEMQSTVREHRDGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSENNHANE 960

Db 1041 SVEEMQSTVREHRDGGHAGGIFNRYNLLKIQVCNKKLWERYTHRRKEVSEENHNHANE 1100
Qy 961 RMLPHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGCPVHKD 1020
Db 1101 RMLPHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGCPVHKD 1160
Qy 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPFGHHSVTGRPSV 1065
Db 1161 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPFGHHSVTGRPSV 1205

Search completed: December 18, 2006, 17:26:52
Job time : 142.536 secs

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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:51:56 ; Search time 132.143 Seconds
(without alignments)
3733.253 Million cell updates/sec

Title: US-10-616-101-3
Perfect score: 5585
Sequence: 1 GFGKRDVVEYLLQNGASVQA.....AMKMAHSPGHHSVTGRPSV 1065

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5585	100.0	1065	5	US-10-616-101-3
2	5585	100.0	1083	5	US-10-616-101-12
3	5585	100.0	1100	5	US-10-616-101-8
4	5582	99.9	1166	4	US-09-972-115A-6
5	5582	99.9	1166	4	US-10-163-587A-15
6	5582	99.9	1166	4	US-10-199-937-135
7	5582	99.9	1169	4	US-10-199-937-2
8	5582	99.9	1169	4	US-10-199-937-101
9	5582	99.9	1240	5	US-10-616-101-4
10	5582	99.9	1262	4	US-10-199-937-107
11	5582	99.9	1385	4	US-10-199-937-133
12	5579	99.9	1100	5	US-10-616-101-11
13	5421	97.1	1074	3	US-09-509-196A-2
14	5363.5	96.0	1227	3	US-09-849-602-26
15	4740.5	84.9	1327	3	US-09-841-835-2
16	4740.5	84.9	1327	3	US-09-972-115A-8
17	4740.5	84.9	1327	3	US-10-199-937-4
18	4739.5	84.9	1333	3	US-09-972-115A-2
19	4663	83.5	1267	3	US-09-972-115A-4
20	3918	70.2	784	4	US-10-199-937-89
21	3775	67.6	756	4	US-10-199-937-91
22	3706.5	66.4	1181	4	US-10-199-937-139
23	3706.5	66.4	1181	6	US-11-097-143-9474
24	3412	61.1	802	3	US-09-964-899-41
25	3412	61.1	802	5	US-10-975-523-41
26	3093	55.4	949	3	US-09-841-835-10
27	2916	52.2	583	5	US-10-616-101-10

28	2367	42.4	522	4	US-10-199-937-99	Sequence 99, Appl
29	2165	38.8	415	4	US-10-276-774-1690	Sequence 1690, Ap
30	1918.5	34.4	673	3	US-09-841-835-8	Sequence 8, Appli
31	1895	33.9	362	4	US-10-199-937-160	Sequence 160, App
32	1869.5	33.5	1099	4	US-10-199-937-178	Sequence 178, App
33	1038	18.6	338	5	US-10-616-101-9	Sequence 9, Appli
34	877.5	15.7	1765	5	US-10-055-877-140	Sequence 140, App
35	875.5	15.7	4274	5	US-10-450-763-31331	Sequence 31331, A
36	875.5	15.7	4377	5	US-10-756-149-4917	Sequence 4917, Ap
37	875.5	15.7	4384	5	US-10-821-234-1120	Sequence 1120, Ap
38	875.5	15.7	4386	5	US-10-450-763-37734	Sequence 37734, A
39	871.5	15.6	1940	5	US-10-055-877-141	Sequence 141, App
40	863.5	15.5	1762	4	US-10-205-194-117	Sequence 117, App
41	860.5	15.4	1330	4	US-10-108-260A-3237	Sequence 3237, App
42	852.5	15.3	4397	5	US-10-450-763-52303	Sequence 52303, A
43	836	15.0	1549	6	US-11-097-143-1776	Sequence 1776, Ap
44	836	15.0	1549	6	US-11-097-143-29028	Sequence 29028, A
45	820	14.7	1159	5	US-10-055-877-139	Sequence 139, App

ALIGNMENTS

RESULT 1

US-10-616-101-3
; Sequence 3, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION: *
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossovskaya, Valeria
; TITLE OF INVENTION: Tankrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1065
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-101-3

Query Match 100.0%; Score 5585; DB 5; Length 1065;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GFGKRDVVEYLLQNGASVQARDGGLIPLHNACSGHAEVWVNLRLRHGADPNARDNWNVT	60
DB	1	GFGKRDVVEYLLQNGASVQARDGGLIPLHNACSGHAEVWVNLRLRHGADPNARDNWNVT	60
QY	61	PLHEAAIKGIDVCIVLLOHGAETIRNTDGRALDLADPSAKAVLTGEYKDELLSAR	120
DB	61	PLHEAAIKGIDVCIVLLOHGAETIRNTDGRALDLADPSAKAVLTGEYKDELLSAR	120
QY	121	SGNEEKWALLTPLNVNCHASDGRKSTPLHAAAGVNRVKIVOLLLOHGAHVHAKDKGLV	180
DB	121	SGNEEKWALLTPLNVNCHASDGRKSTPLHAAAGVNRVKIVOLLLOHGAHVHAKDKGLV	180
QY	181	PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVCVCSLLLSYGADPTLL	240
DB	181	PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVCVCSLLLSYGADPTLL	240
QY	241	NCHNKAIDLAFTPOLKERLAYEFKXGSLLOQAAREADVTRIKKHLSELMVNFKHPQTHET	300

Db 241 NCHNSAIDLAPTPQKRLAYEFKHSLLQAAREADVTRIKHLSLEWVNFKHPQTHET 300
Qy 301 ALHCAASPYPKRKQICELLRRKGANINEKTEFLPLHVASEKAHNDVVEVVVKEAKV 360
Db 301 ALHCAASPYPKRKQICELLRRKGANINEKTEFLPLHVASEKAHNDVVEVVVKEAKV 360
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQMGNEVQQLQEGIS 420
Db 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQMGNEVQQLQEGIS 420
Qy 421 LGNSEADROLLEAAKAGDVETVKKCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 421 LGNSEADROLLEAAKAGDVETVKKCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Qy 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKGAVVNVADLWKFTPLHEAAAKGKYE 540
Db 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKGAVVNVADLWKFTPLHEAAAKGKYE 540
Qy 541 ICKLLLQHAGADPTKQRDGNTPDLVKDGTDIQDLLRGDAALLDAAKKGCLARVKKLS 600
Db 541 ICKLLLQHAGADPTKQRDGNTPDLVKDGTDIQDLLRGDAALLDAAKKGCLARVKKLS 600
Qy 601 PDNVNCRDTQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 601 PDNVNCRDTQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Qy 661 VAALLIKYNACVNAATDKWAFTPLHEAAQKGRTOQLCALLAHGADPTLKQEGQTPDLVLS 720
Db 661 VAALLIKYNACVNAATDKWAFTPLHEAAQKGRTOQLCALLAHGADPTLKQEGQTPDLVLS 720
Qy 721 ADDVSALLTAAMPSPALPSCKYKQVNLGVSPGATADALSSGSPSSLSAASLDNLSG 780
Db 721 ADDVSALLTAAMPSPALPSCKYKQVNLGVSPGATADALSSGSPSSLSAASLDNLSG 780
Qy 781 SFSELSVSSVSSGTEGASSLEKEVPGVDFSIQFVRLGLEHLMDFEREQITLDVLVE 840
Db 781 SFSELSVSSVSSGTEGASSLEKEVPGVDFSIQFVRLGLEHLMDFEREQITLDVLVE 840
Qy 841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQLNPLYTLNTSGSTILIDLSPDDKEFQ 900
Db 841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQLNPLYTLNTSGSTILIDLSPDDKEFQ 900
Qy 901 SVEEEMQSTVREHDCGHAGGIFNRYNLIKQVCKNKLWERYTHRRKEVSEENHNHANE 960
Db 901 SVEEEMQSTVREHDCGHAGGIFNRYNLIKQVCKNKLWERYTHRRKEVSEENHNHANE 960
Qy 961 RMLFHGSPFNALIHKGFDERHAYIGMFGAGIYFAENSCKSNQYVYGGGTGCPVHKD 1020
Db 961 RMLFHGSPFNALIHKGFDERHAYIGMFGAGIYFAENSCKSNQYVYGGGTGCPVHKD 1020
Qy 1021 RSCYICHRQLLFCRVTLGKSFQFSAMKHAHSPPGHHSVTGRPSV 1065
Db 1021 RSCYICHRQLLFCRVTLGKSFQFSAMKHAHSPPGHHSVTGRPSV 1065

RESULT 2

US-10-616-101-12
; Sequence 12, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossoskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25

; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic mutant
US-10-616-101-12

Query Match 100.0%; Score 5585; DB 5; Length 1083;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFGKRDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYTT 60
Db 1 GFGKRDVVEYLLQNGASVQARDGGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYTT 60
Qy 61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTPALDADPSAKAVLTGEYKKOELLESA 120
Db 61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRTPALDADPSAKAVLTGEYKKOELLESA 120
Qy 121 SGNEEKWALLTPLVNCHASDGRKSTPLHLAGYNNRKIVQLLOHGADVHAKDKGDLV 180
Db 121 SGNEEKWALLTPLVNCHASDGRKSTPLHLAGYNNRKIVQLLOHGADVHAKDKGDLV 180
Qy 181 PLHNACSYGHYEYVELLVKHGACVNAWDLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
Db 181 PLHNACSYGHYEYVELLVKHGACVNAWDLWQFTPLHEAASKNRVEVCSLLSYGADPTLL 240
Qy 241 NCHNSAIDLAPTPQKRLAYEFKHSLLQAAREADVTRIKHLSLEWVNFKHPQTHET 300
Db 241 NCHNSAIDLAPTPQKRLAYEFKHSLLQAAREADVTRIKHLSLEWVNFKHPQTHET 300
Qy 301 ALHCAASPYPKRKQICELLRRKGANINEKTEFLPLHVASEKAHNDVVEVVVKEAKV 360
Db 301 ALHCAASPYPKRKQICELLRRKGANINEKTEFLPLHVASEKAHNDVVEVVVKEAKV 360
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQMGNEVQQLQEGIS 420
Db 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQFTALQMGNEVQQLQEGIS 420
Qy 421 LGNSEADROLLEAAKAGDVETVKKCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 421 LGNSEADROLLEAAKAGDVETVKKCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Qy 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKGAVVNVADLWKFTPLHEAAAKGKYE 540
Db 481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKGAVVNVADLWKFTPLHEAAAKGKYE 540
Qy 541 ICKLLLQHAGADPTKQRDGNTPDLVKDGTDIQDLLRGDAALLDAAKKGCLARVKKLS 600
Db 541 ICKLLLQHAGADPTKQRDGNTPDLVKDGTDIQDLLRGDAALLDAAKKGCLARVKKLS 600
Qy 601 PDNVNCRDTQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 601 PDNVNCRDTQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Qy 661 VAALLIKYNACVNAATDKWAFTPLHEAAQKGRTOQLCALLAHGADPTLKQEGQTPDLVLS 720
Db 661 VAALLIKYNACVNAATDKWAFTPLHEAAQKGRTOQLCALLAHGADPTLKQEGQTPDLVLS 720
Qy 721 ADDVSALLTAAMPSPALPSCKYKQVNLGVSPGATADALSSGSPSSLSAASLDNLSG 780
Db 721 ADDVSALLTAAMPSPALPSCKYKQVNLGVSPGATADALSSGSPSSLSAASLDNLSG 780
Qy 781 SFSELSVSSVSSGTEGASSLEKEVPGVDFSIQFVRLGLEHLMDFEREQITLDVLVE 840
Db 781 SFSELSVSSVSSGTEGASSLEKEVPGVDFSIQFVRLGLEHLMDFEREQITLDVLVE 840
Qy 841 MGHKELKEIGINAYGHRHKLIKGVERLISGQQLNPLYTLNTSGSTILIDLSPDDKEFQ 900

Db 841 MGKELKEIGINAYGHRHKLINGVERLSGQGLNPYLTNTSGSTLIDLSPDKEFQ 900
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 960
Qy 961 RMLFHGSPFVNAI IHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD 1020
Db 961 RMLFHGSPFVNAI IHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD 1020
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
RESULT 3
US-10-616-101-8
; Sequence 8, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossovskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: RIGL-GLOCIIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/596,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-101-8
Query Match 100.0%; Score 5585; DB 5; Length 1100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60
Db 1 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60
Qy 61 PLHEAAIKGIDVCIVLQHGAEPTIRNTDGTALDADPSAKAVLTGEYKDELLESAR 120
Db 61 PLHEAAIKGIDVCIVLQHGAEPTIRNTDGTALDADPSAKAVLTGEYKDELLESAR 120
Qy 121 SGNEKMMALLTPLNVNCHASDGRKSTPLHLAAGNRYKIVQLLQHGADVHAKDGLV 180
Db 121 SGNEKMMALLTPLNVNCHASDGRKSTPLHLAAGNRYKIVQLLQHGADVHAKDGLV 180
Qy 181 PLHNACSYGHVEVTELLVKGACVNMADLWQFTPLHEAASKRVEVCSEILLSYGADPTLL 240
Db 181 PLHNACSYGHVEVTELLVKGACVNMADLWQFTPLHEAASKRVEVCSEILLSYGADPTLL 240
Qy 241 NCHNKAISDALPTPOLKERLAYEFKGHSLQQAAREADVTRIKKHSLEWVNFKHPQTHET 300
Db 241 NCHNKAISDALPTPOLKERLAYEFKGHSLQQAAREADVTRIKKHSLEWVNFKHPQTHET 300
Qy 301 ALHCAASAPYKPKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAVY 360
Db 301 ALHCAASAPYKPKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAVY 360
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRELLSYGCDPNIIISLQGFALTQMGNEVQQLLEGIS 420

Db 361 NALDNLGQTSLHRAAYCGHLQTCRELLSYGCDPNIIISLQGFALTQMGNEVQQLLEGIS 420
Qy 421 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGQSTPLHFAAGYNEVSVVEYLL 480
Db 421 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGQSTPLHFAAGYNEVSVVEYLL 480
Qy 481 QHGADVIAKDKGGLVPLHNACSYGHEVVAEALLVKHGA VNVNADLWKFTPLHEAAAKGYE 540
Db 481 QHGADVIAKDKGGLVPLHNACSYGHEVVAEALLVKHGA VNVNADLWKFTPLHEAAAKGYE 540
Qy 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDYDIOQLLRGDAALLDAKKGCLARVKKLSS 600
Db 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDYDIOQLLRGDAALLDAKKGCLARVKKLSS 600
Qy 601 PDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 601 PDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Qy 661 VAALLIKYNACVNATDKWAFPLHEAAQKGTQCALILLAHGADPTLKNQEGOTPLDLVS 720
Db 661 VAALLIKYNACVNATDKWAFPLHEAAQKGTQCALILLAHGADPTLKNQEGOTPLDLVS 720
Qy 721 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSPSSLSAASSLDNLSS 780
Db 721 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSPSSLSAASSLDNLSS 780
Qy 781 SFSSELSSVSSSTEGEGASSLEKKEVPGVDFITOFVRLNGLEHLMDFIEREQITLDLVE 840
Db 781 SFSSELSSVSSSTEGEGASSLEKKEVPGVDFITOFVRLNGLEHLMDFIEREQITLDLVE 840
Qy 841 MGKELKEIGINAYGHRHKLINGVERLSGQGLNPYLTNTSGSTLIDLSPDKEFQ 900
Db 841 MGKELKEIGINAYGHRHKLINGVERLSGQGLNPYLTNTSGSTLIDLSPDKEFQ 900
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 960
Qy 961 RMLFHGSPFVNAI IHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD 1020
Db 961 RMLFHGSPFVNAI IHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD 1020
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
RESULT 4
US-09-972-115A-6
; Sequence 6, Application US/09972115A
; Publication No. US20030032769A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieszyk, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-115A-6

already issued
has issued result No.4

Db 727 VAALLIKYNACVNAIDKWAFTPLHAAQKGRTOQLCALLAHGADPTLKNQEQOTPLDLVS 786
Qy 721 ADDVSALLTAAMPSPSALSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSS 780
Db 787 ADDVSALLTAAMPSPSALSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSS 846
Qy 781 SFSELSVVSSSGTSGASSLEKKEVGVDFSIQFVRNLGLEHLMDFEREQITLDVLVE 840
Db 847 SFSELSVVSSSGTSGASSLEKKEVGVDFSIQFVRNLGLEHLMDFEREQITLDVLVE 906
Qy 841 MGHEKELKEIGINAYGHRHKLKGVRELISGQOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900
Db 907 MGHEKELKEIGINAYGHRHKLKGVRELISGQOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 966
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 967 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 1026
Qy 961 RMLPHGSPFVNAILHKGDFERHAYIGMFGAGIYFAENSSKSNQVYVYIGGTCGCPVHKD 1020
Db 1027 RMLPHGSPFVNAILHKGDFERHAYIGMFGAGIYFAENSSKSNQVYVYIGGTCGCPVHKD 1086
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1087 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1131
RESULT 6
US-10-199-937-135
; Sequence 135, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 135
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-135
Query Match 99.9%; Score 5582; DB 4; Length 1166;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVLLRHGADPNARDNNYNT 60
Db 67 GFRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVLLRHGADPNARDNNYNT 126
Qy 61 PLHEAAKIDVICVILLOHGAEPTRINTDGTALDPSAKAVLTGEYKDELLESAR 120
Db 127 PLHEAAKIDVICVILLOHGAEPTRINTDGTALDPSAKAVLTGEYKDELLESAR 186
Qy 121 SGNEEKOMALLPLNVNCHASDGRKSTPLHLAGYNRVKIVOLLQHGADVHAKDGDIV 180
Db 187 SGNEEKOMALLPLNVNCHASDGRKSTPLHLAGYNRVKIVOLLQHGADVHAKDGDIV 246
Qy 181 PLHNACSYGHEVTELLVHKGACVNAWDLQWFTPLHAAASKNRVEVCSLLSYGADPTLL 240
Db 247 PLHNACSYGHEVTELLVHKGACVNAWDLQWFTPLHAAASKNRVEVCSLLSYGADPTLL 306

RESULT 7
US-10-199-937-2
; Sequence 2, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582

Qy 241 NCHNKSALDAPTQPKERLAYEFKSHLSLQAAAREADVTRIKKHLSELMVNFQHPQTHET 300
Db 307 NCHNKSALDAPTQPKERLAYEFKSHLSLQAAAREADVTRIKKHLSELMVNFQHPQTHET 366
Qy 301 ALHCAASAPYPRKQICELLRLKGANINEKTEFLTPHVAASEKANDNDVVEVVKHEAKV 360
Db 367 ALHCAASAPYPRKQICELLRLKGANINEKTEFLTPHVAASEKANDNDVVEVVKHEAKV 426
Qy 361 NALNIGQTSLHRAAYCCHLOTCLLLSYGCDPNIISLQGFALTALQMGNNENVOQLLOEGIS 420
Db 427 NALNIGQTSLHRAAYCCHLOTCLLLSYGCDPNIISLQGFALTALQMGNNENVOQLLOEGIS 486
Qy 421 LGNSEADQRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 487 LGNSEADQRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 546
Qy 481 QHGADVHAKDGGGLVPLHNACSYGHEVVAELLVKGAVVNVADLWKFTPLHAAAKGYE 540
Db 547 QHGADVHAKDGGGLVPLHNACSYGHEVVAELLVKGAVVNVADLWKFTPLHAAAKGYE 606
Qy 541 ICKLLLOHGADPTTKNRDGNTPDLVKDGDITDIODLLRGDAALDAAKKGCLARVKKLSS 600
Db 607 ICKLLLOHGADPTTKNRDGNTPDLVKDGDITDIODLLRGDAALDAAKKGCLARVKKLSS 666
Qy 601 PDVNCRDTCGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 667 PDVNCRDTCGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 726
Qy 661 VAALLIKYNACVNAIDKWAFTPLHAAQKGRTOQLCALLAHGADPTLKNQEQOTPLDLVS 720
Db 727 VAALLIKYNACVNAIDKWAFTPLHAAQKGRTOQLCALLAHGADPTLKNQEQOTPLDLVS 786
Qy 721 ADDVSALLTAAMPSPSALSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSS 780
Db 787 ADDVSALLTAAMPSPSALSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSS 846
Qy 781 SFSELSVVSSSGTSGASSLEKKEVGVDFSIQFVRNLGLEHLMDFEREQITLDVLVE 840
Db 847 SFSELSVVSSSGTSGASSLEKKEVGVDFSIQFVRNLGLEHLMDFEREQITLDVLVE 906
Qy 841 MGHEKELKEIGINAYGHRHKLKGVRELISGQOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 900
Db 907 MGHEKELKEIGINAYGHRHKLKGVRELISGQOGLNPYLTLNTSGSGTILIDLSPDDKEFQ 966
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 967 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 1026
Qy 961 RMLPHGSPFVNAILHKGDFERHAYIGMFGAGIYFAENSSKSNQVYVYIGGTCGCPVHKD 1020
Db 1027 RMLPHGSPFVNAILHKGDFERHAYIGMFGAGIYFAENSSKSNQVYVYIGGTCGCPVHKD 1086
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1087 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1131

;; PRIOR FILING DATE: 1999-06-29
;; NUMBER OF SEQ ID NOS: 178
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 1169
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-199-937-2

Query Match 99.9%; Score 5582; DB 4; Length 1169;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYT 60
Db 70 GFGKDVVEYLLQNGAVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYT 129

Qy 61 PLHEAAIKGKIDVICIVLQHGAEPTIRNTDGTALDLPADPSAKAVLTGEYKDELLSAR 120
Db 130 PLHEAAIKGKIDVICIVLQHGAEPTIRNTDGTALDLPADPSAKAVLTGEYKDELLSAR 189

Qy 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 180
Db 190 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 249

Qy 181 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
Db 250 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 309

Qy 241 NCHNKSADLAPTQKRLAYEFKSHLSLQAAREADVTRIKKHLSEMVNFKHPQTHET 300
Db 310 NCHNKSADLAPTQKRLAYEFKSHLSLQAAREADVTRIKKHLSEMVNFKHPQTHET 369

Qy 301 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPHVAASEKAHNDVVEVVVYKHEAKV 360
Db 370 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPHVAASEKAHNDVVEVVVYKHEAKV 429

Qy 361 NALNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGFALTALQMGNEVQQLQEGIS 420
Db 430 NALNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGFALTALQMGNEVQQLQEGIS 489

Qy 421 LGNSEADRLLEAAKAGDVETVKKLCVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL 480
Db 490 LGNSEADRLLEAAKAGDVETVKKLCVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL 549

Qy 481 QHGADVHAKDKGGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 540
Db 550 QHGADVHAKDKGGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 609

Qy 541 ICKLLQHGADPTKKNRDNPTPLVKDGDITDQLRGDAALLDAAKGGCLARVKLLSS 600
Db 610 ICKLLQHGADPTKKNRDNPTPLVKDGDITDQLRGDAALLDAAKGGCLARVKLLSS 669

Qy 601 PDVNCRTDQGRHSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 660
Db 670 PDVNCRTDQGRHSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 729

Qy 661 VAALLIKYCNATDKWAFTPLEHAQKGTQCALLLAHGADPTLKNQSGQTPDLVS 720
Db 730 VAALLIKYCNATDKWAFTPLEHAQKGTQCALLLAHGADPTLKNQSGQTPDLVS 789

Qy 721 ADDVSALLTAAMPSPALPSCYKQVNLGVRFGATADALSSGSPSSLSAASLDNLSSG 780
Db 790 ADDVSALLTAAMPSPALPSCYKQVNLGVRFGATADALSSGSPSSLSAASLDNLSSG 849

Qy 781 SPSLSSVSSSGTEGASSLSEKVPVDFISITQFVRLNGLHLMDFPERQITLDLVE 840
Db 850 SPSLSSVSSSGTEGASSLSEKVPVDFISITQFVRLNGLHLMDFPERQITLDLVE 909

Qy 841 MGKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLNTSGSGTILIDLSPPDKKEFQ 900
Db 910 MGKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLNTSGSGTILIDLSPPDKKEFQ 969

RESULT 8

US-10-199-937-101
; Sequence 101, Application US/10199937
; Publication No. US20070190739A1

GENERAL INFORMATION:

;; APPLICANT: Christenson, Erik
;; APPLICANT: Demaggio, Anthony J.
;; APPLICANT: Goldman, Phyllis S.
;; APPLICANT: McElligott, David L.
;; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
;; FILE REFERENCE: 27866/36559
;; CURRENT APPLICATION NUMBER: US/10/199,937
;; CURRENT FILING DATE: 2002-07-22
;; PRIOR APPLICATION NUMBER: US/09/606,035
;; PRIOR FILING DATE: 2000-06-28
;; PRIOR APPLICATION NUMBER: 60/141,582
;; PRIOR FILING DATE: 1999-06-29
;; NUMBER OF SEQ ID NOS: 178
;; SOFTWARE: Patent In Ver. 2.0

;; SEQ ID NO 101

;; LENGTH: 1169

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-10-199-937-101

Query Match 99.9%; Score 5582; DB 4; Length 1169;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYT 60
Db 70 GFGKDVVEYLLQNGAVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYT 129

Qy 61 PLHEAAIKGKIDVICIVLQHGAEPTIRNTDGTALDLPADPSAKAVLTGEYKDELLSAR 120
Db 130 PLHEAAIKGKIDVICIVLQHGAEPTIRNTDGTALDLPADPSAKAVLTGEYKDELLSAR 189

Qy 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 180
Db 190 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 249

Qy 181 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
Db 250 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 309

Qy 241 NCHNKSADLAPTQKRLAYEFKSHLSLQAAREADVTRIKKHLSEMVNFKHPQTHET 300
Db 310 NCHNKSADLAPTQKRLAYEFKSHLSLQAAREADVTRIKKHLSEMVNFKHPQTHET 369

Qy 301 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPHVAASEKAHNDVVEVVVYKHEAKV 360
Db 370 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPHVAASEKAHNDVVEVVVYKHEAKV 429

Qy 361 NALNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGFALTALQMGNEVQQLQEGIS 420
Db 430 NALNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGFALTALQMGNEVQQLQEGIS 489

Qy 421 LGNSEADRLLEAAKAGDVETVKKLCVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL 480
Db 490 LGNSEADRLLEAAKAGDVETVKKLCVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL 549

QY 481 QHGDVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540
DB 550 QHGDVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 609
QY 541 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQLLRGDAALLDAKKGCLARVKKLSS 600
DB 610 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQLLRGDAALLDAKKGCLARVKKLSS 669
QY 601 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLOHGADVNAODKGLPLHNAASYGHVD 660
DB 670 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLOHGADVNAODKGLPLHNAASYGHVD 729
QY 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLLAHAGADPTLKNQEGQTPDLVLS 720
DB 730 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLLAHAGADPTLKNQEGQTPDLVLS 789
QY 721 ADDVSALLTAAMPPSALPSCYKQVNLGVRSFGATADALSSGSPSSLSAASSLDNLSSG 780
DB 790 ADDVSALLTAAMPPSALPSCYKQVNLGVRSFGATADALSSGSPSSLSAASSLDNLSSG 849
QY 781 SFSELSVVSSSGTGASLEKEVPGVDFSTQFVRNLGLEHLMDFEREQITLDVLVE 840
DB 850 SFSELSVVSSSGTGASLEKEVPGVDFSTQFVRNLGLEHLMDFEREQITLDVLVE 909
QY 841 MGHKELKEIGINAYGHRHKLKGVRELISGQOGLNPYLTNTSGSGTILIDLSPDDKEFQ 900
DB 910 MGHKELKEIGINAYGHRHKLKGVRELISGQOGLNPYLTNTSGSGTILIDLSPDDKEFQ 969
QY 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQKCNKKLWERYTHRRKEVSEENHNHANE 960
DB 970 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQKCNKKLWERYTHRRKEVSEENHNHANE 1029
QY 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYIGGGTGPCVHKD 1020
DB 1030 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYIGGGTGPCVHKD 1089
QY 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065
DB 1090 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1134

RESULT 9

US-10-616-101-4
; Sequence 4, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossovskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: RIGI-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-101-4

Query Match 99.9%; Score 5582; DB 5; Length 1240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGRKDVVEYLLQNGASVQARDDGGLPLHNACSFHAEVVNLLLRHGADPNARDNNYT 60
DB 141 GFGRKDVVEYLLQNGASVQARDDGGLPLHNACSFHAEVVNLLLRHGADPNARDNNYT 200
QY 61 PLHBAAIKGIIDVICIVLLOHGABPTIRNTDQRTALDLADPSAKAVLTGEYKDELLESAR 120
DB 201 PLHBAAIKGIIDVICIVLLOHGABPTIRNTDQRTALDLADPSAKAVLTGEYKDELLESAR 260
QY 121 SGNSEKQWALLTPLNVNCHASDGRKSTPLHLAAGYNVRVKI VOLLLOHGADVHAKDKGLV 180
DB 261 SGNSEKQWALLTPLNVNCHASDGRKSTPLHLAAGYNVRVKI VOLLLOHGADVHAKDKGLV 320
QY 181 PLHNACSYGHEVTELLVKHGACVNAMDLMQFTPLHEAASKNRVEVCSLLLSYGDPTLL 240
DB 321 PLHNACSYGHEVTELLVKHGACVNAMDLMQFTPLHEAASKNRVEVCSLLLSYGDPTLL 380
QY 241 NCHNKAIDLAPTQKLERLAYEPKSHSLLOAAREADVTRIKKHLSEMVNPKHPQTHET 300
DB 381 NCHNKAIDLAPTQKLERLAYEPKSHSLLOAAREADVTRIKKHLSEMVNPKHPQTHET 440
QY 301 ALHCAAAAPYPRKQICELLIRKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAKV 360
DB 441 ALHCAAAAPYPRKQICELLIRKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAKV 500
QY 361 NALDNLGOTSLHRAAYCGHLOTCHLLLSYGCDDPMIISLQGFALTQMGNNVQOLLQEGIS 420
DB 501 NALDNLGOTSLHRAAYCGHLOTCHLLLSYGCDDPMIISLQGFALTQMGNNVQOLLQEGIS 560
QY 421 LGNSEADQRLLEAAKAGDVETVKKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVEYLL 480
DB 561 LGNSEADQRLLEAAKAGDVETVKKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVEYLL 620
QY 481 QHGDVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540
DB 621 QHGDVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 680
QY 541 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQLLRGDAALLDAKKGCLARVKKLSS 600
DB 681 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQLLRGDAALLDAKKGCLARVKKLSS 740
QY 601 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLOHGADVNAODKGLPLHNAASYGHVD 660
DB 741 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLOHGADVNAODKGLPLHNAASYGHVD 800
QY 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLLAHAGADPTLKNQEGQTPDLVLS 720
DB 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLLAHAGADPTLKNQEGQTPDLVLS 860
QY 721 ADDVSALLTAAMPPSALPSCYKQVNLGVRSFGATADALSSGSPSSLSAASSLDNLSSG 780
DB 861 ADDVSALLTAAMPPSALPSCYKQVNLGVRSFGATADALSSGSPSSLSAASSLDNLSSG 920
QY 781 SFSELSVVSSSGTGASLEKEVPGVDFSTQFVRNLGLEHLMDFEREQITLDVLVE 840
DB 921 SFSELSVVSSSGTGASLEKEVPGVDFSTQFVRNLGLEHLMDFEREQITLDVLVE 980
QY 841 MGHKELKEIGINAYGHRHKLKGVRELISGQOGLNPYLTNTSGSGTILIDLSPDDKEFQ 900
DB 981 MGHKELKEIGINAYGHRHKLKGVRELISGQOGLNPYLTNTSGSGTILIDLSPDDKEFQ 1040
QY 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQKCNKKLWERYTHRRKEVSEENHNHANE 960
DB 1041 SVEEMQSTVREHRDGGHAGGIFNRYNLIKQKCNKKLWERYTHRRKEVSEENHNHANE 1100
QY 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYIGGGTGPCVHKD 1020
DB 1101 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYIGGGTGPCVHKD 1160
QY 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1065
DB 1161 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1205

```
RESULT 10
; Sequence 107, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 1262
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-107

Query Match 99.9%; Score 5582; DB 4; Length 1262;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFRKDVVEYLLQNGASVQARDGGGLIPLHNACSFGEAEVNVNLLRHGADPNARNWNYT 60
DB 163 GFRKDVVEYLLQNGANVQARDGGGLIPLHNACSFGEAEVNVNLLRHGADPNARNWNYT 222
QY 61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRALDLADPSKAVLTGEYKDELLESAR 120
DB 223 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRALDLADPSKAVLTGEYKDELLESAR 282
QY 121 SGNEEKMMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVQLLOHGADVHAKDGLV 180
DB 283 SGNEEKMMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVQLLOHGADVHAKDGLV 342
QY 181 PLHNACSGHYEVTELLVKHGACVNMADLWOPTPLHVAEAKNRVVCVLSLLSYGADPTLL 240
DB 343 PLHNACSGHYEVTELLVKHGACVNMADLWOPTPLHVAEAKNRVVCVLSLLSYGADPTLL 402
QY 241 NCHNKSALDLAPTQPKERLAYEFKHSLLQAREADVTRIKKHSLEWVNFKHPQTHET 300
DB 403 NCHNKSALDLAPTQPKERLAYEFKHSLLQAREADVTRIKKHSLEWVNFKHPQTHET 462
QY 301 ALHCAAASPYPRKQICELLRLKGANINEKTEFLTPLVHASEKAHNDVVEVVKHEAKV 360
DB 463 ALHCAAASPYPRKQICELLRLKGANINEKTEFLTPLVHASEKAHNDVVEVVKHEAKV 522
QY 361 NALDNLGTSLHRAAYCCHLQTCRLLLSYGCDDPNIISLQGTALQNGENVQQLLEGIS 420
DB 523 NALDNLGTSLHRAAYCCHLQTCRLLLSYGCDDPNIISLQGTALQNGENVQQLLEGIS 582
QY 421 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
DB 583 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 542
QY 481 QHGADVHAKDGGGLVPLHNACSGHYEVAELLVKRGAVNVNADLWKFTPLHEAAAKGYE 540
DB 643 QHGADVHAKDGGGLVPLHNACSGHYEVAELLVKRGAVNVNADLWKFTPLHEAAAKGYE 702
QY 541 ICKLLQHGADPTKQNRGNTPLDLVKGDDTDIQLLRGDAALLDAAKGCLARVKLSS 600
DB 703 ICKLLQHGADPTKQNRGNTPLDLVKGDDTDIQLLRGDAALLDAAKGCLARVKLSS 762
QY 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
DB 763 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 822

RESULT 11
US-10-199-937-133
; Sequence 133, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133
; LENGTH: 1385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-133

Query Match 99.9%; Score 5582; DB 4; Length 1385;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFRKDVVEYLLQNGASVQARDGGGLIPLHNACSFGEAEVNVNLLRHGADPNARNWNYT 60
DB 286 GFRKDVVEYLLQNGANVQARDGGGLIPLHNACSFGEAEVNVNLLRHGADPNARNWNYT 345
QY 61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRALDLADPSKAVLTGEYKDELLESAR 120
DB 346 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRALDLADPSKAVLTGEYKDELLESAR 405
QY 121 SGNEEKMMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVQLLOHGADVHAKDGLV 180
DB 406 SGNEEKMMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVQLLOHGADVHAKDGLV 465
QY 181 PLHNACSGHYEVTELLVKHGACVNMADLWOPTPLHVAEAKNRVVCVLSLLSYGADPTLL 240
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Db 466 PLHNACSYGHEVTELLVKGHCAGVNDLWQFTPLHEAASKNRVVCVCSLLLSYGDPTLL 525
Qy 241 NCHNKSALDLAPTQOLKRLAYEPKGHSLQAAAREADVTRIKCHLSLEWVNFQHPQTHET 300
Db 526 NCHNKSALDLAPTQOLKRLAYEPKGHSLQAAAREADVTRIKCHLSLEWVNFQHPQTHET 585
Qy 301 ALHCAAAAPYPRKQICELLRKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 360
Db 586 ALHCAAAAPYPRKQICELLRKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 645
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISQGTALQMGNEVQOQLQEGIS 420
Db 646 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISQGTALQMGNEVQOQLQEGIS 705
Qy 421 LGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 706 LGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 765
Qy 481 QHGADVHAADKGGVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540
Db 766 QHGADVHAADKGGVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 825
Qy 541 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQDLRGDAALLDAKKGCLARVKKLSS 600
Db 826 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQDLRGDAALLDAKKGCLARVKKLSS 885
Qy 601 PDVNCNCRDTQGRHSTPLHAAAGYNVLEVAEYLLQHGADVNAQDKGGLPLHNAASYGHVD 660
Db 886 PDVNCNCRDTQGRHSTPLHAAAGYNVLEVAEYLLQHGADVNAQDKGGLPLHNAASYGHVD 945
Qy 661 VAALLIKYNACVNAATDKWFTPLHEAAKQRTQLCALLAHGADPTLKNQEGQTPDLVLS 720
Db 946 VAALLIKYNACVNAATDKWFTPLHEAAKQRTQLCALLAHGADPTLKNQEGQTPDLVLS 1005
Qy 721 ADDVSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
Db 1006 ADDVSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 1065
Qy 781 SFSSELSSVSSSGTGASLEKKEVPGVDFSTQFVRNLGLEHLMDFPEREQITLDVLVE 840
Db 1066 SFSSELSSVSSSGTGASLEKKEVPGVDFSTQFVRNLGLEHLMDFPEREQITLDVLVE 1125
Qy 841 MGHKELKEIGNAYGHRHKLKGVERLISGQOGLNPYLTNTSGSGTILIDLSPDKBFQ 900
Db 1126 MGHKELKEIGNAYGHRHKLKGVERLISGQOGLNPYLTNTSGSGTILIDLSPDKBFQ 1185
Qy 901 SVEEMQSTVREHRDGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 1186 SVEEMQSTVREHRDGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE 1245
Qy 961 RMLFHGSPVNAI IHKGDFERHAYIGMFGAGIYFAENSSKNQVYGGIGGTGCPVHKD 1020
Db 1246 RMLFHGSPVNAI IHKGDFERHAYIGMFGAGIYFAENSSKNQVYGGIGGTGCPVHKD 1305
Qy 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSV 1065
Db 1306 RSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSVTGRPSV 1350

RESULT 12

US-10-616-101-11
; Sequence 11, Application US/10616101
; Publication No. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossoskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; CURRENT FILING DATE: 2003-07-08

; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic mutant
US-10-616-101-11

Query Match 99.9%; Score 5579; DB 5; Length 1100;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GFGKDVVEYLLONGASVQARDGGLIPLHNACSFHAEVNVNLLLRHGADPNARNWNT 60
Db 1 GFGKDVVEYLLONGASVQARDGGLIPLHNACSFHAEVNVNLLLRHGADPNARNWNT 60
Qy 61 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRDLDLADPSAKAVLTGEYKDELESAR 120
Db 61 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRDLDLADPSAKAVLTGEYKDELESAR 120
Qy 121 SGNBEKMWALLTPLNVNCHASDGRKSTPLHAAAGYNRVKIVOLLQHGADVNAQDKGLV 180
Db 121 SGNBEKMWALLTPLNVNCHASDGRKSTPLHAAAGYNRVKIVOLLQHGADVNAQDKGLV 180
Qy 181 PLHNACSYGHEVTELLVKGHCAGVNDLWQFTPLHEAASKNRVVCVCSLLLSYGDPTLL 240
Db 181 PLHNACSYGHEVTELLVKGHCAGVNDLWQFTPLHEAASKNRVVCVCSLLLSYGDPTLL 240
Qy 241 NCHNKSALDLAPTQOLKRLAYEPKGHSLQAAAREADVTRIKCHLSLEWVNFQHPQTHET 300
Db 241 NCHNKSALDLAPTQOLKRLAYEPKGHSLQAAAREADVTRIKCHLSLEWVNFQHPQTHET 300
Qy 301 ALHCAAAAPYPRKQICELLRKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 360
Db 301 ALHCAAAAPYPRKQICELLRKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 360
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISQGTALQMGNEVQOQLQEGIS 420
Db 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISQGTALQMGNEVQOQLQEGIS 420
Qy 421 LGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db 421 LGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Qy 481 QHGADVHAADKGGVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540
Db 481 QHGADVHAADKGGVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLHEAAAKGYE 540
Qy 541 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQDLRGDAALLDAKKGCLARVKKLSS 600
Db 541 ICKLLQHGADPTKKNRDNTPDLVKGDDTDIQDLRGDAALLDAKKGCLARVKKLSS 600
Qy 601 PDVNCNCRDTQGRHSTPLHAAAGYNVLEVAEYLLQHGADVNAQDKGGLPLHNAASYGHVD 660
Db 601 PDVNCNCRDTQGRHSTPLHAAAGYNVLEVAEYLLQHGADVNAQDKGGLPLHNAASYGHVD 660
Qy 661 VAALLIKYNACVNAATDKWFTPLHEAAKQRTQLCALLAHGADPTLKNQEGQTPDLVLS 720
Db 661 VAALLIKYNACVNAATDKWFTPLHEAAKQRTQLCALLAHGADPTLKNQEGQTPDLVLS 720
Qy 721 ADDVSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
Db 721 ADDVSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
Qy 781 SFSSELSSVSSSGTGASLEKKEVPGVDFSTQFVRNLGLEHLMDFPEREQITLDVLVE 840

Db 781 SFSLSVSSVSSGTEGASSLEKGVGVDFRISITQFVRLGLEHLMDFEREQITLDLVE 840
Qy 841 MGKHELKEIGINAYGHRHKLKIGVERLISGQGLNPLYLTNTSGSGTILIDLSPDDKEFQ 900
Db 841 MGKHELKEIGINAYGHRHKLKIGVERLISGQGLNPLYLTNTSGSGTILIDLSPDDKEFQ 900
Qy 901 SVEBEMOSTVREHRDGGHAGGIFNRYNLIKQVCKNKKLWERYTHRRKEVSEENHNHANE 960
Db 901 SVEBEMOSTVREHRDGGHAGGIFNRYNLIKQVCKNKKLWERYTHRRKEVSEENHNHANE 960
Qy 961 RMLFHGSPFVNAILTHKGDFERHAYIGMGFGAGIYFAENSSKNQYVYGGTGCPVHKD 1020
Db 961 RMLFHGSPFVNAILTHKGDFERHAYIGMGFGAGIYFAENSSKNQYVYGGTGCPVHKD 1020
Qy 1021 RSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHSVTGRPSV 1065
Db 1021 RSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHSVTGRPSV 1065
RESULT 13
US-09-509-196A-2
; Sequence 2, Application US/09509196A
; Patent No. US20020037582A1
; GENERAL INFORMATION:
; APPLICANT: DALY, Roger J.
; APPLICANT: SUTHERLAND, Robert L.
; TITLE OF INVENTION: A Potential Effector for the Grb7 Family of Signalling
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: 1871-129
; CURRENT APPLICATION NUMBER: US/09/509.196A
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: P09388
; PRIOR FILING DATE: 1997-09-23
; PRIOR APPLICATION NUMBER: PCT AU98/00795
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 2
; LENGTH: 1074
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-509-196A-2
Query Match 97.1%; Score 5421; DB 3; Length 1074;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1034; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 27 IPLHNACSFGEAEVNVNLLRHGADPNARDNNWYTPLEHAAIKGKIDYCVILLOHGASPTI 86
Db 1 IPLHNACSFGEAEVNVNLLRHGADPNARDNNWYTPLEHAAIKGKIDYCVILLOHGASPTI 60
Qy 87 RNTDGRALDADPSAKAVLTGEYKQBELLESARSNGNEEKWALLTPLNVNCHASDGRKS 146
Db 61 RNTDGRALDADPSAKAVLTGEYKQBELLESARSNGNEEKWALLTPLNVNCHASDGRKS 120
Qy 147 TPLHLAGYNRVKIVQLLQHGADVHAKDKGDLVPLHNACSYGHEVTELLVKGACVNA 206
Db 121 TPLHLAGYNRVKIVQLLQHGADVHAKDKGDLVPLHNACSYGHEVTELLVKGACVNA 180
Qy 207 MDLQWFTPLHEAASKNRVEVCSLLSYGADPTLNCNKNKSAIDAPTQPKERLAYBFKG 266
Db 181 MDLQWFTPLHEAASKNRVEVCSLLSYGADPTLNCNKNKSAIDAPTQPKERLAYBFKG 240
Qy 267 HSLQQAAREADVTRIKHLSLEWNVFKHPQTHETALHCAASAPYKPKQICELLRLKGAN 326
Db 241 HSLQQAAREADVTRIKHLSLEWNVFKHPQTHETALHCAASAPYKPKQICELLRLKGAN 300
Qy 327 INEKTKEPLTPLHVAASEKAHNDVVEVVKHAKVNALDNLGQTSILHRAAYCGHLQTCRLL 386
Db 301 INEKTKEPLTPLHVAASEKAHNDVVEVVKHAKVNALDNLGQTSILHRAAYCGHLQTCRLL 360
Qy 387 LSYGCDPNIISLQGFALQMGNEVQQLQEGISLGNSEADQRLLEAAKAGDVETVKLC 446

Db 361 LSYGCDPNIISLQGFALQMGNEVQQLQEGISLGNSEADQRLLEAAKAGDVETVKLC 420
Qy 447 TVQSVNCRDIEGRQSTPLHFAAGYNRVSVVYELLQHGADVHAKDKGDLVPLHNACSYGHY 506
Db 421 TVQSVNCRDIEGRQSTPLHFAAGYNRVSVVYELLQHGADVHAKDKGDLVPLHNACSYGHY 480
Qy 507 EVAELLVKGAVNVADLWKFTPLHEAAGKYEIKCLLLOHGADPTKQRDGNTPDLV 566
Db 481 EVAELLVKGAVNVADLWKFTPLHEAAGKYEIKCLLLOHGADPTKQRDGNTPDLV 540
Qy 567 KDGDITDIDLGRDAALLDAKKGCLARVKLSSPDNVNCRDQGRHSTPLHLAAGYNNL 626
Db 541 KDGDITDIDLGRDAALLDAKKGCLARVKLSSPDNVNCRDQGRHSTPLHLAAGYNNL 600
Qy 627 EVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAPTPLHEA 686
Db 601 EVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNASLNATDKWAPTPLHEA 660
Qy 687 AQKRTQLCALLAHGADPTLKNQEGTQPLDLYSADDSALLTAAMPSPALPSCYKPOVL 746
Db 661 AQKRTQLCALLAHGADPTLKNQEGTQPLDLYSADDSALLTAAMPSPALPSCYKPOVL 720
Qy 747 NGVRSPGATADALSSGSPSSLSAASSLNLGSGFSELSVSVSSSGTEGASSLEKKEVP 806
Db 721 NGVRSPGATADALSSGSPSSLSAASSLNLGSGFSELSVSVSSSGTEGASSLEKKEVP 780
Qy 807 GVDFSITQFVRNLTGLEHLMDFEREQITLDVLEMGHKLKEIGINAYGHRHKLKIGVER 866
Db 781 GVDFSITQFVRNLTGLEHLMDFEREQITLDVLEMGHKLKEIGINAYGHRHKLKIGVER 840
Qy 867 LISGQGLNPLYLTNTSGSGTILIDLSPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRY 926
Db 841 LISGQGLNPLYLTNTSGSGTILIDLSPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRY 900
Qy 927 NILKIQKCNKWLERYTHRRKEVSEENHNHNERMLFHGSPFVNAILHKGDFERHAYIG 986
Db 901 NILKIQKCNKWLERYTHRRKEVSEENHNHNERMLFHGSPFVNAILHKGDFERHAYIG 960
Qy 987 GMFGAGIYFAENSSKNQYVYGGTGCPVHKDRSCYICHRQLLFCRVTLGKSPLOFSA 1046
Db 961 GMFGAGIYFAENSSKNQYVYGGTGCPVHKDRSCYICHRQLLFCRVTLGKSPLOFSA 1020
Qy 1047 MKMAHSPGHSVTGRPSV 1065
Db 1021 MKMAHSPGHSVTGRPSV 1039
RESULT 14
US-09-849-602-26
; Sequence 26, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849.602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 26
; LENGTH: 1227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-26
Query Match 96.0%; Score 5363.5; DB 3; Length 1227;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 1035; Conservative 3; Mismatches 25; Indels 3; Gaps 2;

Qy 1 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNWYT 60
Db 129 GFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNWYT 188
Qy 61 PLHEAAIKGKIDVICVILQHGAEPTIRNTDGRALDADPSAKAVLTGEYKDELESAR 120
Db 189 PLHEAAIKGKIDVICVILQHGAEPTIRNTDGRALDADPSAKAVLTGEYKDELESAR 248
Qy 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDKGLV 180
Db 249 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDKGLV 308
Qy 181 PLHNACSYGHEVTELLVKHGACVNMADLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
Db 309 PLHNACSYGHEVTELLVKHGACVNMADLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 368
Qy 241 NCHNKAIDLAFTPOLKERLAYEFKHSLLQAREADVTRIKKHLSELMVNFKHPQTHET 300
Db 369 NCHNKAIDLAFTPOLKERLAYEFKHSLLQAREADVTRIKKHLSELMVNFKHPQTHET 428
Qy 301 ALHCAAAAPYPRKQICELLIRKGANINEKTEFLTPLHVAESEKAHNDVVEVVKHEAKV 360
Db 429 ALHCAAAAPYPRKQICELLIRKGANINEKTEFLTPLHVAESEKAHNDVVEVVKHEAKV 488
Qy 361 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDPNIIISQGFALQMGNEVQQLIQEGIS 420
Db 489 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDPNIIISQGFALQMGNEVQQLIQEGIS 548
Qy 421 LGNSEADQLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 549 LGNSEADQLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 608
Qy 481 QHGADVHAKDKGLVPLHNACSYGHEVVAELLVKHGAVNVADLWKFTPLHEAAKAGYE 540
Db 609 QHGADVHAKDKGLVPLHNACSYGHEVVAELLVKHGAVNVADLWKFTPLHEAAKAGYE 668
Qy 541 ICKLLQHGADPTKKNRGDPTDLVKGDDTDIQLLRGDAALDAAKGGCLARVKLSS 600
Db 669 ICKLLQHGADPTKKNRGDPTDLVKGDDTDIQLLRGDAALDAAKGGCLARVKLSS 728
Qy 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
Db 729 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 788
Qy 661 VAAALLIKYNACVNAATDKWAFPLHEAAKQGTOLCALLAHGADPTLANOGSTPLDLVS 720
Db 789 VAAALLIKYNACVNAATDKWAFPLHEAAKQGTOLCALLAHGADPTLANOGSTPLDLVS 848
Qy 721 ADDVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
Db 849 ADDVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSLSAASSLDNLSSG 908
Qy 781 SFSELSSVSSSGTSGASLEKKEVPGVDFSIQFVRNLGLEHLMIDIFEREQITLDVLVE 840
Db 909 SFSELSSVSSSGTSGASLEKKEVPGVDFSIQFVRNLGLEHLMIDIFEREQITLDVLVE 968
Qy 841 MGHKELKEIGINAYGHRHKLKGVVERLISGOQGLNPYLTLNTSGSTLIDLSPDKPEFQ 900
Db 969 MGHKELKEIGINAYGHRHKLKGVVERLISGOQGLNPYLTLNTSGSTLIDLSPDKPEFQ 1028
Qy 901 SVEEBMQSTVREHRDGHAGGIFNRYNLTQKVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 1029 SVEEBMQSTVREHRDGHAGGIFNRYNLTQKVCNKKLWERYTHRRKEVSEENHNHANE 1088
Qy 961 RMLFHGSPFVNAIHKGFDERHAYIGGMFGAGIYPAENSSKSNQVYVIGGGTGCPVHK- 1019
Db 1089 RMLFHGSPFVNAIHKGFDERHAYIGGMFGAGIYPAENSSKSNQVYVIGGGTGCPVHK- 1148
Qy 1020 DRSCVICHQQLPCEVTLGKFLQPSAMKMAHSPGHHSVTGRPSV 1065
Db 1149 DLVTFATAALL--PGNLGRVFPVQCNEGTSPPGHHSVTGRPSV 1192

RESULT 15
US-09-841-835-2
; Sequence 2, Application US/09841835
; Patent No. US20020076795A1
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841.835
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1327 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
US-09-841-835-2
Query Match 84.9%; Score 4740.5; DB 3; Length 1327;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 882; Conservative 97; Mismatches 79; Indels 9; Gaps 2;
Qy 1 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNWYT 60
Db 225 GFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNWYT 284
Qy 61 PLHEAAIKGKIDVICVILQHGAEPTIRNTDGRALDADPSAKAVLTGEYKDELESAR 120
Db 285 PLHEAAIKGKIDVICVILQHGADPNIRNTDGRALDADPSAKAVLTGEYKDELESAR 344
Qy 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDKGLV 180
Db 345 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDKGLV 404
Qy 181 PLHNACSYGHEVTELLVKHGACVNMADLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
Db 405 PLHNACSYGHEVTELLVKHGACVNMADLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 464
Qy 241 NCHNKAIDLAFTPOLKERLAYEFKHSLLQAREADVTRIKKHLSELMVNFKHPQTHET 300
Db 465 NCHNKAIDLAFTPOLKERLAYEFKHSLLQAREADVTRIKKHLSELMVNFKHPQTHET 524
Qy 301 ALHCAAAAPYPRKQICELLIRKGANINEKTEFLTPLHVAESEKAHNDVVEVVKHEAKV 360

Db 525 ALHCASVSLHPKRVQVTELLRLKGANVNEKNKDFMTPLHVAERAHNDVMEVLHKHCAKM 584
Qy 361 NALDNLGQTSLSHRAAYCGHLOTCLRLLSYCDPNIIISLQGTALQMGNEVVOQLQEGIS 420
Db 585 NALDNLGQTSLSHRAALAGHLOTCLRLLSYSDPSIISLQGTAAQMGNEAVQOILSESTP 644
Qy 421 LGHSEADROLLEAAKAGDVETVKLCTVQSVNCRDTEGROSTPLHFAAGYVRVSVVEYLL 480
Db 645 IRTSDVDYRLLEASKAGDLETVQLCSSLQNVNCRDLEGRHSTPLHFAAGYVRVSVVEYLL 704
Qy 481 QHGADVHAKDKGGLVPLHNAACSYGHYEVAELLVKHGAVNVNADLWKFTPLHEAAAKGYE 540
Db 705 HHGADVHAKDKGGLVPLHNAACSYGHYEVAELLVPHGASVNVNADLWKFTPLHEAAAKGYE 764
Qy 541 ICKLLLOHGADPTKKNRDGNTPLDLVKGDGTDIQDLLRGDAALLDAAKGCCLARVKKLSS 600
Db 765 ICKLLKHGADPTKKNRDGNTPLDLVKEGDTDIQDLLKGDAALLDAAKGCCLARVQKCLCT 824
Qy 601 PDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 825 PENINCRDTCGRNSTPLHLAAGYNNLEVAEYLLHEHGADVNAQDKGGLIPLHNAASYGHVD 884
Qy 661 VAALLIKYNAQVATDKWFTPLHEAAQKGTOLCALLAHGADPTLKNQEGOTPLDLVS 720
Db 885 IAALLIKYNTCVNATDKWFTPLHEAAQKGTOLCALLAHGADPTMKNQEGOTPLDLAT 944
Qy 721 ADVSALLTAAMPPSALPSCYKQVNLGVRSFGATADALSSGSPSSLSAASSLDNLSC 780
Db 945 ADDIRALLIDAMPEALPTCFKQAT-----VVSASLISPASTPSCLSAASSIDNLG 997
Qy 781 SPSLSSVSVSSSGTEGASSLEKK--EYVGVDFSTQFVRNLGLEHLMDFEREQITLDVL 838
Db 998 PLAEVAVGGASNAGDGAAGTERKEGEVAGLDMNISQFLKSLGLEHLRDIFFETEQITLDVL 1057
Qy 839 VEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTNTSGSGTILIDLSPDDKE 898
Db 1058 ADMGHEELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTTHCVNQGTILDLAPEDKE 1117
Qy 899 FQSVVEEMQSTVREHRDGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHHA 958
Db 1118 YQSVVEEMQSTIREHRDGGNAGGIFNRYNVIRIQKVVNKKLRERFCHRQKEVSEENHH 1177
Qy 959 NERMLFHGSPFVNAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGTCPCPVH 1018
Db 1178 NERMLFHGSPFINAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGTCGCPTH 1237
Qy 1019 KDRSCYICHRQLLFCRVTLGKSLQFSAMKWAHSPGHHSVTGRPSV 1065
Db 1238 KDRSCYICHRQMLFCRVTLGKSLQFSMTKWAHAPPGHHSVIGRPSV 1284

Search completed: December 18, 2006, 17:59:59
Job time : 136.143 secs

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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:34:55 ; Search time 35.577 Seconds
(without alignments)
2620.235 Million cell updates/sec

Title: US-10-616-101-3
Perfect score: 5585
Sequence: 1 GFGKDVVEYLLQNGASVQA.....AMKVAHSPGHHVTVGRPSV 1065

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents_AA:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.psp:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.psp:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.psp:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCRUS_COMB.psp:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.psp:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.psp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Patent (✓)
Art

Result No. Query Match Length DB ID Description

1	5585	100.0	1083	2	US-09-843-1598-10	Sequence 10, Appl
2	5585	100.0	1100	2	US-09-696-668-3	Sequence 3, Appl
3	5585	100.0	1100	2	US-09-843-1598-3	Sequence 3, Appl
4	5582	99.9	1166	2	US-09-972-115A-6	Sequence 6, Appl
5	5582	99.9	1240	2	US-09-696-668-4	Sequence 4, Appl
6	5582	99.9	1240	2	US-09-843-1598-4	Sequence 4, Appl
7	5579	99.9	1100	2	US-09-843-1598-9	Sequence 9, Appl
8	5542.5	99.2	1100	2	US-09-427-154-2	Sequence 2, Appl
9	5533	99.1	1166	2	US-09-350-982C-5	Sequence 5, Appl
10	5363.5	96.0	1227	2	US-09-849-602-26	Sequence 26, Appl
11	4740.5	84.9	1327	2	US-09-196-387-2	Sequence 2, Appl
12	4740.5	84.9	1327	2	US-09-841-835-2	Sequence 2, Appl
13	4740.5	84.9	1327	2	US-09-972-115A-8	Sequence 8, Appl
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16	3412	61.1	802	2	US-09-964-899-41	Sequence 41, Appl
17	3093	55.4	949	2	US-09-196-387-10	Sequence 10, Appl
18	3093	55.4	949	2	US-09-841-835-10	Sequence 10, Appl
19	2916	52.2	583	2	US-09-843-1598-8	Sequence 8, Appl
20	1918.5	34.4	673	2	US-09-196-387-8	Sequence 8, Appl
21	1918.5	34.4	673	2	US-09-841-835-8	Sequence 8, Appl
22	875.5	15.7	4377	2	US-09-949-016-6978	Sequence 6978, Ap
23	860.5	15.4	1839	1	US-09-172-977-4	Sequence 4, Appl
24	860.5	15.4	1839	1	US-09-404-108-4	Sequence 4, Appl
25	860.5	15.4	3924	2	US-09-538-092-1246	Sequence 1246, Ap
26	842	15.1	1719	2	US-09-949-016-6966	Sequence 6966, Ap

ALIGNMENTS

RESULT 1

US-09-843-1598-10
; Sequence 10, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H. Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68252-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic mutant
US-09-843-1598-10

Query Match 100.0%; Score 5585; DB 2; Length 1083;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	181	PLHNACSYGHEVTELLVKHGACVNAMDLWQPTPLHEAASKNRVEVCSLLLSYGADPTLL	240
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Qy 301 ALHCAAASYPKPKQICELLIRKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 360
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Db 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGFALQMGNEVQQLQEGIS 420
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RESULT 2

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; Sequence 3, Application US/09696668
; Patent No. 6617102
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chen, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/696,668
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-696-668-3

Query Match 100.0%; Score 5585; DB 2; Length 1100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 3, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-159B-3

Query Match 100.0%; Score 5585; DB 2; Length 1100;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 NCHNKSATDLATPOLKRLAYEFKHSLLQAREADYTRIKKHSLEWVNFKPHQTHET 300
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DB 481 OHGADVHAKDKGLVPLHNACSYGHYEVAELLVKHGA VVNVADLWKFTPLHEAAAKGYE 540
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DB 541 ICKLLQHGADPTTKNRDGNTPDLVKDGDTDIQLLRGDAALLDAAKGGCLARVKLSS 600
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DB 601 PDVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
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DB 661 VAALLIKYNACVNATDKWAFPLHEAAQKGTOLCALLAHGADPTLKNQSGOTPLDLVS 720
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RESULT 4
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; Sequence 6, Application US/09972115A
; Patent No. 6599228
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieszyk, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-115A-6

Query Match 99.9%; Score 5582; DB 2; Length 1166;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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307 NCHNKSADIDAPTQPKERLAYEFKGHSLLOAAREADVTRIKHLSLEMVNFHKHPQTHET 366
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RESULT 5
US-09-696-668-4
; Sequence 4, Application US/09696668
; Patent No. 6617102
; GENERAL INFORMATION:
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; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Osovskaaya, Valeria
; TITLE OF INVENTION: TANKVRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS (
; FILE REFERENCE: A-68292-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/696,668
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-696-668-4
```

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Query Match          99.9%; Score 5582; DB 2; Length 1240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFGHAEVVNLRLRHGADPNARDNNYNT 60
DB 141 GFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFGHAEVVNLRLRHGADPNARDNNYNT 200
QY 61 PLHEAAIKGIDVICIVLQGAETIRNTDGR TALDLADPSAKAVLTGEYKDELLESAR 120
DB 201 PLHEAAIKGIDVICIVLQGAETIRNTDGR TALDLADPSAKAVLTGEYKDELLESAR 260
121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 180
261 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGDLV 320
181 PLHNACSYGHEVTELLVKGACVNA MDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
321 PLHNACSYGHEVTELLVKGACVNA MDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 380
241 NCHNKSADIDAPTQPKERLAYEFKGHSLLOAAREADVTRIKHLSLEMVNFHKHPQTHET 300
381 NCHNKSADIDAPTQPKERLAYEFKGHSLLOAAREADVTRIKHLSLEMVNFHKHPQTHET 440
301 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPLHVASEKAHNDVVVVVVKHEAKV 360
441 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPLHVASEKAHNDVVVVVVKHEAKV 500
361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLOGFTALQMGNEVQQLLQEGIS 420
501 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLOGFTALQMGNEVQQLLQEGIS 560
421 LGNSEADROLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
561 LGNSEADROLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
481 QHGADVHAKDKGGLVPLHNACSYGHEVVAELLVKHGAVVNVADLWKFTPLHEAAKKGKYE 540
621 QHGADVHAKDKGGLVPLHNACSYGHEVVAELLVKHGAVVNVADLWKFTPLHEAAKKGKYE 680
541 ICKLLQHGADPTKKNRDNPTPLDVKDGTDIQDLRLRGDAALLDAKKGCLARVKKLS 600
681 ICKLLQHGADPTKKNRDNPTPLDVKDGTDIQDLRLRGDAALLDAKKGCLARVKKLS 740
601 PDNVNCRDTQGRHSTPLHLAAGYNRVVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
741 PDNVNCRDTQGRHSTPLHLAAGYNRVVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
661 VAALLIKYNACVNATDKWAFPTPLHEAAKKGRTQICALLAHGADPTLKNOEGQTPDLVS 720
801 VAALLIKYNACVNATDKWAFPTPLHEAAKKGRTQICALLAHGADPTLKNOEGQTPDLVS 860
721 ADDVSALLTAAMPSPALPSCYKPVNLGVRSPGATADALSSGSPSSLSAASSLDNLG 780
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Db 861 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPCATADALLSGPSSLSAASSLONLSG 920
Qy 781 SFSELSVVSSSGTEGASLEKEVGVDFSTQFVRNLGLEHLMDFEREQITLDVLVE 840
Db 921 SFSELSVVSSSGTEGASLEKEVGVDFSTQFVRNLGLEHLMDFEREQITLDVLVE 980
Qy 841 MGHEKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTLNTSGSGTILDLSPDDKEFQ 900
Db 981 MGHEKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTLNTSGSGTILDLSPDDKEFQ 1040
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 1041 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNHANE 1100
Qy 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYGTGGTGCPCVHKD 1020
Db 1101 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYGTGGTGCPCVHKD 1160
Qy 1021 RSCYICHRQLLFCRVTLGKSFQFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1161 RSCYICHRQLLFCRVTLGKSFQFSAMKMAHSPPGHHSVTGRPSV 1205

RESULT 6
US-09-843-159B-4
; Sequence 4, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-159B-4

Query Match 99.9%; Score 5582; DB 2; Length 1240;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFGRKDVVEYLLQNGASVQARDGGILPLHNACSFQHAIEVFNLLLRHGADPNARDNNYNT 60
Db 141 GFGRKDVVEYLLQNGANVQARDGGILPLHNACSFQHAIEVFNLLLRHGADPNARDNNYNT 200
Qy 61 PLHEAAIKGIDVICVILLQHGAEPTIRNTDGTALDADPSAKAVLTGEYKDELLSAR 120
Db 201 PLHEAAIKGIDVICVILLQHGAEPTIRNTDGTALDADPSAKAVLTGEYKDELLSAR 260
Qy 121 SGNEEKWALLPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDGLIV 180
Db 261 SGNEEKWALLPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDGLIV 320
Qy 181 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVVCSSLLSYGADPTLL 240
Db 321 PLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVVCSSLLSYGADPTLL 380
Qy 241 NCHNKSADLAPTPOLKERLAYEFKHSLLQAREADVTIRIKHLSLEWVNFKHPQTHET 300
Db 381 NCHNKSADLAPTPOLKERLAYEFKHSLLQAREADVTIRIKHLSLEWVNFKHPQTHET 440
Qy 301 ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPLVASEKAHNDVVEVVVHKAHV 360

Db 441 ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPLVASEKAHNDVVEVVVHKAHV 500
Qy 361 NALDNLGQTSLHRAAYCGHLOTCHLLLSYCGDPNIIISLOGFTALQMGNNVQOOLLQEGIS 420
Db 501 NALDNLGQTSLHRAAYCGHLOTCHLLLSYCGDPNIIISLOGFTALQMGNNVQOOLLQEGIS 560
Qy 421 LGNSEADRLLEAAKAGADVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 561 LGNSEADRLLEAAKAGADVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 620
Qy 481 QHGADVHAKDGGILVPLHNACSYGHEVVAELLVKGAVVNVADLWKFTPLHFAAAKGYE 540
Db 621 QHGADVHAKDGGILVPLHNACSYGHEVVAELLVKGAVVNVADLWKFTPLHFAAAKGYE 680
Qy 541 ICKLLQHGADPTKQRDNTPLDLVKDGDTDIQLLGRDAALLDAAKGGCLARVKKLSS 600
Db 681 ICKLLQHGADPTKQRDNTPLDLVKDGDTDIQLLGRDAALLDAAKGGCLARVKKLSS 740
Qy 601 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Qy 661 VAALLIKYNACVNATDKWAFPTLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDLVS 720
Db 801 VAALLIKYNACVNATDKWAFPTLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDLVS 860
Qy 721 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPCATADALLSGPSSLSAASSLONLSG 780
Db 861 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPCATADALLSGPSSLSAASSLONLSG 920
Qy 781 SFSELSVVSSSGTEGASLEKEVGVDFSTQFVRNLGLEHLMDFEREQITLDVLVE 840
Db 921 SFSELSVVSSSGTEGASLEKEVGVDFSTQFVRNLGLEHLMDFEREQITLDVLVE 980
Qy 841 MGHEKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTLNTSGSGTILDLSPDDKEFQ 900
Db 981 MGHEKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTLNTSGSGTILDLSPDDKEFQ 1040
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 1041 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEENHNHANE 1100
Qy 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYGTGGTGCPCVHKD 1020
Db 1101 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYGTGGTGCPCVHKD 1160
Qy 1021 RSCYICHRQLLFCRVTLGKSFQFSAMKMAHSPPGHHSVTGRPSV 1065
Db 1161 RSCYICHRQLLFCRVTLGKSFQFSAMKMAHSPPGHHSVTGRPSV 1205

RESULT 7

US-09-843-159B-9
; Sequence 9, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1100

Db 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGTDIHVLRLGDAALLDAAKKGCLARVKCLSS 600
Qy 601 PDVNCRTDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLPLHNAASYGHVD 660
Db 601 PDVNCRTDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLPLHNAASYGHVD 660
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Db 661 VAALLIKYNACVNATDKWAFTPLHAAQKGRTOCALLLAHGADPTLKNQEGOTPLDLVS 720
Qy 721 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
Db 721 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
Qy 781 SFSELSVVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDLVE 840
Db 781 SFSELSVVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDLVE 840
Qy 841 MGHKELKEIGINAYGHRHKLKGVVERLISGQGLNPYLTNTSGGTILIDLSPDDKEFQ 900
Db 841 MGHKELKEIGINAYGHRHKLKGVVERLISGQGLNPYLTNTSGGTILIDLSPDDKEFQ 900
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIKVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIKVCNKKLWERYTHRRKEVSEENHNHANE 960
Qy 961 RMLFHGSPFNVAIIHKGFDERHAYIGMGFAGIYFAENSSKSNQYVYGGTGCPCVHKD 1020
Db 961 RMLFHGSPFNVAIIHKGFDERHAYIGMGFAGIYFAENSSKSNQYVYGGTGCPCVHKD 1020
Qy 1021 RSCYICHRQLLCFRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV 1065
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RESULT 9
US-09-350-982C-5
Sequence 5, Application US/09350982C
Patent No. 6455290
GENERAL INFORMATION:
APPLICANT: Berthelsen, Jens
APPLICANT: Toma, Salvatore
APPLICANT: Isacchi, Antonella
TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, and Methods Rel
TITLE OF INVENTION: Same
FILE REFERENCE: PHRM-0043
CURRENT APPLICATION NUMBER: US/09/350,982C
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 1166
TYPE: PR
ORGANISM: Artificial
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: (1102)..(1102)
OTHER INFORMATION: n is any nucleic acid
NAME/KEY: misc_feature
LOCATION: (2650)..(2650)
OTHER INFORMATION: n is any nucleic acid
US-09-350-982C-5
Query Match 99.1%; Score 5533; DB 2; Length 1166;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1056; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GFGKDVVEYLLQNGASVQARDGGGLPLHNAACSFHAEVFNLLRHHGADPNARDNNYNT 60
Db 67 GFGKDVVEYLLQNGANVQARDGGGLPLHNAACSFHAEVFNLLRHHGADPNARDNNYNT 126

Qy 61 PLHEAAIKGIDVCIIVLLOHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKKDELLESAR 120
Db 127 PLHEAAIKGIDVCIIVLLOHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKKDELLESAR 186
Qy 121 SGNEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIKIVOLLQHGADVNAQDKGLD 180
Db 187 SGNEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIKIVOLLQHGADVNAQDKGLD 246
Qy 181 PLHNACSYGHEVTELLVKHGACVNAMDLWQFTPLHAAASKNRVEVCILLISYGDPTLL 240
Db 247 PLHNACSYGHEVTELLVKHGACVNAMDLWQFTPLHAAASKNRVEVCILLISYGDPTLL 306
Qy 241 NCHNKSADLAPTQPKERLAYEFKSHSLQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Db 307 NCHNKSADLAPTQPKERLAYEFKSHSLQAAREADVTRIKKHLSELMVNFKHPQTHET 366
Qy 301 ALHCAASAPYPRKQICELLRLKGANINEKTEFELPLHVAASEKAHNDVVEVVVHEAKV 360
Db 367 AXHCAASAPYPRKQICELLRLKGANINEKTEFELPLHVAASEKAHNDVVEVVVHEAKV 426
Qy 361 NALDNLGQTSLHRAAYCGHLOTCLLLISYGCDDNIIISLOGETALQMGNNVQOLLQEGIS 420
Db 427 NALDNLGQTSLHRAAYCGHLOTCLLLISYGCDDNIIISLOGETALQMGNNVQOLLQEGIS 486
Qy 421 LGNSEADRLLEAAKAGDVETVKCLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 487 LGNSEADRLLEAAKAGDVETVKCLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 546
Qy 481 QHGADVHAQDKGLVPLHNACSYGHEVVAELLVKHGA VNVVADLWKFTPLHAAAAGKYE 540
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Db 607 ICKLLQHGADPTKKNRDGNTPLDLVKDGTDIQDLRLGDAALLDAAKKGCLARVKCLSS 666
Qy 601 PDVNCRTDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLPLHNAASYGHVD 660
Db 667 PDVNCRTDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLPLHNAASYGHVD 726
Qy 661 VAALLIKYNACVNATDKWAFTPLHAAQKGRTOCALLLAHGADPTLKNQEGOTPLDLVS 720
Db 727 VAALLIKYNACVNATDKWAFTPLHAAQKGRTOCALLLAHGADPTLKNQEGOTPLDLVS 786
Qy 721 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
Db 787 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLSSG 846
Qy 781 SFSELSVVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDLVE 840
Db 847 SFSELSVVSSSGTEGASLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDLVE 906
Qy 841 MGHKELKEIGINAYGHRHKLKGVVERLISGQGLNPYLTNTSGGTILIDLSPDDKEFQ 900
Db 907 MGHKELKEIGINAYGHRHKLKGVVERLISGQGLNPYLTNTSGGTILIDLSPDDKEFQ 966
Qy 901 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIKVCNKKLWERYTHRRKEVSEENHNHANE 960
Db 967 SVEEMQSTVREHRDGGHAGGIFNRYNLIKIKVCNKKLWERYTHRRKEVSEENHNHANE 1026
Qy 961 RMLFHGSPFNVAIIHKGFDERHAYIGMGFAGIYFAENSSKSNQYVYGGTGCPCVHKD 1020
Db 1027 RMLFHGSPFNVAIIHKGFDERHAYIGMGFAGIYFAENSSKSNQYVYGGTGCPCVHKD 1086
Qy 1021 RSCYICHRQLLCFRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV 1065
Db 1087 RSCYICHRQLLCFRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV 1131

RESULT 10
US-09-849-602-26
Sequence 26, Application US/09849602


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QY 1 GFGRKDVVEYLLQNGASVOARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60
Db 225 GFGRKDVVEYLLQNGASVOARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 284
QY 61 PLHEAAIKGKIDVICIVLLOHGAEPITRNTDGTALDPSAKAVLTGEYKDELLESAR 120
Db 285 PLHEAAIKGKIDVICIVLLOHGAEPITRNTDGTALDPSAKAVLTGEYKDELLESAR 344
QY 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLQHGADVHAKDGLV 180
Db 345 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLQHGADVHAKDGLV 404
QY 181 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVCSSLISYGDPTLL 240
Db 405 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVCSSLISYGDPTLV 464
QY 241 NCHNKSADLAPTOLKERLAYEFKHSLLQAAREADVTRIKKHSLEWNVKHPQTHET 300
Db 465 NCHGKSADVMAPTPELRERLTTEYFKHSLLOAAREADLAKVKTTLALEIINFKPQSHET 524
QY 301 ALHCAAAAPYPRKQICELLRLKGANINEKTEFPLTHVASEKAHNDVVEVVVKEAKV 360
Db 525 ALHCAVASLHPKQVTELLRLKGANVNEKDFMTPLHVAERAHNDVMEVLHKGAKM 584
QY 361 NALDNLGOTSLHRAAYCGHLCRLLLSYGCDPNIISLQGTALQMGNEVQQLLQEGIS 420
Db 595 NALDTLQGTALHRAALAGHLQTCRLLLSYGSFPSIISLQGTAAQMGNEAVQQLSESTP 644
QY 421 LGNSADQLLEAAKAGDVETVKLCITVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL 480
Db 645 IRTSDVYRLLEAAKAGDLETVKLCSSQNVNCRDLEGRHSTPLHFAAGYNNRVSVVEYLL 704
QY 481 OHGADVHAKDGLVPLHNACSYGHEVVAELLVKHGAVNVNADLWKFTPLHEAAAKGYE 540
Db 705 HHGADVHAKDGLVPLHNACSYGHEVVAELLVKHGAVNVNADLWKFTPLHEAAAKGYE 764
QY 541 ICKLLQHGADPTKKNRGNTPLDVKDGTDIQDLRGDAALLDAKKGCLARVKLSS 600
Db 765 ICKLLKHGADPTKKNRGNTPLDVKEGDTDIQDLKGDAALLDAKKGCLARVKLCT 824
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Db 825 PENINCRDTQGRNSTPLHLAGYNNLEVAEYLLHGHGADVNAQDKGGLIPLHNAASYGHVD 884
QY 661 VAALLIKYNACVNTDKWAPTPLHEAAOKGRTOLCALLLHGHGADPTLKNQEGTDLVLS 720
Db 885 TAALLIKYNTCVNATDKWAPTPLHEAAOKGRTOLCALLLHGHGADPTMKNQEGTDLVAT 944
QY 721 ADDVSALLTAAMPSPALPCYKQVPLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
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QY 781 SFSELSSVVSSSGTGASLEKK--EVPGVDPSTITQFVRNLEHLMIDIFEREQITLTVL 838
Db 998 PLAEALVAGSAGNAGDGAAGTERKEGEVAGLDMNISQFLKSLGLEHLRIDIFETEQITLTVL 1057
QY 839 VPMGHKEIKGINAYGHRHKLIGVERLISQOGLNPLYTLNTSGSGTILIDLSPDCKE 898
Db 1058 ADMGHEELKEIGINAYGHRHKLIGVERLISQOGLNPLYTLPHVCYNQGTILIDLAPEDKE 1117
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QY 959 NERMLFHGSPFNVAIIHKGDFDRHAYIGMFGAGIYFAENSKSNQYVYGGTGCPVH 1018
Db 1178 NERMLFHGSPFNVAIIHKGDFDRHAYIGMFGAGIYFAENSKSNQYVYGGTGCPVH 1237
QY 1019 KDRSCYIHRQLLFCRVTLGKSFLOFSAMKMAHSPGHHSVTGRPSV 1065
Db 1238 KDRSCYIHRQMLFCRVTLGKSFLOFSAMKMAHSPGHHSVTGRPSV 1284
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RESULT 12
US-09-841-835-2
; Sequence 2, Application US/09841835
; Patent No. 6506587
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841.835
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1327 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
US-09-841-835-2

Query Match 84.9%; Score 4740.5; DB 2; Length 1327;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 882; Conservative 97; Mismatches 79; Indels 9; Gaps 2;

QY 1 GFGRKDVVEYLLQNGASVOARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60
Db 225 GFGRKDVVEYLLQNGASVOARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 284
QY 61 PLHEAAIKGKIDVICIVLLOHGAEPITRNTDGTALDPSAKAVLTGEYKDELLESAR 120
Db 285 PLHEAAIKGKIDVICIVLLOHGAEPITRNTDGTALDPSAKAVLTGEYKDELLESAR 344
QY 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLQHGADVHAKDGLV 180
Db 345 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLQHGADVHAKDGLV 404
QY 181 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVCSSLISYGDPTLL 240
Db 405 PLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVCSSLISYGDPTLV 464
QY 241 NCHNKSADLAPTOLKERLAYEFKHSLLQAAREADVTRIKKHSLEWNVKHPQTHET 300
Db 465 NCHGKSADVMAPTPELRERLTTEYFKHSLLOAAREADLAKVKTTLALEIINFKPQSHET 524
QY 301 ALHCAAAAPYPRKQICELLRLKGANINEKTEFPLTHVASEKAHNDVVEVVVKEAKV 360
```

Db 525 ALHCAVASLHPKRVQVTELLRLKGANVNEKNKDFMTPLHVAARAHNDVMEVLKHGAKM 584
Qy 361 NALNLGQTSLHRAAYCHLQTCRLLLSYGCDPNIISLQGFALOMGNVNVQQLQSGIS 420
Db 585 NALDTLGTALHRAALAGHLQTCRLLLSYGDPSIISLQGFATAQMGNEAVQQLSESTP 644
Qy 421 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYL 480
Db 645 IRTSDVDYRLLEAKAGDLETVVKQLSSQNVNCRDLGRHSTPLHFAAGYNRVSVVEYL 704
Qy 481 QHGADVHAKDGGGLVPLHNAACSYGHEVAELLVHVGAVNVADLWKFTPLHEAAKAGYE 540
Db 705 HHGADVHAKDGGGLVPLHNAACSYGHEVAELLVHVGASVNVADLWKFTPLHEAAKAGYE 764
Qy 541 ICKLLHGHGADPTKKNRDGNTPLDVKDGTDIQDLRGDAALLDAKKGCLARVKKLSS 600
Db 765 ICKLLHGHGADPTKKNRDGNTPLDVKEGDTDIQLLKGDAALLDAKKGCLARVQKLC 824
Qy 601 PDVNCRDTOGRHSTPLHNAAGYNNLEVAEYLLQHGADVNAODKGGIPLHNAASYGHVD 660
Db 825 PENINCRDTOGRNSTPLHNAAGYNNLEVAEYLLHGHGADVNAODKGGIPLHNAASYGHVD 884
Qy 661 VAALLIKYNACVNATDKWFTPLHEAAKAGRTQCALLLAHGADPTLKNQEGQTPDLVS 720
Db 885 IAALLIKYNTCVNATDKWFTPLHEAAKAGRTQCALLLAHGADPTMKNQEGQTPDLAT 944
Qy 721 ADDVSALLTAAMPSPALPSCYKQVNLGVNRSFGATADALSSGSPSSLSAASLDNLG 780
Db 945 ADDIRALLIDAMPPEALPTCFKQAT-----VVSASLISPASTPSCLSAASIDNLG 997
Qy 781 SFSELSSVSSSGTEGASSLEKK--EVPGVDFSTQFVRNLGLEHLMIDIFEREQITLDVL 838
Db 998 PLAELAVGASNAGDGAAGTERKEGEVAGLDMNISQFLKSIGLEHLADI FETEQITLDVL 1057
Qy 839 VEMGHKELKEIGINAYGHRHKLKGVVERLLSGQGLNPYLTLNTSGSGTILIDISPDK 898
Db 1058 ADMGHEELKEIGINAYGHRHKLKGVVERLLSGQGTNPYLTFHCVNQGTILDLAPDKE 1117
Qy 899 FQSVVEEMQSTVREHRDGHAGGIFNRYNLIKIKVCNKKLWERYTHRRKEVSENNHA 958
Db 1118 YQSVVEEMQSTIREHRDGNAGGIFNRYNIRIKQVNVKKLRERFCHRQKEVSENNHH 1177
Qy 959 NERMLFHGSPFNALIHKGDFERHAYTGGMGAGIYFAENSSKSNQYVYGGTGCPCPVH 1018
Db 1178 NERMLFHGSPFNALIHKGDFERHAYTGGMGAGIYFAENSSKSNQYVYGGTGCPCPT 1237
Qy 1019 KDRSICYICRQLLFCRVTLGKSFQFSAMKMAHSPGHHSVTGRPSV 1065
Db 1238 KDRSICYICRQMLFCRVTLGKSFQFSTMKMAHAPPGHHSVIGRPSV 1284

RESULT 13

US-09-972-115A-8
; Sequence 8, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972.115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent in version 3.1
; LENGTH: 1327
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-972-115A-8
Query Match 84.9%; Score 4740.5; DB 2; Length 1327;
Best Local Similarity 82.7%; Pred. No. 0;
Matches 882; Conservative 97; Mismatches 79; Indels 9; Gaps 2;
Qy 1 GFRKQDVVEYLLQNGASVQARDGGGLPLHNACSFHAEVNVNLLRRHAGDAPNADNNYT 60
Db 225 GFRKQDVVEYLLQNGANVHARDGGGLPLHNACSFHAEVNVNLLRRHAGDAPNADNNYT 284
Qy 61 PLHEAAIKGIDVICIVLQHGAEPTIRNTDGRALDADPSAKAVLTGEYKQDLELSAR 120
Db 285 PLHEAAIKGIDVICIVLQHGADPNIRNTDGSALDADPSAKAVLTGEYKQDLELSAR 344
Qy 121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNRVKTIVQLLQHGADVHAKDGDV 180
Db 345 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNRVKTIVQLLQHGADVHAKDGDV 404
Qy 181 PLHNACSYGHEVTELLVHKGACVNAAMDQWFTPLHEAASKNRVEVCSLLLSYCADPTLL 240
Db 405 PLHNACSYGHEVTELLVHKGACVNAAMDQWFTPLHEAASKNRVEVCSLLLSHAGDPTLV 464
Qy 241 NCHNKSALDAPTPOKRLAYEFKSHLSLQAAEADVTIRIKKHLSELMVNFKHQTHET 300
Db 465 NCHGKSADVAPTPELRELTIEFKSHLSLQAAEADLAKVKKTALALEINFKQPSHET 524
Qy 301 ALHCAAAAPSPKQKQICELLRLKGANINTEKGFPLPLHVAASEKAHNDVVEVVKHAKV 360
Db 525 ALHCAVASLHPKRVQVTELLRLKGANVNEKNKDFMTPLHVAARAHNDVMEVLKHGAKM 584
Qy 361 NALNLGQTSLHRAAYCHLQTCRLLLSYGCDPNIISLQGFALOMGNVNVQQLQSGIS 420
Db 585 NALDTLGTALHRAALAGHLQTCRLLLSYGDPSIISLQGFATAQMGNEAVQQLSESTP 644
Qy 421 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYL 480
Db 645 IRTSDVDYRLLEAKAGDLETVVKQLSSQNVNCRDLGRHSTPLHFAAGYNRVSVVEYL 704
Qy 481 QHGADVHAKDGGGLVPLHNAACSYGHEVAELLVHVGAVNVADLWKFTPLHEAAKAGYE 540
Db 705 HHGADVHAKDGGGLVPLHNAACSYGHEVAELLVHVGASVNVADLWKFTPLHEAAKAGYE 764
Qy 541 ICKLLHGHGADPTKKNRDGNTPLDVKDGTDIQDLRGDAALLDAKKGCLARVKKLSS 600
Db 765 ICKLLHGHGADPTKKNRDGNTPLDVKEGDTDIQLLKGDAALLDAKKGCLARVQKLC 824
Qy 601 PDVNCRDTOGRHSTPLHNAAGYNNLEVAEYLLQHGADVNAODKGGIPLHNAASYGHVD 660
Db 825 PENINCRDTOGRNSTPLHNAAGYNNLEVAEYLLHGHGADVNAODKGGIPLHNAASYGHVD 884
Qy 661 VAALLIKYNACVNATDKWFTPLHEAAKAGRTQCALLLAHGADPTLKNQEGQTPDLVS 720
Db 885 IAALLIKYNTCVNATDKWFTPLHEAAKAGRTQCALLLAHGADPTMKNQEGQTPDLAT 944
Qy 721 ADDVSALLTAAMPSPALPSCYKQVNLGVNRSFGATADALSSGSPSSLSAASLDNLG 780
Db 945 ADDIRALLIDAMPPEALPTCFKQAT-----VVSASLISPASTPSCLSAASIDNLG 997
Qy 781 SFSELSSVSSSGTEGASSLEKK--EVPGVDFSTQFVRNLGLEHLMIDIFEREQITLDVL 838
Db 998 PLAELAVGASNAGDGAAGTERKEGEVAGLDMNISQFLKSIGLEHLADI FETEQITLDVL 1057
Qy 839 VEMGHKELKEIGINAYGHRHKLKGVVERLLSGQGLNPYLTLNTSGSGTILIDISPDK 898
Db 1058 ADMGHEELKEIGINAYGHRHKLKGVVERLLSGQGTNPYLTFHCVNQGTILDLAPDKE 1117
Qy 899 FQSVVEEMQSTVREHRDGHAGGIFNRYNLIKIKVCNKKLWERYTHRRKEVSENNHA 958
Db 1118 YQSVVEEMQSTIREHRDGNAGGIFNRYNIRIKQVNVKKLRERFCHRQKEVSENNHH 1177
Qy 959 NERMLFHGSPFNALIHKGDFERHAYTGGMGAGIYFAENSSKSNQYVYGGTGCPCPVH 1018

Db 1178 NERMLFHGSPFFINAIHHKGFDERHAYIGCMFGAGIYFAENSKSNQYVYGIGGTGCPH 1237
QY 1019 KDRSCVICHROLFCRVTLGKSFLOFSAMKMAHSPGHHSVTGPRSV 1065
Db 1238 KDRSCVICHROLFCRVTLGKSFLOFSAMKMAHSPGHHSVTGPRSV 1284

RESULT 14
US-09-972-115A-2
Sequence 2, Application US/09972115A
Patent No. 6599728
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Mieczyslaw, Piatyvezek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1333
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(1)
OTHER INFORMATION: The 'Xaa' at location 1 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (2)..(2)
OTHER INFORMATION: The 'Xaa' at location 2 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (3)..(3)
OTHER INFORMATION: The 'Xaa' at location 3 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (4)..(4)
OTHER INFORMATION: The 'Xaa' at location 4 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (5)..(5)
OTHER INFORMATION: The 'Xaa' at location 5 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (6)..(6)
OTHER INFORMATION: The 'Xaa' at location 6 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (7)..(7)
OTHER INFORMATION: The 'Xaa' at location 7 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (8)..(8)
OTHER INFORMATION: The 'Xaa' at location 8 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (9)..(9)
OTHER INFORMATION: The 'Xaa' at location 9 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
OTHER INFORMATION: The 'Xaa' at location 10 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (10)..(10)
OTHER INFORMATION: The 'Xaa' at location 11 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (11)..(11)
OTHER INFORMATION: The 'Xaa' at location 12 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (12)..(12)
OTHER INFORMATION: The 'Xaa' at location 13 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (13)..(13)
OTHER INFORMATION: The 'Xaa' at location 14 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (14)..(14)
OTHER INFORMATION: The 'Xaa' at location 15 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (15)..(15)
OTHER INFORMATION: The 'Xaa' at location 16 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (16)..(16)
OTHER INFORMATION: The 'Xaa' at location 17 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (17)..(17)
OTHER INFORMATION: The 'Xaa' at location 18 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (18)..(18)
OTHER INFORMATION: The 'Xaa' at location 19 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (19)..(19)
OTHER INFORMATION: The 'Xaa' at location 20 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (20)..(20)
OTHER INFORMATION: The 'Xaa' at location 21 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (21)..(21)
OTHER INFORMATION: The 'Xaa' at location 22 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (22)..(22)
OTHER INFORMATION: The 'Xaa' at location 23 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T
NAME/KEY: misc feature
LOCATION: (23)..(23)
OTHER INFORMATION: The 'Xaa' at location 24 stands for Lys, Asn, Arg, Ser, Thr, Ile, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T


```

; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyzek A.
; FILE OF INVENTION: A Second Mammalian Telomerase
; CURRENT APPLICATION NUMBER: US 09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1267
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(11)
; OTHER INFORMATION: The 'Xaa' at location 1 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (42)-(42)
; OTHER INFORMATION: The 'Xaa' at location 42 stands for Lys, Arg, Thr, or Met.
; NAME/KEY: misc feature
; LOCATION: (98)-(98)
; OTHER INFORMATION: The 'Xaa' at location 98 stands for Lys, Arg, Thr, or Met.
; NAME/KEY: misc feature
; LOCATION: (110)-(110)
; OTHER INFORMATION: The 'Xaa' at location 110 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (114)-(114)
; OTHER INFORMATION: The 'Xaa' at location 114 stands for Asn, Ser, Thr, or Ile.
; NAME/KEY: misc feature
; LOCATION: (126)-(126)
; OTHER INFORMATION: The 'Xaa' at location 126 stands for Lys, or Asn.
; NAME/KEY: misc feature
; LOCATION: (139)-(139)
; OTHER INFORMATION: The 'Xaa' at location 139 stands for Ile, Val, Leu, or Phe.
; NAME/KEY: misc feature
; LOCATION: (144)-(144)
; OTHER INFORMATION: The 'Xaa' at location 144 stands for Thr.
; NAME/KEY: misc feature
; LOCATION: (153)-(153)
; OTHER INFORMATION: The 'Xaa' at location 153 stands for Thr.
; NAME/KEY: misc feature
; LOCATION: (166)-(166)
; OTHER INFORMATION: The 'Xaa' at location 166 stands for Ser, Gly, Arg, or Cys.
; NAME/KEY: misc feature
; LOCATION: (173)-(173)
; OTHER INFORMATION: The 'Xaa' at location 173 stands for Ile, Val, Leu, or Phe.
; NAME/KEY: misc feature
; LOCATION: (174)-(174)
; OTHER INFORMATION: The 'Xaa' at location 174 stands for Glu, or Lys.
; NAME/KEY: misc feature
; LOCATION: (183)-(183)
; OTHER INFORMATION: The 'Xaa' at location 183 stands for Val.
; NAME/KEY: misc feature
; LOCATION: (185)-(185)
; OTHER INFORMATION: The 'Xaa' at location 185 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (188)-(188)
; OTHER INFORMATION: The 'Xaa' at location 188 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (202)-(202)
; OTHER INFORMATION: The 'Xaa' at location 202 stands for His, or Pro.
; NAME/KEY: misc feature
; LOCATION: (204)-(204)
; OTHER INFORMATION: The 'Xaa' at location 204 stands for Glu, or Lys.
; NAME/KEY: misc feature
; LOCATION: (205)-(205)
; OTHER INFORMATION: The 'Xaa' at location 205 stands for Asn, Ser, Thr, or Ile.
; NAME/KEY: misc feature
; LOCATION: (207)-(207)
; OTHER INFORMATION: The 'Xaa' at location 207 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (211)-(211)
; OTHER INFORMATION: The 'Xaa' at location 211 stands for Gln, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (213)-(213)
; OTHER INFORMATION: The 'Xaa' at location 213 stands for Ser, Gly, Arg, or Cys.
; NAME/KEY: misc feature
; LOCATION: (215)-(215)
; OTHER INFORMATION: The 'Xaa' at location 215 stands for Lys, Asn, Glu, Asp, Gln, His
; OTHER INFORMATION: , a stop codon, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (227)-(227)
; OTHER INFORMATION: The 'Xaa' at location 227 stands for His, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (228)-(228)
; OTHER INFORMATION: The 'Xaa' at location 228 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (237)-(237)
; OTHER INFORMATION: The 'Xaa' at location 237 stands for Glu, or Asp.
; NAME/KEY: misc feature
; LOCATION: (238)-(238)
; OTHER INFORMATION: The 'Xaa' at location 238 stands for Asn, Ser, Thr, Ile, Asp, Gly
; OTHER INFORMATION: , Ala, Val, His, Arg, Pro, Leu, Tyr, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (667)-(667)
; OTHER INFORMATION: The 'Xaa' at location 667 stands for Tyr, Cys, Ser, or Phe.
; NAME/KEY: misc feature
; LOCATION: (725)-(725)
; OTHER INFORMATION: The 'Xaa' at location 725 stands for Lys, or Asn.
; NAME/KEY: misc feature
; LOCATION: (727)-(727)
; OTHER INFORMATION: The 'Xaa' at location 727 stands for His, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (735)-(735)
; OTHER INFORMATION: The 'Xaa' at location 735 stands for Glu, or Asp.
; NAME/KEY: misc feature
; LOCATION: (741)-(741)
; OTHER INFORMATION: The 'Xaa' at location 741 stands for Met, Val, or Leu.
; NAME/KEY: misc feature
; LOCATION: (763)-(763)
; OTHER INFORMATION: The 'Xaa' at location 763 stands for Leu, or Phe.
; NAME/KEY: misc feature
; LOCATION: (764)-(764)
; OTHER INFORMATION: The 'Xaa' at location 764 stands for Tyr, Cys, Ser, or Phe.
; NAME/KEY: misc feature
; LOCATION: (787)-(787)
; OTHER INFORMATION: The 'Xaa' at location 787 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (788)-(788)
; OTHER INFORMATION: The 'Xaa' at location 788 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (789)-(789)
; OTHER INFORMATION: The 'Xaa' at location 789 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (790)-(790)
; OTHER INFORMATION: The 'Xaa' at location 790 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (791)-(791)
; OTHER INFORMATION: The 'Xaa' at location 791 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:27:10 ; Search time 32.8048 Seconds
(without alignments)
3123.657 Million cell updates/sec

Title: US-10-616-101-3

Perfect score: 5585

Sequence: 1 GFGKRDVVEYLLQNGASVQA.....AMKMAHSPPGHHVSGRPSV 1065

Scoring table: , BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	877.5	15.7	1765	T42714	ankyrin 3, splice
2	877.5	15.7	1961	T42716	ankyrin 3, splice
3	875.5	15.7	4377	A55575	ankyrin 3, long sp
4	873.5	15.6	1943	T42713	ankyrin 3, splice
5	871.5	15.6	1940	T42715	ankyrin 3, splice
6	860.5	15.4	3924	S37431	ankyrin 2, neurona
7	844	15.1	1856	B35049	ankyrin 1, erythro
8	844	15.1	1880	A35049	ankyrin 1, erythro
9	842	15.1	1881	SUHUK	ankyrin 1, erythro
10	839.5	15.0	1848	S37771	ankyrin, erythrocy
11	837.5	15.0	1862	I49502	ankyrin - mouse
12	834	14.9	1549	T13940	ankyrin - fruit fl
13	814.5	14.6	2039	T15347	ankyrin-related un
14	828	11.2	791	T42691	hypothetical prote
15	545.5	9.8	1411	S30355	alpha-latroinsecto
16	514	9.2	934	H71274	probable ankyrin -
17	496.5	8.9	1062	T30255	inversin - mouse
18	491.5	8.8	1062	T14151	Inv protein - mous
19	464.5	8.3	1401	S11527	alpha-latrotoxin p
20	456.5	8.2	1188	T19552	hypothetical prote
21	451	8.1	1058	D82654	ankyrin-like prote
22	431.5	7.7	426	AE2149	hypothetical prote
23	426	7.6	991	T25412	hypothetical prote
24	405.5	7.3	1184	T00253	gene Ankhzn protei
25	388	6.9	397	T46445	hypothetical prote
26	372.5	6.7	2584	T24158	hypothetical prote
27	372.5	6.7	2606	T24157	hypothetical prote
28	363.5	6.5	1031	T43458	hypothetical prote
29	350	6.3	557	T46507	hypothetical prote

ALIGNMENTS

RESULT 1

T42714

ankyrin 3, splice form 2 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T42714

R:Peterson, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.

J. Cell Biol. 130, 313-330, 1995

A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene f the repeat domain.

A:Reference number: Z22237; MUID:95340633; PMID:7615634

A:Accession: T42714

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1765 <P>

A:Cross-references: UNIPROT:Q61307; UNIPARC:UPI0000029AB8; EMBL:L40632; NID:g710548; PID:

A:Experimental source: strain C57BL/6J; kidney

C:Genetics:

A:Gene: Ank3

A:Map position: 10

A:Introns: 1587/1

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

Query Match 15.7%; Score 877.5; DB 2; Length 1765;

Best Local Similarity 30.9%; Pred. NO. 4.1e-46;

Matches 277; Conservative 125; Mismatches 377; Indels 117; Gaps 22;

QY 3 GRKDVVEYLLQNGASVQARDGGLIPLHNACSFQHAENVNLLRHGADPNARDNNYTP 62

Db 68 GHVEVVELLOREANVDATKKGNTALHISLAGQAEVVKVLVTNGANVNAQSQNGFTPL 127

QY 63 HEAAIKGKIDVICVLLQHGAEPTIRNTDGRTPALDLA-----DPSAKAVLTGYK---KDE 114

Db 128 YMAAQENHLEVVRELLDNGASQSLATEDGFTPLAVALQQGHQDVVLSLENDTKGKRLP 187

QY 115 LLESARSGNEEMKALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVOLLLOHGADVHAK 174

Db 188 ALHIAARKDDTKAAALLLQNDTNADVESKSGFTPLHIAAHYGNINVTALLNRAAAVDFT 247

QY 175 DKGDLVPLHNACSGHYEVTELLVKHGACVNMDLWQFTPLHKAASKNRVECSLLSYG 234

Db 248 ARNDITPLHVAASKGNANMVKLLLDORGAKIDAKTRDGLTPLHCGARSHEQVEMLLDRS 307

QY 235 ADPTLLNCHNKSAIDLAPTPOLKERLAYEFKGHSLLOQAAREADVTRIKKHLSELMVNFKH 294

Db 308 A-PILSKTN-----GLSPHMTQGD-----HLNCVQLLQ 339

QY 295 -----PQTHETALHCAAAPYPRKQICELLKKGANINEKTEFLTPLHVAASEKAHN 347

Db 340 NVPPDDVTNDYLTALHVAACHGCHKV---VAKVLLDKKASPNKALNGFTPLHIACKCKRI 396

30 348.5 6.2 606 2 AC2508 hypothetical prote
31 345 6.2 1423 1 I37275 death-associated p
32 336.5 6.0 1107 2 T21280 hypothetical prote
33 321 5.7 1398 2 T21884 hypothetical prote
34 310 5.6 1435 2 T29230 hypothetical prote
35 306 5.5 1322 2 A59288 myosin heavy chain
36 305 5.5 679 2 B45771 2-SA-dependent RNA
37 300.5 5.4 1016 2 T19006 ankyrin related pr
38 299.5 5.4 633 2 T27499 hypothetical prote
39 299 5.4 247 2 D84448 probable ankyrin f
40 294.5 5.3 900 2 A42024 transcription fact
41 290 5.2 1004 2 A55142 myosin-light-chain
42 287.5 5.1 656 2 A34793 sex-determining pr
43 287 5.1 1295 2 T21720 hypothetical prote
44 285 5.1 1083 2 S48460 probable membrane
45 284 5.1 237 2 T50984 related to 26a pro

C;Keywords: alternative splicing; peripheral membrane protein

F:73-105/Domain: ankyrin repeat homology <AN01>
F:106-138/Domain: ankyrin repeat homology <AN02>
F:139-171/Domain: ankyrin repeat homology <AN03>
F:172-200/Domain: ankyrin repeat homology <AN04>
F:201-233/Domain: ankyrin repeat homology <AN05>
F:234-266/Domain: ankyrin repeat homology <AN06>
F:267-299/Domain: ankyrin repeat homology <AN07>
F:300-332/Domain: ankyrin repeat homology <AN08>
F:333-365/Domain: ankyrin repeat homology <AN09>
F:366-398/Domain: ankyrin repeat homology <AN10>
F:399-431/Domain: ankyrin repeat homology <AN11>
F:432-464/Domain: ankyrin repeat homology <AN12>
F:465-497/Domain: ankyrin repeat homology <AN13>
F:498-530/Domain: ankyrin repeat homology <AN14>
F:531-563/Domain: ankyrin repeat homology <AN15>
F:564-596/Domain: ankyrin repeat homology <AN16>
F:597-629/Domain: ankyrin repeat homology <AN17>
F:630-662/Domain: ankyrin repeat homology <AN18>
F:663-695/Domain: ankyrin repeat homology <AN19>
F:696-728/Domain: ankyrin repeat homology <AN20>
F:729-761/Domain: ankyrin repeat homology <AN21>
F:762-794/Domain: ankyrin repeat homology <AN22>
F:795-827/Domain: ankyrin repeat homology <AN23>

Query Match 15.7%; Score 875.5; DB 2; Length 4377;
Best Local Similarity 30.5%; Pred. No. 2.3e-45;
Matches 273; Conservative 126; Mismatches 362; Indels 135; Gaps 21;

Qy 3 GRKDVVEYLLQNGASVQARDGGGLPLHNACSFHAEVNVNLLRHGADPNARDNNWYTPL 62
Db 85 GHVEVSELLQREANVDAATKGNATLHSLAGQAEVVKVLTNGANVNAQSQNGFTPL 144

Qy 63 HEAAIKGKIDVICVILQHGAEPTIRNTDGTALDLA-----DPSAKAVLTGEYK---KDE 114
Db 145 YMAAQENHLEVVEVFLDNGASQSLATEDGFTPLAVALQOQHDQVVSLLLENDTKGKVRLP 204

Qy 115 LLESARSGNEBKMAILLPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAK 174
Db 205 ALHTAARKDDTKAALLLQNDNADVESKSGFTPLHIAAHYGNINVTALLNRAAANDFT 264

Qy 175 DKGLVPLHNACSGHYEVTELLVKHGACVNMADLQFTPLHEAASKNRVCVCSLLLSYG 234
Db 265 ARNDITPLHVASKGNANVMKLLDRGAKIDAKTRDGLTPLHCGARSHEQVEMLLDRA 324

Qy 235 ADPTLLCHNKSAIDLAPTPOLKERLAYEFKGHSLQAAAREADVTRIKKHLSELMVNFKH 294
Db 325 A-PILSKTKN-----GLSPLHMAATQGD-----HLNCVQLLIQH 356

Qy 295 -----PQTHETALHCAASAPYPRKQICELLLRKGANINEKTEFLTPHLHVAASEKAHN 347
Db 357 NVPVDDVTNDYLTALHVAHCHGYK---VAKVLDKKANPNKALNGFTPLHIAACKNRI 413

Qy 348 DVVEVVKHEAKVNDLNLGQADVHAKDQGLVPLHNACSGHYEVTELLVKHGADVHAK 407
Db 414 KVMELLKHGASIQAVTESGLTPHVAAFMGHNVISQLMHGHASPTNVTNRGETALHMA 473

Qy 408 -----NENVQQLQEGISLGNSEADRO---LLEAAKAGDVETVKKLCVV-QSNCRDIEGR 459
Db 474 ARSQGAQVVRVYLQDGAQVEAKAKDDQTPHISARLGRADIVQQLQOQASPNAAATTSG- 532

Qy 460 QSTPLHFAAGYNRVSVVEYLLQHGADVHAKDQGLVPLHNACSGHYEVTELLVKHGAVV 519
Db 533 -YTPHLHSAAREGHEVDAALPDHGHASUSITTKKFTPLHVAAKYKGKUEVANILLQKSGSP 591

Qy 520 NVADLWKFTEPLHEAAAKGYEICKLLQHGADPTKKNRDGNTPDL-LVKQGDITDIQILL- 577
Db 592 DAAGKSGITPLHVAHYDNQKVALLLDQGHASPHAAKNGYTPHLHIAAKNQMDIATILL 651

Qy 578 -----RGDAALLDAKKGLARVKKLSPPD-NVNCRDQTQGRHSTPLHLAAGVNN 625
Db 652 EYGDANAVTRQGTASVHLAAQEGHVDVMSVLLGRNANVNLNKSQ--LTPLHLAAQEDR 709

Qy 626 LEVAEYLLQHGADVNAQDKGGLIPLHNAAASYGHVDVVAALLIKYACVNAATDKWAFTPLHE 685
Db 710 VNVAEVLVQNGAHVDAQTKMGYTPHLVGHYCHYGNIKIVNFFLQHSKAKVNAKTNGYTPHLQ 769

Qy 686 AAQKGRQQLCALLAHGADPTLKNQSGQTPDL-----VSADDVSALLT-AAAPPSPALP 738
Db 770 AAQOQGHTHIIVLLQNNASPNELTVNGNTALGIARRLGYSVVDPTLKIIVTETMTTITVT 829

Qy 739 SCYK---POVLNVSFGATADALSSGSPSSLSAASSLDNLGSGFSELSSVSVSSSGTE 795
Db 830 EKHKNVPETNEVLD-----MSDDEVKNAPEMLSDG----- 863

Qy 796 GASSLEKKEVGVDFSITQFVRNLGLEHLMDFEREQ-ITLDVLVEMGHKELKEIG 850
Db 864 -----EVIDSEGEDAMTGDTKYLGPDQLKEIG 893

RESULT 4
T42713
ankyrin 3, splice form 1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42713
J;Cell Biol. 130, 313-330, 1995
A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene 1 the repeat domain.
A;Reference number: Z22237; MUID:95340633; PMID:7615634
A;Accession: T42713
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1943 <PET>
A;Cross-references: UNIPROT:Q61307; UNIPARC:UPI0000028367; EMBL:L40632; NID:G710548; PID: J;Experimental source: strain C57BL/6J; kidney
C;Genetics:
A;Gene: Ank3
A;Map position: 10
A;Introns: 855/1
C;Function:
A;Description: supposed to play an important role in the polarized distribution of many ;
A;Note: major kidney ankyrin
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing

Query Match 15.6%; Score 873.5; DB 2; Length 1943;
Best Local Similarity 30.6%; Pred. No. 8.6e-46;
Matches 274; Conservative 122; Mismatches 365; Indels 135; Gaps 21;

Qy 3 GRKDVVEYLLQNGASVQARDGGGLPLHNACSFHAEVNVNLLRHGADPNARDNNWYTPL 62
Db 68 GHVEVSELLQREANVDAATKGNATLHSLAGQAEVVKVLTNGANVNAQSQNGFTPL 127

Qy 63 HEAAIKGKIDVICVILQHGAEPTIRNTDGTALDLA-----DPSAKAVLTGEYK---KDE 114
Db 128 YMAAQENHLEVVEVFLDNGASQSLATEDGFTPLAVALQOQHDQVVSLLLENDTKGKVRLP 187

Qy 115 LLESARSGNEBKMAILLPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAK 174
Db 188 ALHTAARKDDTKAALLLQNDNADVESKSGFTPLHIAAHYGNINVTALLNRAAANDFT 247

Qy 175 DKGLVPLHNACSGHYEVTELLVKHGACVNMADLQFTPLHEAASKNRVCVCSLLLSYG 234
Db 248 ARNDITPLHVASKGNANVMKLLDRGAKIDAKTRDGLTPLHCGARSHEQVEMLLDRA 307

Qy 235 ADPTLLCHNKSAIDLAPTPOLKERLAYEFKGHSLQAAAREADVTRIKKHLSELMVNFKH 294
Db 308 A-PILSKTKN-----GLSPLHMAATQGD-----HLNCVQLLIQH 339

Qy 295 -----PQTHETALHCAASAPYPRKQICELLLRKGANINEKTEFLTPHLHVAASEKAHN 347
Db 340 NVPVDDVTNDYLTALHVAHCHGYK---VAKVLDKKASPNKALNGFTPLHIAACKNRI 396

Qy 348 DVVEVVKHEAKVNDLNLGQADVHAKDQGLVPLHNACSGHYEVTELLVKHGADVHAK 407

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Db 397 RVMLLLKHGASIQAVTESGLTPIHVAAPFMGHVNIIVSLMHGASPNITNVGETALHMA 456
Qy 408 -----NENVQQLQGGISLGNSEADQ--LLEAAKAGDVETVKKLCV-QSVNCRDIEGR 459
Db 457 ARSGQAEVVRVLVDQGAQVEAKKDDQTPHLSARLGKADIIVQQLLQCGASPNAAATTS- 515
Qy 460 QSTPLHFAAGYNRVSVVEYLLOHGADVHAKDGGGLVPLHNACSYGHYEVAELLVKHGAVV 519
Db 516 -YTPLHLAAREGHEDVAAPFLLOHGASLSITTKGFTPLHVAAYGKLEVASLLQKSASP 574
Qy 520 NVADLWKFTPLHHEAAKGYEICKLLLOHGADPTKKNRDGNTPLDL-VKDGDTDIQDILL- 577
Db 575 DAAGKSGLTPLHVAHYDNQKVALLLDOGASPHAAAKNGYTPHLIAAKNQMDIATSL 634
Qy 578 -----RGDAALDAKKGCLARKVKKLSPPD-NVNCRDTOGRHSTPLHLAAGYNN 625
Db 635 EYGADANAVTRQGTASVHLAAQEGHVDVMSLLSRNANVNLNKS- -LTPHLAAQEDR 692
Qy 626 LEVAEYLLOHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFPLHE 685
Db 693 VNVAEVLVNOGAHVDAQTGMGYTPLHVGHYGNIKIVNFLQHSKAKVNAKTNGYTAHQ 752
Qy 739 SCYK---POVLNGVRSPGATADALSGSPSSLSAASLDNLS-GSFSELSSVSSSGT 794
Db 813 EKHKMNPETMNEVLDD-----MSDDEVKASAPEKLSGGEY-----ISDGE 853
Qy 795 EGASSELKEVPGVDPSITQFVRNLGLEHMDIFEREQITLDVIVEMGHKELKEIG 850
Db 854 EG-----EDAITGDTDKYLGPDQDLKELG 876

RESULT 5
T42715
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42715
J:Peterson, L.L.; John, K.M.; Lu, F.M.; Bicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.
R:Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: Z22237; PMID:95340633; PMID:7615634
A:Accession: T42715
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1940 <PET>
A:Cross-references: UNIPROT:Q61307; UNIPARC:UPI0000029ABD; EMBL:L40632; NID:g710548; PID
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Introns: 834/1
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match 15.6%; Score 871.5; DB 2; Length 1940;
Best Local Similarity 28.3%; Pred. No. 1.1e-45;
Matches 320; Conservative 159; Mismatches 464; Indels 189; Gaps 35;

Qy 3 GRKDVVEYLLONGASVQARDGGGLPLHNACSFHGAEVVNLRLRHGADPNARDNNYTP 62
Db 68 GHVEVVELLQREANVDATKGNATLHSLAGQAEVVKLVLTNGANVNAQSQNGFTPL 127

Qy 63 HEAAATKGIDVCIVLLQHGAEPTIRNTDGRALDLA-----DPSKAVLTGYK---KDE 114
Db 128 YMAAQENHLEVVRFLDNGASQSLATEDGFTPLAVALQGHQDVVSLLENDTKGKVRLP 187
Qy 115 LLESARGNEEKWMALLPLNVLNCHASDGRKSTPLHLAAGYNRVKIVQLLLOHGADVHAK 174
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Db 188 ALHIAARKDDTKAAALLQNDTNADVESKSGFTPLHIAAHYGNINVATLLLNRAAAVDFT 247
Qy 175 DKGDVLPLHNACSYGHYEVTETLLVKGACVNAMDLMQFTPLHHEAAKRNVEVECSLLISYG 234
Db 248 ARNDITPLHVAKRGNNANVKLLDRGAKIDAKTRDGLTPLHCGARSGHGEVQVEMMLDLS 307
Qy 235 ADPTLLNCHNKSAIDLAPTPQLKERLAYBFKGHSLQAAREADVTRIKKHLSELMVNFKH 294
Db 308 A-PILSKTKN-----GLSPHMAATQGD-----HLNCVQLLQ 339
Qy 295 -----POTHETALHCAAASPYPKKQICEILLRKGANINEKTEKFLTPLHVAASEKAHN 347
Db 340 NVPVDDVTNDYLTALHVAACHGHYK---VAKVLLDKASPNAKALNGFTPLHIACKNRI 396
Qy 348 DVVEVVHKEAKVNALDNIGQTSLHRAAYCGHLOTCRLLLSYGCDDPNILSQFTALOMG 407
Db 397 RVMLLLKHGASIQAVTESGLTPIHVAAPFMGHVNIIVSLMHGASPNITNVGETALHMA 456
Qy 408 -----NENVQQLQGGISLGNSEADQ--LLEAAKAGDVETVKKLCV-QSVNCRDIEGR 459
Db 457 ARSGQAEVVRVLVDQGAQVEAKKDDQTPHLSARLGKADIIVQQLLQCGASPNAAATTS- 515
Qy 460 QSTPLHFAAGYNRVSVVEYLLOHGADVHAKDGGGLVPLHNACSYGHYEVAELLVKHGAVV 519
Db 516 -YTPLHLAAREGHEDVAAPFLLOHGASLSITTKGFTPLHVAAYGKLEVASLLQKSASP 574
Qy 520 NVADLWKFTPLHHEAAKGYEICKLLLOHGADPTKKNRDGNTPLDL-VKDGDTDIQDILL- 577
Db 575 DAAGKSGLTPLHVAHYDNQKVALLLDOGASPHAAAKNGYTPHLIAAKNQMDIATSL 634
Qy 578 -----RGDAALDAKKGCLARKVKKLSPPD-NVNCRDTOGRHSTPLHLAAGYNN 625
Db 635 EYGADANAVTRQGTASVHLAAQEGHVDVMSLLSRNANVNLNKS- -LTPHLAAQEDR 692
Qy 626 LEVAEYLLOHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFPLHE 685
Db 693 VNVAEVLVNOGAHVDAQTGMGYTPLHVGHYGNIKIVNFLQHSKAKVNAKTNGYTAHQ 752
Qy 686 AAQKGTQQLCALLAHGADPTLKNQEGQTPDLVS-----ADDVSALLTAAMPSPALP 738
Db 753 AAQGGHTHIINVLQNNASPNELTVNGNTALAIARRLGYSIVVDTLKVTEEIMTTIT 812
Qy 739 SCYK---POVLNGVRSPG-----ATADALSS-----GP----- 763
Db 813 EKHKMNPETMNEVLDDMSDEGKCTWFKIPKQEVLVKSEDAITGDTDKYLGPDQDLKEL 872
Qy 764 ---SSPSSLSAASLDNLSGSFSELSSVVS-----SSGTEGASSELKEKVPVGVDFSTQF 815
Db 873 GDDSLPAEGYVGFSLGARSASLSFSSDRSYTLNRSYARDSMMIEBELLVPSKEQHLT-F 931
Qy 816 VNLGLEHMDIFEREQITLDV-----VEMGHKELKEIGINAYG-----HRHKL 861
Db 932 TREFDSDSLRH-YSWAADTLDNVNLVSSPVHSGF--LVSPFVMDARGSGMRGSRHGMRII 988
Qy 862 -----KGVRLISQOGLNPYLTNTSSGTTILDLSPDDKEFQS-VEEMQSTV 910
Db 989 IPPRCKTAPTRITCRVLKHKLANPPMVEGEGSLRKLVEWGAGAQFLGPVIEIP--- 1045
Qy 911 REHRDGGHAGGIFNRYNLIKIQVCNKKLWE--RYTHRRKEVSE-----ENHNHANERML 963
Db 1046 -----HFGSMRGKRELIVLRSENGETWKEHQFDSKNEDLAELLNGMBEELDSPEEL- 1097
Qy 964 FHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENS---SKSNQYVYVIGGG 1012
Db 1098 --GTRKICRIITKDFPQ-----YFAVWSRIKQESNQ--IGPEGG 1132
```

RESULT 6
S37431

ankyrin 2, neuronal long splice form - human

N:Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid
N:Contains: ankyrin 2, short form

Query Match	15.4%;	Score	860.5;	DB	2;	Length	3924;
Best Local Similarity	29.8%;	Pred.	No. 1.7e-44;				
Matches	283;	Conservative	127;	Mismatches	386;	Indels	153;
Gaps	21;						

Qy	3	GRKDVVEYLQNGASVQARDGGGLPLPHNACSFCHAEVNNLLLRHGDAPNARDNNVTPPL	62
Db	75	GHVGLVQELLGRSSVDVSATKGNWTALHIALAGQAEVVKVLVEGANINNAQSQNGFTPL	134
Qy	63	HEAAIKGKIDVICVLLQHGAEPTIRNTDGR-----ALDLADPSKAVLTVGBYKKDEL---	115
Db	135	YMAAQENHIDVVKYLLLENGANQSTATEDGFTPLAVALQOQHNOQAVALLLENDTGKVRPL	194
Qy	116	LESARSGNEEKWALLTPLNVNCHASDGRKS-----TPLHLAAGYNVKIVQL	163
Db	195	ALHIAARKDDTKSAALLQ---NDHNADVQSKMNVNRTTSGFTPLHIAAHYGNVNVATL	251
Qy	164	LLOHGADVHAKDGDVLVPLHNACSYGHEYETELLVKGACVNA MDLWQFTPLHEAASKNR	223
Db	252	LLNRGAADVFTARNGITPLHVASKRGNTNMVKLLDRGGQIDAKTRDGLTPLHCAARSGH	311
Qy	224	VEVCSLLLSVGAODPTLLNCHNKSAIDLAPTPQLKERLAYEPKSHLSLQAAREADVTRIKK	283
Db	312	DQVVELLLERGA-PLIARTKN-----GLSPHMAAQGHVHEVCVK	349
Qy	284	HLISLEWNVFKHP-----QTHE TALHCAAA SPYPKRKQICELLRLKGANINEKTRFEFTPL	338
Db	350	HL-----LQHKAPVDDVTLDYTLTALHVA-----HCHYRVTKLLDKRPNARALNGFTPL	402
Qy	339	HVASEKAHNDVVEVVKHAEKVNALDNGOTSLHRAAYCGHLOTCRILLSYSGCDPNIIISL	398
Db	403	HIACKNRKIVMELLVKYGASIQAITESGLTPIHVAAFMGHLNIVLLLLQNGASPDVTNI	462
Qy	399	QGTALOMGN-----ENVQQLQEGI-----SLGNSADRRQLLE-----	432
Db	463	RGETALHMAARAGQVEVRCLLRNGALVDARAREEQTPLHIASRLGKTEIVQLLEQHMWH	522
Qy	433	-----AAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEY	478
Db	523	PDAATNGYTPLHISAREGQDVASVLEGAHSLATK-KGFTPLHVAAYKGSLDVAKL	581
Qy	479	LLOHGADVHAKDGGVLVPLHNACSYGHEYAEVALLVKGAVNVNADLWKFTPLHEAAAAGK	538
Db	582	LLQRRAAADSAGKNGLTPLHVAAHYDNQKVALLLLEKASPHATAKNGYTPLHIAAKNQ	641
Qy	539	YEICKLLLOHGADPTKKRDCNTPLDV-KGDPTDIDLLRGDAALLDAAKKGCLARVKK	597
Db	642	MQIASTLLNAGAEVTNVTQGVTPPLHASQEGHTDMVTLLLDKANTHMTKSGL-----	696
Qy	598	LSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYG	657
Db	697	-----TSHLAAQEDKVNVDILTKHGADQDQDHTKGLYTPLVIVACHYG	739
Qy	658	HVDVAALLIKYNACVNATDKWAFPTPLHEAAQKGTQLCALLLAHGADPTLKNQEGQTPLD	717
Db	740	NVKWNVFLLKQGANVNAKTNGYTPPLHQAQQOQHTHII NVLLQHGAKPNATTANGNTALA	799
Qy	718	L-----VSADDVSALLTAAMPSPALPSCYKQVNLNVRSPGATADALSSGPPSPSLSA	771
Db	800	IAKRLGVISVVDTLKVVTESVTTTTTITETK-----HKLNVPTETWTEVL-----DVSD	847
Qy	772	ASSLDNLGSSFSLEL-----SSVSSSGTEGASSLEKKEVCPQVDFPSITQFV--RN	818
Db	848	EEGDDTWTGCGEYLRPEDLKELGDDSLSSQFPLDGNVYLYRISLEGRSDLSLRSFSSDRS	907
Qy	819	LGLEHLMIDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERL	867
Db	908	HTLSHAS--YLRDSAVMDDSVIIPSHQVSTLAKAEARNSVRLSWGTENL	954

RESULT	7
B35049	
ankyrin 1, erythrocyte splice form 3 - human	

N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N:Contains: ankyrin 2.2, erythrocyte

C:Species: Homo sapiens (man)

C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998

C:Accession: B35049

R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K

A:Title: cDNA sequence for human erythrocyte ankyrin.

A:Reference number: A35049; MUID:90175370; PMID:1689849

A:Accession: B35049

A:Molecule type: mRNA

A:Residues: 1-1856 <LAM>

A:Cross-references: UNIPARC:UPI0000177546

C:Genetics:

A:Gene: GDB:ANK1; ANK

A:Cross-references: GDB:118737; OMIM:182900

A:Map position: 8p11.2-8p11.2

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>

F:12-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>

F:44-76/Domain: ankyrin repeat homology <AN01>

F:77-109/Domain: ankyrin repeat homology <AN02>

F:110-142/Domain: ankyrin repeat homology <AN03>

F:143-171/Domain: ankyrin repeat homology <AN04>

F:172-204/Domain: ankyrin repeat homology <AN05>

F:205-237/Domain: ankyrin repeat homology <AN06>

F:238-270/Domain: ankyrin repeat homology <AN07>

F:271-303/Domain: ankyrin repeat homology <AN08>

F:304-336/Domain: ankyrin repeat homology <AN09>

F:337-369/Domain: ankyrin repeat homology <AN10>

F:370-402/Domain: ankyrin repeat homology <AN11>

F:403-435/Domain: ankyrin repeat homology <AN12>

F:436-468/Domain: ankyrin repeat homology <AN13>

F:469-501/Domain: ankyrin repeat homology <AN14>

F:502-534/Domain: ankyrin repeat homology <AN15>

F:535-567/Domain: ankyrin repeat homology <AN16>

F:568-600/Domain: ankyrin repeat homology <AN17>

F:601-633/Domain: ankyrin repeat homology <AN18>

F:634-666/Domain: ankyrin repeat homology <AN19>

F:667-699/Domain: ankyrin repeat homology <AN20>

F:700-732/Domain: ankyrin repeat homology <AN21>

F:733-765/Domain: ankyrin repeat homology <AN22>

F:766-798/Domain: ankyrin repeat homology <AN23>

Query Match 15.1%; Score 844; DB 2; Length 1856;

Best Local Similarity 25.7%; Pred. No. 5.5e-44;

Matches 281; Conservative 151; Mismatches 355; Indels 306; Gaps 28;

Qy 3 GRKDVVEYLLQNGASVQARDGGLIPLHNACSGFHAENVNLLRHGADPNARDNNWYTP 62

Db 89 GQDEVVELVNGVNVNAQSQGFTPLYMAAQENHLEVVKFLLENGANQNVATEDGFTPL 148

Qy 63 HEAAIKGKIDVICVLLQHGAEPTI-----RNTDGTALDLDADPSAKAVLTGEYK 113

Db 149 AVALQQGHENVAHLINYGKVRPLPALHIAARNDTRTA-----AVLLQNDPNP 199

Qy 114 ELLEGARGNEKMWALLTPLNVNCHASD-----GRKS-----TPLHLAAGY 155

Db 200 DVL--SKTG-----FTPLHIAHYENLVNAQQLLNKSSVNTFPQNGITPLHIAARR 249

Qy 156 NRKTVQLLLQHGADVHAKDGLVPLHNACSGHYEVTELVKYGACVNAVDLMQFTPL 215

Db 250 GNVIMVRLLDGRGAQIETKTDELTPHCAARNGHVRISIELLDHGAQIAKTNGLSPI 309

Qy 216 HEAAKRNVEVCSLLSYGADFTLLNCHNKSIDLAFTPLKRLAYEFKHSLLQAARE 275

Db 310 HMAAGDHLDCVRLLLQYDAE-----ID----- 332

Qy 276 ADVTRIKKHLSEVMVNFKHPQTHETALHCAASPYKPKQICELLIRKGANINEKTKEPL 335

Db 333 -DIT-----LDHLTPHVA-----HGHHRVAKVLLDKGAKPNSRALNGF 372

Qy 336 TPLHVASEKANDVVEVVVKHEAKYNALDNLGOTSLHRAAYCGHLQTCRLLLSVGCDPNI 395

Db 373 TPLHIAACKNQHVVRVMEILLTKTGASIDVETSLPLHVASFMGLHFIVKLLQRGASPNV 432

Qy 396 ISLQGFALQMG-----NENVQQLQEQ-----GISLGNSEADROLLE- 432

Db 433 SNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKAKDDOTPLHCAARIGHTNNVKKLLEN 492

Qy 433 -----AAKAGDVETVKKLTQVQ--SVNCRDIEGROSTPLHFAAGYNRVS 474

Db 493 NANPNLATTAGHTPLHIAAREGHVETVLALLEKEASQACWTKKG--FTPLHVAAYKGV 550

Qy 475 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVAELLVKGAVNVVADLWK--FTPLHEA 533

Db 551 VAEILLERDAHPNAAGKGLTPLHVAVHNHNDIVKLLLPGRGSPH-SPAWNGYTPHIA 609

Qy 534 AAKGYEICKLLLOHGADPTKKNRDGNTPLDL--VKDGDITDIQLLRGDAALLDAAKKGCL 592

Db 610 AKQNVAVARSLLQYGGSANAESVQGVTPHLHAAQEGHAEVALL----- 654

Qy 593 ARVKLSSPDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHN 652

Db 655 -----LSKQANGNLGNKSG--LTPLHLVAQEGHVPVADVLKHKGVMDATTRMGYTP 707

Qy 653 AASYGHVDVVAALLIKYNACVNATDKWAFPLHAAQKGRGTQLCALLAHGADPTLKNQEG 712

Db 708 ASHYGNIKLVKRFLLQHQADVNAKTKLGYSPLHQAQOQGHDTIVTLLKNGASPNVSSDG 767

Qy 713 QTPDL-----VSADVDVSAITLTAAMPSPALPSC----- 740

Db 768 TPLAIAKRLGIYSVTDVLKVTDETSFVLVSDKHRMSPETVDEILDVSEGEELISF 827

Qy 741 -----YKQVNLNGVRSPGATADALSSGSPSPSSLS-----AASSLDN 777

Db 828 KAERRDRDVBEEKLLDFVKLDQVVESPA-----PRIPCAMPETVWIRSEREQ 879

Qy 778 LSGSPSELSSVSSSGTEGASLSLEKEVQGVDFSIQFVRNLGLEHLMDFEREQITLDV 837

Db 880 ASKEYDEDSLIPSSPATETSDNISPVASPVHTGFLVSEF----- 918

Qy 838 LVEMGHKELKEIGINAYGHRHKLKIGVE-----RLISGQGLNPVLTNTSG 884

Db 919 -----VDARGSGNRGSRHNLRVVIPPRTCAAPTRICRLVKPKQLSTPPPLAEEG 970

Qy 885 STILIDLSP-----DDKEFQSEEEEMQSTVREHRRDGHGAGGIF 923

Db 971 LASRIIALGPTGAQFLSPVIVEIPHPFASHGRGDRDLVLRSENGSVWKEHR----- 1021

Qy 924 NRYNLIKIQKVCN 936

Db 1022 SYGESYLDQILN 1034

RESULT 8

A35049

R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K

N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N:Contains: ankyrin 2.2, erythrocyte

C:Species: Homo sapiens (man)

C:Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004

C:Accession: A35049

R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K

proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A:Title: cDNA sequence for human erythrocyte ankyrin.

A:Reference number: A35049; MUID:90175370; PMID:1689849

A:Accession: A35049

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1880 <LAM>

A:Cross-references: UNIPROT:P16157; UNIPARC:UPI0000177545; GB:M28880

C:Genetics:

A:Gene: GDB:ANK1; ANK

A:Accession: A35443
A:Molecule type: protein
A:Residues: 'X', 'S', '7-12; 403-417, 'X', '419-422, 'H', '424, 'LQ', '797-800, 'L', '802-814; 862-863,
A:Cross-references: UNIPARC:UPI0000173DD1; UNIPARC:UPI0000173DD2; UNIPARC:UPI0000173DD3;
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing; phosphoprotein
F:2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>
F:2-1512, 1675-1881/Product: ankyrin 2, erythrocyte #status predicted <MAT2>
F:2-827/Domain: 89K #status predicted <DOM1>
F:2-827/Region: anion exchange protein binding
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>
F:568-600/Domain: ankyrin repeat homology <AN17>
F:601-633/Domain: ankyrin repeat homology <AN18>
F:634-666/Domain: ankyrin repeat homology <AN19>
F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>
F:828-1382/Domain: 62K #status predicted <DOM2>
F:828-1382/Region: spectrin binding
F:1383-1981/Domain: 55K #status predicted <DOM3>

Query Match 15.1%; Score 842; DB 1; Length 1881;
Best Local Similarity 25.5%; Pred. No. 7.5e-44;
Matches 279; Conservative 152; Mismatches 356; Indels 306; Gaps 27;
Qy 3 GRKDYVEYLLQNGASVQARDGGLIPLHNACSFGEAEVYVNNLLRHGADFNARDNNYTP 62
Db 89 GQDEVVRELNVYGVANVAQSQGFTPLYMAAQENHLEVVKFLENGANQNVATEDGFTPL 148
Qy 63 HEAAIKGIDVICVLLQHGAEPTI-----RNTDGRALDLADPSAKAVLTGEYK 113
Db 149 AVALQQGHENVAHLINTGTGKVKRLPALHIAARNDTRTA-----AVLLQNDPNP 199
Qy 114 ELLSARGNEEKQWALLTPLNVNCHASDGRKS-----TPLHLAAGY 155
Db 200 DVL--SKTG-----FTPLHAAHYENLVNAQVLLNRGASVNTPPQNGITPLHIAER 249
Qy 156 NRKIVQLLQHGADVHAKGDLVPLHNACSYGHYEVTTELVAKHGACVNMADLWQFTPL 215
Db 250 GNWIMVRLLDGAGIETKTDELTPHCAARNGHVRISIELLDHGAPIQAKTKNGLSPI 309
Qy 216 HEAAKRVNVCSSLLSAGADPTLNCNCHKSADIAPTPOLKRLAYEFKGHSLQAARE 275
Db 310 HMAAQGDHLDVRLLLQYDAE-----ID----- 332
Qy 276 ADVTRIKHLSLEMYNFKHPTQTHALCAASAPYKPKQICELLRLKGANINEKTEPL 335
Db 333 -DIT-----LDHLLTPLHVA-----HGHHRVAKVLLDGAENSRALNGF 372
Qy 336 TPLHVASEKAHNDVVEVVVGHAEKAVNDLNGQTSLSHRAAYCGHLQTCRLLLSYGCDFNI 395
Db 373 TPLHTACKNHRVVMELLKTKGASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNV 432

Qy 396 ISLQGFALQMG-----NENVQQLLOE-----GISLGNSEADROLLE- 432
Db 433 SNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKAKDDQTPHCAARIGHINMVKLLLEN 492
Qy 433 -----AAKAGDVETVKKLCTVQ-SVNCRDIEGROSTPLHFAAGYNRV 474
Db 493 NANPNLATTAGHTPLHIAAREGHVEITLALLEKEASQACWTKG--FTPLHVAAYKVKR 550
Qy 475 VVEYLLQHGADVHAKGDLVPLHNACSYGHYEVAELLVKHGAVNVADLWK--FTPLHEA 533
Db 551 VAELLERDAHPNAAGKNGLTPLHVAHNNLDIVKLLPRGGSPH--SPAWNGYTPHLHIA 609
Qy 534 AAKGYEICKLLOHGADPTKKNRDGNTPLDL-VKDGDTDIQDLRGDAALLDAKKGCL 592
Db 610 AKONQVEVARSLLQYGSANAESVQGVTPHLHAAQEGHAEWVALL----- 654
Qy 593 ARVKLSSPDNVNCRDQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHN 652
Db 655 -----LSKQANGNLGNKSG--LTPLHVAQEGHVPVADVLKHGVMVDAATTRMGYTELHV 707
Qy 653 AASYGHVDVAALLIKYNACVNATDKWAFPLHBAOKGRQTOLCALLAHGADPTLNQEG 712
Db 708 ASHYGNIKLVKFLQCADVNATKLGYSPLHQAQQGHTDIVTLLKNGASPNVSSDG 767
Qy 713 QTPLDL-----VSADDVSALLTAAMPSPALPSC----- 740
Db 768 TTPLAIAKGLVSVTVLVKVTDETSFVLVSKHRMSPETVDEILDVSEDEGEELISP 827
Qy 741 -----YKQVNLNGVSPGATADALSSQSPSPSSLS-----AASSLDN 777
Db 828 KAERDRSDVDDEKELLDVFKLDQVVEPAI-----PRIPCAMPETVWIRSEBEQ 879
Qy 778 LSGSFSELSVSSVSSGTEGASLEKKEVPGVDSITQFVNGLGLEHLMDFPERQITLDV 837
Db 880 ASKEYDEDSLIPSPATETSDNISPVASPVHTGLVSEF----- 918
Qy 838 LVEMGHKELKEGINAYGHRHKLKIGVE-----RLISGQGLNPYLTLNTSG 884
Db 919 -----VDARGGMRGSRHNGLRVPIPTCAAPTRICRLVKPKQJSTPPPLASEEG 970
Qy 885 SGTILIDLSP-----DDKEFQSVSEEMQSTVREHRDGGHAGGIF 923
Db 971 LASRIIALGPTGAQFLSPVIVEIPHFASHGRGDRDLVLRSENGSVWKEHR----- 1021
Qy 924 NRYNLIKIOKVN 936
Db 1022 SRYGESYLDQILN 1034

RESULT 10

S37771
ankyrin, erythrocyte - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S37771
R:Birkmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.B.
J. Biol. Chem. 268, 9533-9540, 1993
A:Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found am
A:Reference number: S37771; MUID:93252825; PMID:8486643
A:Accession: S37771
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1848

A:Cross-references: UNIPROT:Q61302; UNIPARC:UPI0000028360; EMBL:X69063; NID:G311816; PIDN
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:48-80/Domain: ankyrin repeat homology <AN01>
F:81-113/Domain: ankyrin repeat homology <AN02>
F:114-146/Domain: ankyrin repeat homology <AN03>
F:147-175/Domain: ankyrin repeat homology <AN04>
F:176-208/Domain: ankyrin repeat homology <AN05>
F:209-241/Domain: ankyrin repeat homology <AN06>
F:242-274/Domain: ankyrin repeat homology <AN07>

F:275-307/Domain: ankyrin repeat homology <AN08>
F:308-340/Domain: ankyrin repeat homology <AN09>
F:341-373/Domain: ankyrin repeat homology <AN10>
F:374-406/Domain: ankyrin repeat homology <AN11>
F:407-439/Domain: ankyrin repeat homology <AN12>
F:440-472/Domain: ankyrin repeat homology <AN13>
F:473-505/Domain: ankyrin repeat homology <AN14>
F:506-538/Domain: ankyrin repeat homology <AN15>
F:539-571/Domain: ankyrin repeat homology <AN16>
F:572-604/Domain: ankyrin repeat homology <AN17>
F:605-637/Domain: ankyrin repeat homology <AN18>
F:638-670/Domain: ankyrin repeat homology <AN19>
F:671-703/Domain: ankyrin repeat homology <AN20>
F:704-736/Domain: ankyrin repeat homology <AN21>
F:737-769/Domain: ankyrin repeat homology <AN22>
F:770-802/Domain: ankyrin repeat homology <AN23>

Query Match 15.0%; Score 839.5; DB 2; Length 1848;
Best Local Similarity 29.5%; Pred. No. 1e-43;
Matches 237; Conservative 127; Mismatches 262; Indels 177; Gaps 20;

QY 3 GRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNWYTP 62
DB 93 GDEVVRELVNNGANNAQSGKFTPLNMAQENHLEVVVKFLLNGANQNVADEGFTPL 152
QY 63 HEAAIKGKIDVICVLLQHGAEPTI-----RNTDGRALDLADPSAKAVLTGEYK 113
DB 153 AVALQOQHENVVAHLINVTGKVRPLPALHIAARNDDTRTA-----AVLLQNDPNP 203
QY 114 ELLESARGNEEKMMALLTPLNVNCHASDGRKS-----TPHLAAGY 155
DB 204 DVL--SKTG-----FTPLHIAAHYENLVNVAQLLNRGASVNFPPQNGITPLHIAARR 253
QY 156 NRKIVQLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPL 215
DB 254 GNVMIVRLLDRGAQIETRTKDELTPHCAARNHVRISSEILLDHGAPIQAKTKNGLSPI 313
QY 216 HEAAKSRVEVCSLLSYGADPTLLNCHNKSAIDLAFTPOLKERLAYEFKHSLLQAARE 275
DB 314 HMAAQGDHLDVRLLLQYNAE-----ID----- 336
QY 276 ADVTRIKKHSLEWMVNFKHPQTHETALHCAASPYPKRKQICELLRRKANINEKTEFL 335
DB 337 -DIT-----LDHLTPHVA--HCGHVRVAKVLLDKGAPNSRALNGP 376
QY 336 TPLHVAEKAHNDVVEVVKHAKVNDLNGQTSIHLAAVYCHGLQTCRLLLSYCCDNI 395
DB 377 TPLHTACKNHIRVNMELLKTKGASIDAVTESGLTPLHVASPMGHLPIVKNILLQRGASNV 436
QY 396 ISLOGFTALOM---GNENVQOLLQEGISLGNSEAD-----ROLLE- 432
DB 437 SNVKVETPLHMAARAGHTEVAKYLLQNKAKANAKAKDDQTPHCAARIGHGTGMVKLLLEN 496
QY 433 -----AAKAGDVEVTKLCTVQ--SVNCRDIEGRQSTPLHPAAGYNRVS 474
DB 497 GASPNLATTAGHTPLHTAAREGHVDTALALLEKEASQACWTKG--FTPLHVAAYKVR 554
QY 475 VVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNVNADLWK--FTPLHEA 533
DB 555 LAELLEHDHAFNAAAGKNGLTPLHVAVHNHNLDIIVKLLLPGRGSPH-SPAWNNGYTPHIA 613
QY 534 AAKGYEICKLLQHGADPTKKNRDGNTPLDI--VKDGDITDQLDLRGDAALLDAKKGCL 592
DB 614 AKQNGIEVARSLLQYGGGNAESVQGVTPHLHAAQEGHTEMVALL----- 658
QY 593 ARVKKLSPPDNVNCRDQTRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHN 652
DB 659 -----LSQANGNLGNKSG--LTPLHVSQEGHVPVADVLKGVTVDAFTMGVTPHLV 711
QY 653 AASYGHVDVAALLIKYNAVNAATDKWFTPLHAAQKGTQICALLLAHAGADPTLKNQEG 712
DB 712 ASHYGNIKLVKFLQHQADVNAKTKLGYSPHQAQOQGTDTIVTLLKNGASPNVESSNG 771

QY 713 OTPLDL-----VSADVDVSALLT 729
DB 772 TTPLAIKRLGYSIVTDVLKVT 794

RESULT 11

I49502
ankyrin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49502
R:White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
Mamm. Genome 3, 281-285, 1992
A:Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory doma
A:Reference number: I49502; MUID:92345717; PMID:1386265
A:Accession: I49502
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1862 <RES>
A:Cross-references: UNIPROT:Q02357; UNIPARC:UPI000002921E; GB:M84756; NID:gi91939; PIDN:
C:Genetics:
A:Gene: Ank-1
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:40-72/Domain: ankyrin repeat homology <AN01>
F:73-105/Domain: ankyrin repeat homology <AN02>
F:106-138/Domain: ankyrin repeat homology <AN03>
F:139-167/Domain: ankyrin repeat homology <AN04>
F:168-200/Domain: ankyrin repeat homology <AN05>
F:201-233/Domain: ankyrin repeat homology <AN06>
F:234-266/Domain: ankyrin repeat homology <AN07>
F:267-299/Domain: ankyrin repeat homology <AN08>
F:300-332/Domain: ankyrin repeat homology <AN09>
F:333-365/Domain: ankyrin repeat homology <AN10>
F:366-398/Domain: ankyrin repeat homology <AN11>
F:399-431/Domain: ankyrin repeat homology <AN12>
F:432-464/Domain: ankyrin repeat homology <AN13>
F:465-497/Domain: ankyrin repeat homology <AN14>
F:498-530/Domain: ankyrin repeat homology <AN15>
F:531-563/Domain: ankyrin repeat homology <AN16>
F:564-596/Domain: ankyrin repeat homology <AN17>
F:597-629/Domain: ankyrin repeat homology <AN18>
F:630-662/Domain: ankyrin repeat homology <AN19>
F:663-695/Domain: ankyrin repeat homology <AN20>
F:696-728/Domain: ankyrin repeat homology <AN21>
F:729-761/Domain: ankyrin repeat homology <AN22>
F:762-794/Domain: ankyrin repeat homology <AN23>

Query Match 15.0%; Score 837.5; DB 2; Length 1862;
Best Local Similarity 29.5%; Pred. No. 1.4e-43;
Matches 237; Conservative 127; Mismatches 262; Indels 177; Gaps 20;

QY 3 GRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNWYTP 62
DB 85 GDEVVRELVNNGANNAQSGKFTPLNMAQENHLEVVVKFLLNGANQNVADEGFTPL 144
QY 63 HEAAIKGKIDVICVLLQHGAEPTI-----RNTDGRALDLADPSAKAVLTGEYK 113
DB 145 AVALQOQHENVVAHLINVTGKVRPLPALHIAARNDDTRTA-----AVLLQNDPNP 195
QY 114 ELLESARGNEEKMMALLTPLNVNCHASDGRKS-----TPHLAAGY 155
DB 196 DVL--SKTG-----FTPLHIAAHYENLVNVAQLLNRGASVNFPPQNGITPLHIAARR 245
QY 156 NRKIVQLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPL 215
DB 246 GNVMIVRLLDRGAQIETRTKDELTPHCAARNHVRISSEILLDHGAPIQAKTKNGLSPI 305
QY 216 HEAAKSRVEVCSLLSYGADPTLLNCHNKSAIDLAFTPOLKERLAYEFKHSLLQAARE 275
DB 306 HMAAQGDHLDVRLLLQYNAE-----ID----- 328
QY 276 ADVTRIKKHSLEWMVNFKHPQTHETALHCAASPYPKRKQICELLRRKANINEKTEFL 335

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Db 329 -DIT-----LDHLTPHVA-----HGHHRVAKVLLDGGKAPNSALNGF 368
Qy 336 TPLHVASEKANDVVEVVVKGAKVNALDNLTQTSLHRAAYCGHILQTCRLLLSYGCDPNI 395
Db 369 TPLHACKNHRVWELLKTKGASIDAVTESGLTPLHVASFHGLPIVKNLLIQRGASPNV 428
Qy 396 ISLQGFALOM-----GNENVQQLLEGISLGNSEAD-----RQLLE- 432
Db 429 SNVKVETPLHMAARAGHTEVAKYLLQNKAKANAKAKDDQTPHCAARIGHTGMVKLLLEN 488
Qy 433 -----AAKAGDVETVKLCVQ-SVNCRDTEGRQSTPLHFAAGVNRVS 474
Db 489 GASPNLATTAGHTPLHTAAREGHVDITALALLEKEASQACWTYKG--FTPLHVAAYKVR 546
Qy 475 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVNVVADLWK-FTPLHHEA 533
Db 547 LAELLEHDHAPNAAGKNGLTPLHVAHVHNNLDIVKLLPRGSPH-SPANNGYTPLHIA 605
Qy 534 AAKGYEICKLLQHGADPTKQNRDGTPLDL-VKGDGTDIQDILLRGDAALLDAAKGGL 592
Db 606 AKQNGIEVARSLLOYGGSANASVQGVTPHLAAQEGHTEMVALL----- 650
Qy 593 ARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAODKGGILPLHN 652
Db 651 -----LSQKQNGNLNKGSG--ITPLHLVSOEGHVLVADVLIKGVTVDTTRNGYTPHLV 703
Qy 653 AASYGHVDVVAALLIKYNACVNATDKWAFPTPLHHEAAQKGTQTCALLAHAGADPTLKNQEG 712
Db 704 ASHYGNILKVLKQLHQADVNAKTKLGYSPHQAQOQGTDIVTLLKNGASPNESVSSNG 763
Qy 713 QTPDL-----VSADDVSGALLT 729
Db 764 TTPLAIAKELGYISVTDVLKVV 786

RESULT 12
T13940
Ankyrin - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13940
R:Dubreuil, R.R.; Yu, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994
A:Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in Drosophila
A:Reference number: Z17820; PMID:95024098; PMID:7937942
A:Accession: T13940
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1549 <DUB>
A:Cross-references: UNIPROT:Q24241; UNIPARC:UPI000007E386; EMBL:L35601; NID:g557083; PIR:
C:Genetics:
A:Cross-references: FlyBase:FBgn0011747

Query Match 14.9%; Score 834; DB 2; Length 1549;
Best Local Similarity 27.4%; Pred. No. 1.7e-43;
Matches 298; Conservative 165; Mismatches 470; Indels 154; Gaps 32;

Qy 3 GRKDVVEYLLQNGASVOARDGGLIPLHNACSPGHAEVNNLLRHGADPNARDNNMYTPL 62
Db 84 GYVDICELLRRGIKIDNATKGNATLHSLAGQHDVINQLLYNANVQSLNGFTPL 143
Qy 63 HBAAIKGIIDVICVLQHGAEPIRNTDGRALDLA-----DPSAKAVLTGEYK----KDE 114
Db 144 YMAAQENHDNCCKTLLANGANPSLSTEDGFTPLAVAMQOCHDKIVAVLLENDVRGKVRLP 203
Qy 115 LLESARSGNEEKMMALLTPLNVNCHASDGRKSTPLHAGYNNVKIVQLLQHGADVHAK 174
Db 204 ALHIAAKNDVNAKLLQHDQPNADIVSGSGFTPLHIAHYGNVDIATLLNNKADNVY 263
Qy 175 DKGDVPLHNACSYGHYEVELLVKHGACVNAMDLWQFTPLHFAASKNRVVEVCSLLISYG 234
Db 264 AKGNITPLHVACKWGLSLCTLLLCRGAKIDATRDGLTPLHCAASRGHVEVIKHLQQN 323
```

```
Qy 235 ADPTLLNCHN-KSAIDLAPTOLKERLAYEFKGHSILOAAREADVTRI KKHLSLE----- 288
Db 324 A-PILTKYKXGSLAHMAAQE-----HDEAAHLLDNKAPDVEVTVDYLTALHVAACH 376
Qy 289 -----MVNFK-HPQTHE-----TALHCAAAAPYPRKQICELLURKGANINEKTEKFL 335
Db 377 GHVKVAKLLDYKANPNARALNGFTPLHIAACK--NRIMKVELLIKGANIGATTESGL 433
Qy 336 TPLHVASEKANDVVEVVVKGAKVNALDNLTQTSLHRAAYCGHILQTCRLLLSYGCDPNI 395
Db 434 TPLHVASFPGCINIVLYLQHEASADLPTIRGETPLHAAARANQADIIRILLR-SAKVDA 492
Qy 396 ISLQGFAL-----OMGNEN-VQQLLEGISLGNSEADR--QLLEAAKAGDVETVKLCITV 448
Db 493 IVREGQTPHVASRLGNINIMLLQHGAEINAQSNKYSAHLHIAKEGOENIVQVLEEN 552
Qy 449 QSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEV 508
Db 553 GAEN-NAVTKKGTPLHLACKYKQNVVQILLQNGASIDFQGNQDVTPLHVATHYNNPSI 611
Qy 509 AELLVKHGVNVVADLWKFTPLHHEAAAKGYEICKLLQHGADPTKQNRDGTPLDL-VK 567
Db 612 VELLKNGSSPNLCARNGQCAIHIACKNYLEIAMQLLQHGADVNIISKSGFSPHLHAAQ 671
Qy 568 DGDGTDIQDILLRGDAALLDAAKGGLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLE 627
Db 672 GGNVDMVQQLLEYGVISAANKGL-----TPLHVAQAEGHVL 708
Qy 628 VAEYLLQHGADVNAODKGGILPLHNAAASYGHVDVVAALLIKYNACVNATDKWAFPTLHHEAA 687
Db 709 VSQILLEHGANISERTNGYTPPLHMAAHYGLDLVKFFIENDADIEMSSNIGYTPHLHQA 768
Qy 688 QKQRTQLCALLAHAGADPTLKNQEGTPLDLYSADDSALLTRAMPSPALPSCYKQVPLN 747
Db 769 QQGHIMIINLLLRKANPNALTQDGNATLHASN-----LGYYTVMESLKIIVTSTSVIN 822
Qy 748 G-----VRSPGATADALSSGSPSSLSAAS-----SLDNLSGSFSELSSVVS 790
Db 823 SNIGAIIEKLLKWTPELMQETLLSDDESDCDLLDHNHYKYWATDDLKANYGQDQKQNF 882
Qy 791 SSGTE-----GASLEKKEVPGVDFSIQFVRNIGLEHLMQ--IFEREQITDLVLVEMGHK 844
Db 883 TTNTDHLDTDVSVLNKEILPNEMSCIELTE---IGHKPDNVVIARSQVHLGFLVSP--- 936
Qy 845 ELKEITGINAYHRRKLIKGV-----RLISGOQGLNPYLTNTSGSGTILID 891
Db 937 LVDARGSGMRGYRHNGVRIIVPPKACAEPTITCRYVKQVRVNPVPPPLMEGEALVSRILE 996
Qy 892 LSPDDKEFOS---VBEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRK 948
Db 997 MGPVDGMFLSPITLEVPHVGTLRK-----NEREII-ILRSDNGESWREH-NLYK 1043
Qy 949 EVSEENHNHANERMLPHGSPFVNAIHKGFDERHAYIGMGAGIYFAENSSKSNQVYVG 1008
Db 1044 DIIGEDINQTEE---FHSDRIVR-IVTQNVPHFAVV-----SRVRQEVHV 1085
Qy 1009 IG--GGT 1013
Db 1086 IGPDDGT 1092

RESULT 13
T15347
Ankyrin-related unc-44 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15347; T15346; T15345; A57282; B57282; C57282
R:Gottung, S.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid B0350.
A:Reference number: Z18332
A:Accession: T15347
```

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2039 <GAT>
 A:Cross-references: UNIPROT:Q17489; UNIPARC:UPI0000077B65; EMBL:U50071; NID:g1208871; PID:g1208871
 A:Accession: T15346
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1000, 'SKLQHRT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVA
 32', 'S', 2034-2035, 'GSPTSRSEPEHRHSQHEHGGST' <GA2>
 A:Cross-references: UNIPARC:UPI0000077BDB; EMBL:U50071; NID:g1208871; PID:g1208875; PIDN
 A:Accession: T15344
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1718, 'KW', 1903-1905, 'NRLADESSPS', 1916-1917, 'QRSTIVASTSEQVPE', 1934-1935, 'E
 <GA3>
 A:Cross-references: UNIPARC:UPI000007878C; EMBL:U50071; NID:g1208871; PID:g1208874; PIDN
 A:Accession: T15345
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVPE
 PTRSRSEPEHRHSQHEHGGST' <GA4>
 A:Cross-references: UNIPARC:UPI000007D1A6; EMBL:U50071; NID:g1208871; PID:g1208876; PIDN
 A:Otsuka, A.; Franco, R.; Yang, B.; Shim, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontrakulpo
 J. Cell Biol. 129, 1081-1092, 1995
 A>Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in Cae
 A:Reference number: A57282; MUID:95263663; PMID:7744957
 A:Accession: A57282
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-852, 'GGG', 856-1000, 'SKLQHRT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWE
 'SHRED', 2007-2008, 'TI', 2011, 2017, 'TT', 2020-2022, 'SHIS' <OTS>
 A:Cross-references: UNIPARC:UPI0000080E35; GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:
 A:Accession: B57282
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'E
 V', 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'STRSRSEPEHRHS', 1984-1985, 'EDHEGS', 1
 A:Cross-references: UNIPARC:UPI000017754A; GB:U21731
 A:Accession: C57282
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 194, 'F', 196, 'I', 198, 'DC', 201, 'G', 409, 'AV', 412, 'Q', 414, 824, 'S', 826, 'ER', 829, 'E
 4, 'TIV', 1828, 'ESTS', 1833, 'QV', 1836, 'E', 1934-1935, 'EQS', 1939, 'ESES', 1944, 'REDDGIVTT', 194
 A:Cross-references: UNIPARC:UPI0000076E32; GB:U21732; NID:g790603; PIDN:AAA85853.1; PID:
 C:Genetics:
 A:Gene: CESP:unc-44
 A:Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979
 A:Superfamily: ankyrin; ankyrin repeat homology
 F:164-192/Domain: ankyrin repeat homology <AN04>
 F:358-390/Domain: ankyrin repeat homology <AN1>
 F:391-423/Domain: ankyrin repeat homology <AN11>
 Query Match 14.6%; Score 814.5; DB 2; Length 2039;
 Best Local Similarity 26.1%; Pred. No. 4.4e-42;
 Matches 301; Conservative 156; Mismatches 418; Indels 279; Gaps 36;
 QY 3 GRKDVVEYLLONGASVQARDGGLIPLHNACSGHAEVNNLLRHGADPNARDNNWTPL 62
 DB 77 GHSEVVELIKROAQVDAATRKGNALHTIASLQSLVITLVENGANNVNVQSVNGFTPL 136
 QY 63 HEAAIKGKIDVCIVLQHGAEPTIRNTDGRALTDLADPSAKAVLTGCEYKDELLESARG 122
 DB 137 YMAQENHEEVKYLKHGNALSTEDGFTPLAVA-----LQOG 176
 QY 123 NEEKMALLTPLNVNCHASGRKSTP-LHLAAGYNRVKIVQLLQHGADVHAKDKGLVP 181
 DB 177 HDRVVAVLE-----NDSKGKVRPLALHIAKKDDTTAATLLQLQNEHPDVTSKSGFTP 230
 QY 182 LHNACSYGHEVTELLVKHGACVNDMLQFTPLHEAASKNRVEVCILLISVGADTTLN 241
 DB 231 LHIAAHYGHENVQQLLEKGANVYQARHNISPLHVATKWGRTNMANLLLSRGA---IID 287
 QY 242 CHNKSAIDLAPTQLKERLAYEPKGLSLLOAAREADVTRIKKHLISLEWNVFKHPQTHEYA 301

RESULT 14

T42691

hypoetical protein DKFp434D2328.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

R:Accession: T42691

R:Biocheck: H.; Boscher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: Z22230

A:Accession: T42691
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-791 <AAA>
A:Cross-references: UNIPROT:Q9UFA4; UNIPARC:UPI000006DC92; EMBL:AL133087
A:Experimental source: adult testis; clone DKFzp434D2328
C:Genetics:
A>Note: DKFzp434D2328.1

```
Query Match          11.2%; Score 628; DB 2; Length 791;
Best Local Similarity 27.7%; Pred. No. 4.3e-31;
Matches 232; Conservative 119; Mismatches 313; Indels 174; Gaps 28;

QY 3 GRKDVVEYLQNGASVQARDGGLIPLHNACSFHAEVNVLLRHGADPNARDNNYTPLE 62
DB 14 QGINVYKLLNLGVDEINVTGNTALHIACVNGQDVAVVELIDYGANVQNNNGFTPL 73

QY 63 HEAAIKGKIDVCI-VLLOHGAGAEPTIRNTDGRALDLADPSAKAVLTGEYKDELL- 116
DB 74 HFAAASHTGALCLELVNNGADVNTQSKDGKSPLM- - - - -TAVGRTRSTQTLIQGG 127

QY 117 - - - - -SSASGNEKEMWALLT- - - - -PLN- - - - -VNCHA- - - - - 140
DB 128 EIDCVVDKDGNTPLHVAARYGHHELLINTLITSGADTAKCGIHSMFPLHLAALNAHSDCCRK 187

QY 141 - - - - -SDGRK- - - - -STP- - - - -LHLAAGYNRVKIVOLLQHGADVH 172
DB 188 LLSGQKYSIVSLFNEHVSLSAGFIDTPDKFGRITCLHAAAAGAGNVECIKLQSSGADPH 247

QY 173 AKDKGDLPLHNACSYGHVEVELLVKHGACVNAWDLQFPTLHRAAASKNRVEVCSSLIS 232
DB 248 KDKCGRTPLHYAANCHFHCIETLVTTGANVNETDDMGRTALHTAASD- - - - - 297

QY 233 YGADPTLL-NCHNKSAIDLAPTPOLKER- - - - -LAYEFKGHSLLOAAREADVTRIKKLSLE 288
DB 298 MDRNKTILGNADNSE-ELERARELKEKATCLF- - - - -LLQ- - - - - 335

QY 289 MVNFKHPQTHE- - - - -TALHCAAASYPYKQKQICELLRLKGANINKEKFLT- - - - -PLHVAS 342
DB 336 - - - - -NDANPSIRDKEGYNSIHYAAAYGH- - - - -RQCLELLERTNSGFESDGSATKSPHLHAA 390

QY 343 EKAHNDVVEVVKHEAKVNALDNLGQTSIHRAAAYCGHLQTCRLLSYCGDPNIISLQGT 402
DB 391 YNGHQALEVLQSLVDLDIRDEKGRITLDAAFKRGHTECEVALIN- - - - -QGAS 440

QY 403 ALQMGNEVQQLQGIISLGNSEADRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQST 462
DB 441 IFVKDNTKRTPLHASVINGHTLCRLLEIAD- - - - -NPEADVVKDAQGQ--T 487

QY 463 PLHFAAGYNRVSVVEYLLOHGADVHAKKGLVPLHNACSYGHEVAELLVKHGAVNVA 522
DB 488 PLMLAVAYGHIDAVSLLEKEANVDVTDILGCTALHRTGIMTGHCEVCQMLLEQEVSLICK 547

QY 523 DLWKFPTLHEAAAKGYBEICKLLQLHG- - - - -ADPTKKNRDGNTPLD- - - - -LVKDGDTDIQDL 577
DB 548 DSRGRTPLHYAARAHATWSELLOWALSEEDCCFDKQGYTPLHWACVNGNENCIEVLL 607

QY 578 R- - - - -GD- - - - -AALLDAAKKGCLARVKKLSSPDNVNCRDTOGRHSTPLHLAAG 622
DB 608 EOKCFRKFIGNPFTPLHCAIINDHG- - - - -NCASLLLGAIIDSSIIVSCRDDKGR--TPLHAAAF 663

QY 623 YNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHDVVAALLI-KYNACVNATDKWAPT 681
DB 664 ADHVECLQLLRHSAPVNAVDSNGKTALMMAAENGQAGAVDILVNSAQLTVKDKDLNT 723

QY 682 PLHEAAQKGRQLCALLAHGADPTL- - - - -KNOEGOTPLDLVSADDSALLTAAMPSSA 736
DB 724 PLHLACSGHGKCALLILDKIQDESLINEKNALQTPPLHVAARNGLVVVEELLAKGA 781
```

RESULT 15
S30355
alpha-latroinsectotoxin precursor - black widow spider (fragment)

C:Species: Latrodectus mactans tredecimguttatus (black widow spider)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: S30355; S29864
R:Kiyatkin, N.; Dulubova, I.; Grishin, E.
Eur. J. Biochem. 213, 121-127, 1993
A:Title: Cloning and structural analysis of alpha-latroinsectotoxin cDNA. Abundance of ar
A:Reference number: S30355; MUID:93238678; PMID:8477689
A:Accession: S30355
A:Molecule type: mRNA
A:Residues: 1-1411 <KIY>
A:Cross-references: UNIPROT:Q02989; UNIPARC:UPI000007A3C2; EMBL:Z14086; NID:G9536; PIDN:C
A>Note: it is uncertain whether Met-26 is the initiator or whether translation is initial
C:Keywords: presynaptic neurotoxin
F:533-565/Domain: ankyrin repeat homology <AN1>
F:1001-1032/Domain: ankyrin repeat homology <AN2>
F:1146-1178/Domain: ankyrin repeat homology <AN3>

```
Query Match          9.8%; Score 545.5; DB 2; Length 1411;
Best Local Similarity 23.7%; Pred. No. 1.5e-25;
Matches 239; Conservative 136; Mismatches 378; Indels 257; Gaps 33;

QY 11 LQNGASVQARDGGLIPLHNACSFHAEVNVLLR- - - - -HGADPNARDNNYTPLEH 64
DB 486 LQNGANVSETFELGRGATHAAASAGNYDVGELLNKDINLEKADKN- - - - -GYTELHI 540

QY 65 AAIKGKIDVICIVLLQHGAEPTIRNTDGRALDLADPSAKAVLTGEYKDELLSARSNE 124
DB 541 AADSNNKDFVMEFLIGNADV- - - - -RTKSDLFTP- - - - -LHLAARDLT 581

QY 125 EKMWALLTPLNVNCHASDCRKSSTPLHLAGYNRVKIVQLLQHGADVHAKDGLVPLHN 184
DB 582 DVTQTLIDITEIDLNAQDKSGFTPLHLSISSTSETAAILIRNTNAVNIKSKVGLTPLHL 641

QY 185 ACSYGHYEVELLVKHGACVNAWDLQFPTLHRAAASKNRVEVCSSLISYCGADPTLLNCHN 244
DB 642 ATLQNNLSVSKLAGKAYLNDGDANGMTPLHYAAMTGNLEWVDFLL- - - - -N 689

QY 245 KSAIDLAPTPOLKE- - - - -RLAYEFKGHSLQ- - - - - 271
DB 690 QQYININAAATKEKWTPLHLAILFKNDVAERLLSDENLIRLETNGGINPLHLASATGN 749

QY 272 - - - - -AAREADVTRI-KKHLSELMVNFKPHQTHETALHCAAASYPYKQKQICELLRK 323
DB 750 KQLVTIELAKNADVTRLTSGFS- - - - -ALHLGIIG- - - - -KNEEIPFFLVEK 792

QY 324 GANINKEKTEFLTPLHVASEKARNDDVVEVVKHEAKVNALDNLGQTSIHRAAAYCGHLQTC 383
DB 793 GANVNDKINSVGTPLHFAAGLKCANIFRLLSRGADIKAEDINSQMPIHEAVSNGHLEIV 852

QY 384 RLLSYGCDPNIISLQGTALQMGNEVQQLQGE-GISLGNSEADRLLEAAKAGDVETV 442
DB 853 RILIEK--DPSLM- - - - -NVKNIRNEYPFYLAVERKYKIDIFYFVSKD- - - - - 893

QY 443 KKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLOHGADVHAKD- - - - - 490
DB 894 - - - - -ANVNEVDHNGNTLHLFSSTGELEVQFLMQNGANFRLNKNERKTFDFDLAIE 945

QY 491 - - - - -KGGILVPLHNACSYGHEVAELLVKHGAVNVAADLWKFT 528
DB 946 NGRNLNVAFAVEKNKVNQLQAAHRGKTILYHAICDSAKYDKIEIVKYFIEKLNSE- - - - -N 1002

QY 529 PLHEAAAKGYBEICKLLQ-HGADPTKKNRDGN-TPLDLVKOG- - - - -DTIQDLRG 579
DB 1003 PLHEAAVAHLDLVKYFVQERGINFAEFNEENQASPFCTIHGAPCGYSLDCTPDRLV 1062

QY 580 DAALLDAAKKGCLARVKKLSSPD-VNVCRDTOGRHSTPLHLAAGYNVLEVAEYLLQHGAD 638
DB 1063 VEYLS- - - - -KIPDINGKC-DVQ--ENTPITVAIFANKVSLNVLVIGAD 1106

QY 639 VNAQDKGGLIPLHNAASYGHVDVAALLIK-VNACVNATDKWAPTPLHEAAKGRQLCAL 697
DB 1107 PNQVQDGD-PPLVIAARQGRFEIVRCLIEVHKVDINTRNKERTALHAAAARNDFMDVVKY 1165
```


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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:21:50 ; Search time 213 Seconds
(without alignments)
4625.078 Million cell updates/sec

Title: US-10-616-101-3

Perfect score: 5585

Sequence: 1 GFGKDVVEYLQNGASVQA.....AMKMAHPPGHHSVTGRPSV 1065

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5582	99.9	1166	1 TNKS2 HUMAN	Q9h2k2 homo sapien
2	5350	95.8	1167	2 Q80E0 CHICK	Q80E0 gallus gall
3	4742.5	84.9	1320	2 Q8PFX9 MOUSE	Q8PFX9 mus musculu
4	4740.5	84.9	1327	1 TNKS1 HUMAN	Q95271 homo sapien
5	4732.5	84.7	1327	2 Q4G0F2 HUMAN	Q4G0F2 homo sapien
6	4730.5	84.7	1266	2 Q800D9 CHICK	Q800D9 gallus gall
7	4674.5	83.7	1303	2 Q5XGK5 XENLA	Q5XGK5 xenopus lae
8	4631.5	82.9	1212	2 Q4RG97 TETNG	Q4RG97 tetraodon n
9	4532.5	81.2	1055	2 Q59FX0 HUMAN	Q59FX0 homo sapien
10	4136.5	74.1	976	2 Q8BX62 MOUSE	Q8BX62 mus musculu
11	3849	68.9	1168	2 Q7PYH8 ANOGA	Q7PYH8 anopheles g
12	3706.5	66.4	1181	2 Q9VBP3 DROME	Q9VBP3 drosophila
13	3706.5	66.4	1181	2 Q9XZ37 DROME	Q9XZ37 drosophila
14	3179	56.9	1047	2 Q4S372 TETNG	Q4S372 tetraodon n
15	2833	50.7	589	2 Q3UES1 MOUSE	Q3UES1 m adult mal
16	2731	48.9	601	2 Q8BXH7 MOUSE	Q8BXH7 mus musculu
17	1883	33.7	408	2 Q6P537 MOUSE	Q6P537 mus musculu
18	1795.5	32.1	471	2 Q4FZM0 XENLA	Q4FZM0 xenopus lae
19	886	15.9	1806	2 Q574D8 RAT	Q574D8 rattus norv
20	886	15.9	1984	2 Q574D7 RAT	Q574D7 rattus norv
21	877.5	15.7	1765	2 Q4U258 MOUSE	Q4U258 mus musculu
22	877.5	15.7	1961	2 Q4U256 MOUSE	Q4U256 mus musculu
23	876.5	15.7	1861	2 Q7Z3G4 HUMAN	Q7Z3G4 homo sapien
24	875.5	15.7	1726	2 Q8VC68 MOUSE	Q8VC68 mus musculu
25	875.5	15.7	1377	1 ANK3 HUMAN	Q12955 homo sapien
26	873.5	15.6	1861	2 Q5CZH9 HUMAN	Q5CZH9 homo sapien
27	873.5	15.6	1943	2 Q4U259 MOUSE	Q4U259 mus musculu
28	871.5	15.6	1940	2 Q4U257 MOUSE	Q4U257 mus musculu
29	867.5	15.5	1136	2 Q9N180 BOVIN	Q9N180 bos taurus
30	865	15.5	4372	2 Q5VXD5 HUMAN	Q5VXD5 homo sapien
31	864.5	15.5	2622	2 Q70511 RAT	Q70511 rattus norv

32	864	15.5	1863	2 Q7Z3L5 HUMAN	Q7Z3L5 homo sapien
33	863.5	15.5	1762	2 Q88521 RAT	Q88521 rattus norv
34	860.5	15.4	3924	1 ANK2 HUMAN	Q01484 homo sapien
35	854.5	15.3	1219	2 Q8C8E3 MOUSE	Q8C8E3 mus musculu
36	851.5	15.2	4408	2 Q4RNF0 TETNG	Q4RNF0 tetraodon n
37	842	15.1	1719	2 Q13768 HUMAN	Q13768 homo sapien
38	842	15.1	1880	1 ANK1 HUMAN	P16157 homo sapien
39	841.5	15.1	843	2 P97582 RAT	P97582 rattus norv
40	840.5	15.0	1856	2 Q99407 HUMAN	Q99407 homo sapien
41	840.5	15.0	1899	2 Q59FP2 HUMAN	Q59FP2 homo sapien
42	839.5	15.0	1848	2 Q61302 MOUSE	Q61302 mus musculu
43	839.5	15.0	1878	2 Q3UH42 MOUSE	Q3UH42 mus musculu
44	839.5	15.0	1907	2 Q3UHP2 MOUSE	Q3UHP2 mus musculu
45	837.5	15.0	1862	1 ANK1 MOUSE	Q02357 mus musculu

ALIGNMENTS

RESULT 1

TNKS2 HUMAN STANDARD; PRT; 1166 AA.
 ID Q9H2K2; Q9H8P2; Q9HAS4;
 AC 27-MAR-2002, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2001, sequence version 1.
 DT 07-MAR-2006, entry version 41.
 DE Tankyrase 2 (EC 2.4.2.30) (TANK2) (Tankyrase II) (TNKS-2) (TRF1-
 interacting ankyrin-related ADP-ribose polymerase 2) (Tankyrase-like
 protein) (Tankyrase-related protein).
 DE Name=TNKS2; Synonyms=PARP5B, TANK2, TNKL;
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Fetal brain;
 RX MEDLINE=21072550; PubMed=11205898;
 RA Monz D., Munia A., Comtesse N., Fischer U., Steudel W.-I., Feiden W.,
 RA Glass B., Meese E.U.;
 RT "Novel tankyrase-related gene detected with meningioma-specific
 sera.";
 RL Clin. Cancer Res. 7:113-119(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mammary carcinoma;
 RX MEDLINE=21190090; PubMed=11294570; DOI=10.1038/sj.gene.6363722;
 RA Kuimov A.N., Kuprash D.V., Petrov V.N., Vdovichenko K.K.,
 RA Scanlan M.J., Jongeneel C.V., Lagarkova M.A., Nedospasov S.A.;
 RT "Cloning and characterization of TNKL, a member of tankyrase gene
 family.";
 RL Genes Immun. 2:52-55(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE, AND SUBCELLULAR LOCATION.
 RC TISSUE=Liver;
 RX MEDLINE=21264473; PubMed=11278563; DOI=10.1074/jbc.M009756200;
 RA Lyons R.J., Deane R., Lynch D.K., Ye Z.-S.J., Sanderson G.M.,
 RA Eyre H.J., Sutherland G.R., Daly R.J.;
 RT "Identification of a novel human tankyrase through its interaction
 with the adaptor protein Grb14.";
 RL J. Biol. Chem. 276:17172-17180(2001).
 RN [4]
 RP NUCLEOTIDE SEQUENCE, AND SUBCELLULAR LOCATION.
 RC TISSUE=Placenta;
 RX MEDLINE=21443728; PubMed=11454873; DOI=10.1074/jbc.M105968200;
 RA Kaminker P.G., Kim S.-H., Taylor R.D., Zebardjian Y., Funk W.D.,
 RA Morin G.B., Yaswen P., Campisi J.;
 RT "TANK2, a new TRF1-associated poly(ADP-ribose) polymerase, causes
 rapid induction of cell death upon overexpression.";
 RL J. Biol. Chem. 276:35891-35899(2001).
 RN [5]
 RP NUCLEOTIDE SEQUENCE, FUNCTION, AND INTERACTIONS WITH TRF1 AND

RA LNPEP/OTASE.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=21661361; PubMed=11802774; DOI=10.1042/0264-6021:3610451;
 RA SbioD J.I., Lodish H.F., Chi N.-W.;
 RT "Tankyrase-2 oligomerizes with tankyrase-1 and binds to both TRF1
 RT (telomere-repeat-binding factor 1) and IRAP (insulin-responsive
 RT aminopeptidase).";
 RL Biochem. J. 361:451-459(2002).
 RN [6]
 RA YIN Y., Gelmann E.P.;
 RP NUCLEOTIDE SEQUENCE.
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15164054; DOI=10.1038/nature02462;
 RA Deloukas P., Earthworm M.E., Grafham D.V., Rubinfeld M., French L.,
 RA Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K.,
 RA Hunt S.E., Andrews T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,
 RA Taylor A., Battles J., Bird C.P., Ainscough R., Almeida J.P.,
 RA Ashwell R.I.S., Ambrose K.D., Babbage A.K., Baggeley C.L., Bailey J.,
 RA Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,
 RA Brown J.Y., Burford J.C., Burrill W., Burton J., Cahill P., Camire D.,
 RA Carter N.P., Chapman D.C., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
 RA Corby N., Coulson A., Dhani P., Dutta I., Dunn M., Faulkner L.,
 RA Frankish A., Frankland J.A., Garner P., Garnett J., Gribble S.,
 RA Griffiths C., Grocock R., Gustafson E., Hammond S., Harley J.D.,
 RA Hart E., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,
 RA Huckle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,
 RA Kimberley A.M., Kershaw J.K., Kokkinaki M., Laird G.K., Lawlor S.,
 RA Lee H.M., Leongamert D.A., Laird G., Lloyd C., Lloyd D.M.,
 RA Loveland J., Lovell J., McLaren S., McLeay K.E., McMurray A.,
 RA Mashreghi-Mohammadi M., Matthews L., Milne S., Nickerson T.,
 RA Nguyen M., Overton-Larty E., Palmer S.A., Pearce A.V., Peck A.I.,
 RA Pelan S., Phillimore B., Porter K., Rice C.M., Rogosin A., Ross M.T.,
 RA Sarafidou T., Sehra H.K., Shownkeen R., Skuce C.D., Smith M.,
 RA Stranding L., Sycamore N., Tester J., Thorpe A., Torcaso W.,
 RA Tracey A., Tromans A., Toolas J., Wall M., Walsh J., Wang H.,
 RA Weinstein K., West A.P., Willey D.L., Whitehead S.L., Wilming L.,
 RA Wray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,
 RA Siebert R., Fichtel K., Bentley D., Durbin R., Hubbard T.,
 RA Doucette-Stamm L., Beck S., Smith D.R., Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 10.";
 RL Nature 429:375-381(2004).
 RN [8]
 RA NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 838-1151.
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa M., Yanazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hottu T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Inose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiya H., Satoh N., Takami S., Terashima F., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Okamoto S.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigetani K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada I., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [9]
 RA FUNCTION, AND ADP-RIBOSYLATION.
 RX MEDLINE=21602874; PubMed=11739745; DOI=10.1128/MCB.22.1.332-342.2002;
 RA Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
 RT "Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and 2
 RT at human telomeres.";
 RL Mol. Cell. Biol. 22:332-342(2002).
 CC -1- FUNCTION: May regulate vesicle trafficking and modulate the
 CC subcellular distribution of SLC2A4/GLUT4-vesicles. Has PARP
 CC activity and can modify TRF1, and thereby contribute to the
 CC regulation of telomere length.
 CC -1- CATALYTIC ACTIVITY: NAD(+) + (ADP-D-riboseyl)(n)-acceptor =
 CC nicotinamide + (ADP-D-riboseyl)(n+1)-acceptor.
 CC -1- SUBUNIT: Oligomerizes and associates with TNKS. Interacts with the
 CC cytoplasmic domain of LNPEP/Otase in SLC2A4/GLUT4-vesicles. Binds
 CC to the N-terminus of Grb14 and TRF1 with its ankyrin repeat
 CC region.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and
 CC with juxtanuclear SLC2A4/GLUT4-vesicles. Also found around the
 CC pericentriolar matrix of mitotic centrosomes. During interphase, a
 CC small fraction of TNKS2 is found in the nucleus, associated with
 CC TRF1.
 CC -1- TISSUE SPECIFICITY: Highly expressed in placenta, skeletal muscle,
 CC liver, brain, kidney, heart, thymus, spinal cord, lung, peripheral
 CC blood leukocytes, pancreas, lymph nodes, spleen, prostate, testis,
 CC ovary, small intestine, colon, mammary gland, breast and breast
 CC carcinoma, and in common-type meningioma. Highly expressed in
 CC fetal liver, heart and brain.
 CC -1- PTM: ADP-ribosylated (-auto).
 CC -1- SIMILARITY: Contains 15 ANK repeats.
 CC -1- SIMILARITY: Contains 1 PARP catalytic domain.
 CC -1- SIMILARITY: Contains 1 SAM (sterile alpha motif) domain.
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: AF305081; AAG25674.1; ALT_INIT; mRNA.
 CC EMBL: AF264912; AAG44694.1; -; mRNA.
 CC EMBL: AF329696; AAK13463.1; -; mRNA.
 CC EMBL: AF342982; AAK25811.1; -; mRNA.
 CC EMBL: AF309033; AAK82330.1; -; mRNA.
 CC EMBL: AF438201; AAL40795.1; -; mRNA.
 CC EMBL: AL359707; CAC78760.1; -; Genomic DNA.
 CC EMBL: AK023746; BAB14665.1; ALT_INIT; mRNA.
 CC HSSP: P16157; IN11.
 CC Ensembl: ENSG00000107854; Homo sapiens.
 CC HGNC: HGNC:15677; TNKS2.
 CC MIM: 607128; gene.
 CC InterPro: IPR001290; PARP.
 CC InterPro: IPR012317; PARP_catalytic.
 CC InterPro: IPR01660; SAM.
 CC InterPro: IPR011510; SAM_2.
 CC Pfam: PF00644; PARP; 1.
 CC Pfam: PF00644; PARP; 1.
 CC SMART: SM00248; ANK; 15.
 CC SMART: SM00454; SAM; 1.
 CC PROSITE: PS0297; ANK_REPEAT; 1.
 CC PROSITE: PS0088; ANK_REPEAT; 15.
 CC PROSITE: PS1059; PARP_CATALYTIC; 1.
 CC PROSITE: PS0105; SAM_DOMAIN; 1.
 CC ADP-ribosylation; ANK repeat; Chromosomal protein;
 CC Glycosyltransferase; Golgi stack; NAD; Nuclear protein; Repeat;
 CC Telomere; transferase.
 CC CHAIN 1 1166 /FTId=PRO_0000211334.
 FT REPEAT 57 89 ANK 1.
 FT REPEAT 90 122 ANK 2.

248 PLHNACSYGHVEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSSLLSYGADPTLL 307
241 NCHNKSALDLAPTOLKERLAYEFKGHSLLOAAREADVTRIKKHLSLELVNVPKHPQTHET 300
308 NCHNKSITDLAPTOLKERLAYEFKGHSLLOAARESDVARIKKHLSTLVNVPKHPQTHET 367
301 ALHCAAAAPYKPKQICELLIRKGANINEKTEFLTPLHVAASEKAKHNDVVEVVVKEAKV 360
368 ALHCAAAAPYKPKQVCELLIRKGANINEKTDFTPLHVAASEKAKHNDVVEVVVKEAKV 427
361 NALDNLGTSLHRAAYCCHLOTCRLLSYGCDPNIIISLQGFALTQMGNEVQQLQEGIS 420
428 NALDNLGTSLHRAACHCHLOTCRLLSSGCDPSIVISLQGFALTQMGNESVQQLQEGIP 487
421 LGNSEADQLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
488 LGNSDADRQLLEAAKAGDVTVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 547
481 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKGVAVNVADLWKFTPLHEAAAKGKYE 540
548 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGVAVNVADLWKFTPLHEAAAKGKYE 607
541 ICKLLQHGADPTKKNRDGNTPLDIVKDGDDTDIQLLRGDAALLDAAKKGLARVKLLSS 600
608 ICKLLQHGADPTKKNRDGNTPLDIVKDGDDTDIQLLRGDAALLDAAKKGLARVKLLCS 667
601 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
668 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 727
661 VALLIKYNACVNAQDKWAFPLHFAAGYNNLEVAEYLLQHGADPTLNQEGOTPLDLVS 720
728 VALLIKYNACVNAQDKWAFPLHFAAGYNNLEVAEYLLQHGADPTLNQEGOTPLDLVT 787
721 ADDVSALLTAAMPSPALPCYKQVNLGVSRPCATADALLSPGSPSSLSAASSLDNLSSG 780
788 ADDVSALLTAAMPSPALPCYKQVNLGVSRPCATADALLSPGSPSSLSAASSLDNLSSG 847
781 SFSELSSVSSSTEGASLEKKEVPGVDFSTQFVRNLGLEHLMIDIFEREQITLDLVE 840
848 SFSELSPVVGTSNASEGATVLEKKEVSGVDFSIQFVRNLGLEHLMIDIFEREQITLDLVE 907
841 MGHKELKEIGINAYGHRHKLKGVRELISGQOGLNPYLTNTSSGTTILDLSPDKKEFQ 900
908 MGHKELKEIGINAYGHRHKLKGVRELISGQOGLNPYLTNTSSGTTILDLSSDEKFEQ 967
901 SVEEEMQSTVREHROGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHNANE 960
968 SVEEEMQSTVREHROGGHAGGIFNRYNLIKIOKVCNKKLWERYTHRRKEVSEENHNANE 1027
961 RMLFHGSPFVNAIHHKGFDERHAYIGMFGAGIYFAENSCKSNQVYIGGTCGCPVHKD 1020
1028 RMLFHGSPFVNAIHHKGFDERHAYIGMFGAGIYFAENSCKSNQVYIGGTCGCPVHKD 1087
1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPGHHSTVGRPSV 1065
1088 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPGHHSTVGRPSV 1132

RESULT 3
Q6PFY9 MOUSE PRELIMINARY; PRT; 1320 AA.
AC Q6PFY9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Tks protein.
GN Name=Tks;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1] NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2] NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC057370; AAH57370.1; -; mRNA.
DR HSSP; Q00420; 1AWC.
DR Ensembl; ENSMUSG00000031529; Mus musculus.
DR MGI; MGI:1341087; Tks.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003950; F:NAD+ ADP-riboseyltransferase activity; IEA.
DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001290; PARP.
DR InterPro; IPR012317; PARP_catalytic.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR011510; SAM_2.
DR Pfam; PF00023; Ank; 19.
DR Pfam; PF0644; PARP; 1.
DR Pfam; PF07647; SAM 2; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 15.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00297; ANK_REPEAT; 1.
DR PROSITE; PS00088; ANK_REPEAT; 15.
DR PROSITE; PS01059; PARP_CATALYTIC; 1.
DR PROSITE; PS01059; PARP_CATALYTIC; 1.
DR ANK repeat; Repeat.
SQ SEQUENCE 1320 AA; 140944 MW; A90360DC665FFCC0 CRC64;
Query Match 84.9%; Score 4742.5; DB 2; Length 1320;
Best Local Similarity 82.7%; Pred. No. 1e-271;
Matches 882; Conservative 98; Mismatches 78; Indels 9; Gaps 2;
QY 1 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVLLRHGADPNARDNNYIT 60
DB 218 GFGRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVLLRHGADPNARDNNYIT 277
QY 61 PLHEAAIKGKIDVCIVLLOHGAEPITRTDGRALDADPSAKAVLTGEYKDELLESAR 120
DB 278 PLHEAAIKGKIDVCIVLLOHGAEPITRTDGRALDADPSAKAVLTGEYKDELLESAR 337
QY 121 SGNEEKWALLTFLPNVNCNCHASGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 180
DB 338 SGNEEKWALLTFLPNVNCNCHASGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 397

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RP [1]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.W., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.
 RC NIH MGC Project;
 RG Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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DR EMBL: BC098394; AAH98394.1; -: mRNA.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
 DR GO: GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR012317; PARP_catalytic.
 DR InterPro: IPR001660; SAM.
 DR Pfam: PF00023; ANK; 18.
 DR Pfam: PF00644; PARP; 1.
 DR Pfam: PF07647; SAM 2; 1.
 DR PRINTS: PR01415; ANKYRIN.
 DR SMART: SM00248; ANK; 15.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS50088; ANK_REPEAT; 15.
 DR PROSITE: PS51059; PARP_CATALYTIC; 1.
 DR PROSITE: PS50105; SAM_DOMAIN; 1.
 KW ANK repeat. Repeat.
 SQ SEQUENCE 1327 AA; 141980 MW; 21A8309DF979CA21 CRC64;

Query Match 84.7%; Score 4732.5; DB 2; Length 1327;
 Best Local Similarity 82.6%; Pred. No. 46-271;
 Matches 881; Conservative 97; Mismatches 80; Indels 9; Gaps 2;
 QY 1 GFRKDVVEYLLQNGASVQARDGGILPLHNACSFGEAEVNVLLRHGADPNARDNNWYT 60
 DB 225 GFRKDVVEYLLQNGASVQARDGGILPLHNACSFGEAEVNVLLRHGADPNARDNNWYT 284
 QY 61 PLHEAAIKGKIDVCIVLQHGAEPIRTNDGRTALDLADPSAKAVLTGEYKKDELLESA 120
 DB 285 PLHEAAIKGKIDVCIVLQHGADPNIRNTDGSALDLADPSAKAVLTGEYKKDELLESA 344
 QY 121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDKGLV 180
 DB 345 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHGADVHAKDKGLV 404

QY 181 PLHNACSYGHEVTELLAVKHGACVNMADLMQFTPLHEAASKNRVEVCSSLLSYGADPTLL 240
 DB 405 PLHNACSYGHEVTELLAVKHGACVNMADLMQFTPLHEAASKNRVEVCSSLLSHGADPTLV 464
 QY 241 NCHNKAIDLAPTOLKRLAYEFKSHSLQAAREADVTRIKGHLSELVNFKPQTHET 300
 DB 465 NCHGKSAVDMAPTPELRERLTYEFKSHSLQAAREADLAKVKTLALBIINFKQPSHET 524
 QY 301 ALHCAASAPYPRKQICELILKRGANINEKTEFLPLHVAESEKANHNDVVEVVEHKA 360
 DB 525 ALHCAVASLHPRKQVTELLRLKRGANVNEKNQDPMFTPLHVAERAHNDVMEVLHKGAKM 584
 QY 361 NALNDLQGTSLHRAAYCGHLQTCRLLLSYGCDPMNIIISQGTALQMGNEVQQLIQEGIS 420
 DB 595 NALDTLQGTALHRAALAGHLQTCRLLLSYGSDPSIISQGTAAQMGNEVQQLISESTP 644
 QY 421 LGNSEADQLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNNRVSVVEYLL 480
 DB 645 IRTSDVYRLLEASKAGDLETVKQLCSSONVNCRDLEGRHSTPLHFAAGYNNRVSVVEYLL 704
 QY 481 QHGADVHAKDKGGLVPLHNACSYGHEVVAELLVKGAVNVVADLWKFTPLHEAAKGYE 540
 DB 705 HGGADVHAKDKGGLVPLHNACSYGHEVVAELLVRHGASVNVADLWKFTPLHEAAKGYE 764
 QY 541 ICKLLQHGADPTKKNRGNTPLDLVKDGDTDIODLLRGDAALLDAAKKGCLARVKLSS 600
 DB 765 ICKLLKHGADPTKKNRGNTPLDLVKEGDDTDIODLLRGDAALLDAAKKGCLARVKLCT 824
 QY 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAODKGGLIPLHNAASYGHVD 660
 DB 825 PENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLHEGADVNAODKGGLIPLHNAASYGHVD 884
 QY 661 VAALLIKYNACVNATDKWAFPLHEAAKQGTQICALLLAHGADPTLKNQSGQPTDLVLS 720
 DB 885 IAAALLIKYNTCVNATDKWAFPLHEAAKQGTQICALLLAHGADPTMKNQSGQPTDLAT 944
 QY 721 ADDVSALLTAAMPSPALPCYKPVQNLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG 780
 DB 945 ADDTRALLIDAMPPEALPTCFKPOAT-----VVSASLISPASTPSCLSAASSIDNLITG 997
 QY 781 SFSBELSVVSSSGTEGASSLEKK--EVPGVDFSITQFVRNLGLEHLMDFEREQITLDVL 838
 DB 998 PLAGLAVGSGASNAGDGAAGTERKEGEVAGLDWNISQFLKSLGLEHLRDI FETEQITLDVL 1057
 QY 839 VEMGHKEIKETGINAYGHRHKLKIGVERLISGQOGLNPYLTLNTSGSTILIDLPDKE 898
 DB 1058 ADMGHEELKEITGINAYGHRHKLKIGVERLLGGQGTNPYLTFHCVNQGTILLDLAPEDKE 1117
 QY 899 FQSVVEEMQSTVREHSDGAGGIFNRVNLKIOKVCNKLWERYTHRRKEVSEENHHA 958
 DB 1118 YQSVVEEMQSTIREHSDGAGGIFNRVNVIRIOKVVNKLRERFCHQKEVSEENHHA 1177
 QY 959 NERMLFHGSPFVNAI IHKGFDERHAYIYGMFGAGIYFAENSCKSNQYVYGGGTCFVH 1018
 DB 1178 NERMLFHGSPFINAI IHKGFDERHAYIYGMFGAGIYFAENSCKSNQYVYGGGTCFPH 1237
 QY 1019 KDRSCYICHRQLLFCRVTLGKSFLOFSAMKVAHSPGHHSVTGRPSV 1065
 DB 1238 KDRSCYICHRQMLFCRVTLGKSFLOFTIKMAHAPPGHHSVIGRPSV 1284
 RESULT 6
 Q800D9 CHICK PRELIMINARY; PRT; 1266 AA.
 AC Q800D9;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 14.
 DE Tankyrase 1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.

OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22615216; PubMed=12589701; DOI=10.1042/BJ20021450;
RA De Rycker M., Venkatesan R.N., Wei C., Price C.M.;
RT "Vertebrate tankyrase domain structure and sterile alpha motif (SAM)-
RL mediated multimerization.";
RL Biochem. J. 372:87-96(2003).
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CC -----
DR EMBL; AY142108; AAN41651.1; -; mRNA.
DR HSSP; P16157; IN11.
DR Ensembl; ENSGALG00000011438; Gallus gallus.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001290; PARP.
DR InterPro; IPR012317; PARP_catalytic.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR011510; SAM_2.
DR Pfam; PF00023; ANK; 19.
DR Pfam; PF07647; SAM_2; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00249; ANK; 15.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS0297; ANK_REPEAT; 1.
DR PROSITE; PS0088; ANK_REPEAT; 15.
DR PROSITE; PS1059; PARE_CATALYTIC; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1266 AA; 136212 MW; 14B8617BF930E6E0 CRC64;

Query Match 84.7%; Score 4730.5; DB 2; Length 1266;
Best Local Similarity 82.6%; Pred. No. 4.8e-271;
Matches 881; Conservative 97; Mismatches 80; Indels 9; Gaps 2;

QY 1 GFGKRDVVEYLLQNGASVQARDGGGLIPLHNACSFGEVNVNLLRHGADPNARDNNWYT 60
DB 164 GFGKRDVVEYLLQNGASVQARDGGGLIPLHNACSFGEVNVNLLRHGADPNARDNNWYT 223

QY 61 PLHEAAIKGIDVCIVLQHGAEPIRNTDGTALDADPSAKAVLTGKYKDELLESAR 120
DB 224 PLHEAAIKGIDVCIVLQHGAEPIRNTDGTALDADPSAKAVLTGKYKDELLESAR 283

QY 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRKYIVOLLQHGADVHAKDKGLV 180
DB 284 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRKYIVOLLQHGADVHAKDKGLV 343

QY 181 PLHNACSYGHVEVTELLVKHGACVNMADLWQFTPLHEAASKRVEVCSLLLSYGADPTLL 240
DB 344 PLHNACSYGHVEVTELLVKHGACVNMADLWQFTPLHEAASKRVEVCSLLLSYGADPTLL 403

QY 241 NCHNKAIDLAPTPOLKERLAYEFKHSLLQAREADVTRIKNHLSLEMVNFKPHQTHET 300
DB 404 NCHGKSAVDMAPTPELRRLTYEFKHSLLQAREADVTRIKNHLSLEMVNFKPHQTHET 463

QY 301 ALHCAASAPYKPKKICELLRLKGANINEKTEFLTPLHVAEKANDVVEVVVKEAVK 360
DB 464 ALHCAVAAVHPKPKKQVTELLRLKGANINEKTEFLTPLHVAEKANDVVEVVVKEAVK 523

QY 361 NALDNLGQTSLHRAAYCGHLOTCRLLLSYGCDPNTIISLQGTALQMGENVQOLLQEGIS 420
DB 524 NALDNLGQTSLHRAAYCGHLOTCRLLLSYGCDPNTIISLQGTALQMGENVQOLLQEGIS 583

QY 421 LGNSEADPQLLEAAKAGDVETVKLCITVQSVNCRDIEGRQSTPLHFAAGYNNRVSVYELL 480
DB 584 VRTSDVDYVRLLEAAKAGDVETVKLCITVQSVNCRDIEGRQSTPLHFAAGYNNRVSVYELL 643

QY 481 QHGADVHAKDKGLVPLHNACSYGHVEVTELLVKHGADVHAKDKGLV 540

DB 644 QHGADVHAKDKGLVPLHNACSYGHVEVTELLVKHGADVHAKDKGLV 703

QY 541 ICKLLLOHGADPTKKNRDNCTPLDVKDGTDTIDQLLRGDAALLDAKKGCLARVKKLSS 600
DB 704 ICKLLLOHGADPTKKNRDNCTPLDVKDGTDTIDQLLRGDAALLDAKKGCLARVKKLCT 763

QY 601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
DB 764 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 823

QY 661 VAALIKYNACVNAATDKWAFTPLHEAAQKGTQOLCALLAHAGADPTLKNQEGTPTDLVS 720
DB 824 IAALLIKYNTCVNATDKWAFTPLHEAAQKGTQOLCALLAHAGADPTLKNQEGTPTDLAT 883

QY 721 ADDVSALLTAAMPSPALPCYKPOVLNGVSPCATADALSSGSPSSLSAASLNLG 780
DB 884 ADDIRALLIDAMPPEALPTCFKQAT-----VWSAISLSPASTPSCLSAASLNLG 936

QY 781 SPSSELSSVVSSSGTEGASLEKK--EVPGVDFSIQFVRNLGLEHLMDFEREQITLDVL 838
DB 937 PLAEALVGGASNTGDGAAGTERKEGEVSLDMNITQFLKSLGLEHLRDFETEQITLDVL 996

QY 839 VEMGHKELKEIGINAYGHRHKLINGVERLISQOGLNPNYLTNTSGSTLIDLSPPDKE 898
DB 997 ADMGHEELKEIGINAYGHRHKLINGVERLISQOGLNPNYLTNTSGSTLIDLSPPDKE 1056

QY 899 FQSVVEEMQSTVREHRDGGHAGGINFRNINILKIOKCNKLMERYTHRRKEVSEENHHA 958
DB 1057 FQSVVEEMQSTVREHRDGGHAGGINFRNINILKIOKCNKLMERYTHRRKEVSEENHHA 1116

QY 959 NERMLPHGSPFFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGTCPCPVH 1018
DB 1117 NERMLPHGSPFFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGTCPCPVH 1176

QY 1019 KDRSCYICHRQLLCRVTLGKSLQFSAAMKMAHSPGHHSVTGRPSV 1065
DB 1177 KDRSCYICHRQLLCRVTLGKSLQFSAAMKMAHSPGHHSVTGRPSV 1223

RESULT 7
Q5XGK5 XENLA PRELIMINARY; PRT; 1303 AA.
ID Q5XGK5 XENLA PRELIMINARY; PRT; 1303 AA.
AC Q5XGK5
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE LOC495279 protein.
GN Name=LOC495279;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splicein;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splicein;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3].
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE-Spleen;
 RA Klein S., Gerhard D.S.;
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; BC084432; AAB84432.1; -; mRNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
 DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR001290; PARP.
 DR InterPro; IPR012317; PARP_catalytic.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR011510; SAM_2.
 DR Pfam; PF00023; Ank; 18.
 DR Pfam; PF00644; PARP; 1.
 DR Pfam; PF07647; SAM_2; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 15.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS0297; ANK_REPEAT; 1.
 DR PROSITE; PS00888; ANK_REPEAT; 15.
 DR PROSITE; PS1059; PARP_CATALYTIC; 1.
 DR PROSITE; PS0105; SAM_DOMAIN; 1.
 KW ANK repeat; Repeat.
 SQ SEQUENCE 1303 AA; 140271 MW; 5F4C3F89329D5F8B CRC64;

Query Match 83.7%; Score 4674.5; DB 2; Length 1303;
 Best Local Similarity 81.6%; Pred. No. 1.1e-267;
 Matches 871; Conservative 99; Mismatches 88; Indels 9; Gaps 2;
 QY 1 GFGKDVVEYLLQNGASVOARDGGGLPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60
 DB 201 GFGKDVVEYLLQNGASVOARDGGGLPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 260
 QY 61 PLHEAARIGKIDVCIVLLQHGAEPTIRNTDGTALDLADPSAKAVLTGEYKKDELLESAR 120
 DB 261 PLHEAARIGKIDVCIVLLQHGADPSIRNTDGTALDLADPSAKAVLTGEYKKDELLEAAR 320
 QY 121 SGNEEKMAILLTPLNVNCHASDGRKSTPLHLAAGNVRVIVOLLQHGADVHAKDKGLV 180
 DB 321 SGNEEKMAILLTPLNVNCHASDGRKSTPLHLAAGNVRVIVOLLQHGADVHAKDKGLV 380
 QY 181 PLHNACSYGHVEVTELLVKGHCACVNMOLWQPTPLHEAASKNRVEVCILLSYGDPTLL 240
 DB 381 PLHNACSYGHVEVTELLVKGHCACVNMOLWQPTPLHEAASKNRVEVCILLSYGDPTLL 440
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 DB 441 NCHGKSAVDMAPTPELKERLSYFKGHSLLQAAAREADYTRIKCHLSLEMVNFKHPQTHET 500
 QY 301 ALHCAAAASYPKQKQICELLRLKGANINEKTEFUTPLHVASEKANNDDVEVVKHEAKV 360
 DB 501 ALHCAVASLHPKQKQITELLRLKGANINEKTEFUTPLHVASEKANNDDVEVVKHEAKV 560

QY 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYSGDPPNIISLQGFALQMGNNVQQLQOEGIS 420
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 QY 421 LGNSEARQOLLEAAKAGDVETVKKLCVTQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
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 QY 481 OHGADVHAKDKGLVPLHNACSYGHVEVAELLVKGHCACVNMOLWQPTPLHEAASKNRVEVC 540
 DB 681 HHGADVHAKDKGLVPLHNACSYGHVEVAELLVKGHCACVNMOLWQPTPLHEAASKNRVEVC 740
 QY 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDGTDIQLLLRGDAALDAAKKGCLARVKLSS 600
 DB 741 ICKLLQHGADPTKKNRDGNTPLDLVKDGDGTDIQLLLRGDAALDAAKKGCLARVKLCT 800
 QY 601 PDNVNCRDPTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAODKGGGLPLHNAASYGHVD 660
 DB 801 QENINCRDPTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAODKGGGLPLHNAASYGHVD 860
 QY 661 VAALLIKYNAQVATDKWAFPTPLHEAAGKGTQLCALLAHGADPTLKNQSGQTPDLVLS 720
 DB 861 IAALLIKYNAQVATDKWAFPTPLHEAAGKGTQLCALLAHGADPTLKNQSGQTPDLVLS 920
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 DB 921 ADDIRALLIDAMPPEALPCFKPOAT-----VVSASIIISPASTPSCLSAASSIDNLSSG 973
 QY 781 SFSELSVSSSGTEGASSLEKK--EVPQVDFTITQVNRNLGLEHLMIDIPREQITLDVL 838
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 QY 899 FQSVVEEMQSTVREHRDGHAGGIFNRYNLIKIKVCNKKLWERYTHRRKEVSEENHHA 958
 DB 1094 HQSVVEEMQSTVREHRDGHAGGIFNRYNLIKIKVCNKKLWERYTHRRKEVSEENHHA 1153
 QY 959 NERMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVGGTGCPCVH 1018
 DB 1154 NERMLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVGGTGCPCVH 1213
 QY 1019 KDRSCYICHRQLLCRVTLGKSFLOFSAMKMAHSPGPHSHSVTGPRSV 1065
 DB 1214 KDRSCYICHRQLLCRVTLGKSFLOFSAMKMAHSPGPHSHSVTGPRSV 1260
 RESULT 8
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 AC Q4RG97;
 DT 19-JUL-2005, integrated into UniProtKB/TREMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Chromosome 12 SCAP15104, whole genome shotgun sequence. (Fragment).
 GN ORFNames=GSTENG00034904001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontinae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthonard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Biewont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

RA Craud C., Duprat S., Brothier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Landier E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RN Nature 431:946-957(2004).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBSJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
CC EMBL; CAAB01015104; CAG12585.1; -; Genomic DNA.
CC GO; GO:0005634; C:nucleus; IEA.
CC GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
CC GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
CC InterPro; IPR002110; ANK.
CC InterPro; IPR012317; PARP_catalytic.
CC InterPro; IPR001660; SAM.
CC Pfam; PF00023; Ank; 15.
CC Pfam; PF06644; PARP; 1.
CC Pfam; PF07647; SAM; 2; 1.
CC PRINTS; PR01415; ANKYRIN.
CC SMART; SM00248; ANK; 13.
CC SMART; SM00454; SAM; 1.
CC PROSITE; PS0297; ANK REP REGION; 1.
CC PROSITE; PS0088; ANK REPEAT; 13.
CC PROSITE; PS1059; PARF CATALYTIC; 1.
CC PROSITE; PS0105; SAM_DOMAIN; 1.
CC ANK repeat.
KW ANK repeat.
FT NON TER 1 1
FT NON TER 1212 1212
SQ SEQUENCE 1212 AA; 131719 MW; 973307E7FF92C219 CRC64;

Query Match 82.9%; Score 4631.5; DB 2; Length 1212;
Best Local Similarity 77.2%; Pred. No. 3.3e-265;
Matches 872; Conservative 103; Mismatches 78; Indels 77; Gaps 7;

QY 3 GRKDVVEYLLQNGASVQARDGGLIPLHNACSGFHAEEVNVNLLRHGADPNARDNNYTP 62
DB 50 GEKTWNTFLOTGANVHARDGGLIPLHNACSGFHAEEVNVNLLRHGADPNARDNNYTP 109

QY 63 HEAAIKGKIDVICVILQHGAEPTINTDGTALDADPSAKAVLTGEYKDELLSARSG 122
DB 110 HEAAIKGKIDVICVILQHGADPNIRNTDGSALDADPSAKAVLTGEYKDELLSARSG 169

QY 123 NEEKMALLTPLNVNCHASDGRKSTPLHLAAGVNRVKIVOLLQHGADVHAKDGLVPL 182
DB 170 NEEKMALLTPLNVNCHASDGRKSTPLHLAAGVNRVIVOLLQHGADVHAKDGLVPL 229

QY 183 HNACSYGHEVTELVKHGACVNMVLMQFTPLHEAASKNRVEVCSLLSYGADPTLLNC 242
DB 230 HNACSYGHEVTELVKHGACVNMVLMQFTPLHEAASKNRVEVCSLLSHGADPTLLNC 289

QY 243 HNKSADLAPTQPKERLAYEFGHSLQQAAREADVTRIKGHLSEMVNFKPQTHETAL 302
DB 290 HSKSAVDNAPTPELKDRLTYEFKGHSLQQAAREADMAKVKTKLALIEIISFKPQNTD 349

QY 303 -----HCAASPYPKRKQICELLIRKGNINEKTEFLTPHLVASEKAHNDVVEV 353
DB 350 MLKVAAVFQHCVAVPFPKQVTELLIRKGNINDKDFMTPLHVAERAHNDILEVL 409

QY 354 VKHEAKVNALDNLGOTSLSHRAAYCGHLOQTCRLLSYGCDPNIIISLGFTALQWGNVQ 413
DB 410 QKHGAKVNVADILGQTLHRAALAGHIQTKULLSYGADPAIVSLQGTAAQWGNVQ 469

RESULT 9

Q59FX0 HUMAN PRELIMINARY; PRT; 1055 AA.
ID Q59FX0 HUMAN PRELIMINARY; PRT; 1055 AA.
AC Q59FX0;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
DE variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain.
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBSJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

QY 414 LLEQGISLGNSEADRLLEAAKAGDVETV-----KKLCTVQ 449
DB 470 ILNENVPTNSVDYRFLFAAAGDLDTVQVSWSLALRLVSEGMRLQKVLVSQQLCSPQ 529
QY 450 SYNCRDIEGRQSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHEVA 509
DB 530 NVNCRDLEGRHSTPLHFAAGYNNRVAVVEYLLHGGADVHAKDGLVPLHNACSYGHEVA 589
QY 510 ELLVKGAVNVVADLWKFTPLHEAAAKGYEICKLLQHGADPTKKRDGNTPLDLVKDG 569
DB 590 ELLVRHGASVNVADLWKFTPLHEAAAKGYEICKLLKHGADPTKKRDGNIPLDMVKDG 649
QY 570 PDDIOLLRGDAALDAAKGCLARVKKLSPPNVNCRDTQGRHSTPLHLAAGYNNLEVA 629
DB 650 DTDIOLLRGDAALDAAKGCLARVKKLSPPNVNCRDTQGRHSTPLHLAAGYNNLEVA 709
QY 630 EYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNAATDKWAFTELHEAAQK 689
DB 710 EYLLHGGADVNAQDKGGLIPLHNAASYGHVDIAALLIKYNTCVNATDKWAFTELHEAAQK 769
QY 690 GRTQLCALLLAHGAFTLKNQSGQTPLD-----LVSADDV 724
DB 770 GRTQLCALLLAHGAFTLKNQSGQTALDLYNLPLFIVSTLYSRRAHGVFWLLQADDI 829
QY 725 SALLTAAMPSPALPSCYKPKQ---VLNGVSPGATADALSSGSPSSLSAASLDNLGSG 781
DB 830 RALLIDAMPDPPDALPSCFKPQATVVSASVSPAST-----PSCLSAASIDNLGAP 879
QY 782 FSELSSVSSSGT---EGASSLEKK--EVPGVDFSIQFVRNLGLEHLMDFEREQITL 835
DB 880 LTELAAAVSTGSSGVADGATGSEKGEWMLDMNISQFLKSLGLDHLRDIEREQITL 939
QY 836 DVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGOGLNPYLTNTSGSTLIDLSPD 895
DB 940 DVLADMGHEELKEIGINAYGHRHKLKIGVERLISGOGLNPYLTFFHCASQGTILIDLAPD 999
QY 896 DKEFQSVSEEMOSTVREHDDGGHAGGIFNRYNLTIKQVCKNKKLWERYTHRRKEVSEENH 955
DB 1000 DKEYQSVSEEMOSTIREHDDGGNAGGVFRYNIKIQVNVKKLRERYTHRQKEIADENH 1059
QY 956 NHANERMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYIGGGTGC 1015
DB 1060 NHNEMLFHGSPPFINAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYIGGGTGC 1119
QY 1016 PVHKORSCHVCHRLQFLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSV 1065
DB 1120 PTHKORSCHVCHRLQFLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSV 1169

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CC EMBL; AB209339; BAD92576.1; -; mRNA.
DR Ensembl; ENSG00000173273; Homo sapiens.
DR GO; GO:0003634; C:nucleus; IEA.
DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001290; PARP.
DR InterPro; IPR012317; PARP_catalytic.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR011510; SAM_2.
DR Pfam; PF00023; ANK; 17.
DR Pfam; PF00644; PARP; 1.
DR Pfam; PF07647; SAM_2; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 13.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS50297; ANK REP REGION; 1.
DR PROSITE; PS50088; ANK REPEAT; 13.
DR PROSITE; PS51059; PARP CATALYTIC; 1.
DR PROSITE; PS50105; SAM_DOMAIN; 1.
KW ANK repeat.
FT NON TER 1 1
SQ SEQUENCE 1055 AA; 115234 MW; 9210519D299EB805 CRC64;

Query Match 81.2%; Score 4532.5; DB 2; Length 1055;
Best Local Similarity 82.6%; Pred. No. 28-259;
Matches 842; Conservative 93; Mismatches 75; Indels 9; Gaps 2;

QY 49 ADPNARDNNYTPLEHAALGKIDVICVILLOHGAEPRTINTDGTALDIALDPSAKAVLTG 108
DB 1 ADPNARDNNYTPLEHAALGKIDVICVILLOHGAEPRTINTDGTALDIALDPSAKAVLTG 60

QY 109 EYKDELLESARSNGNEKWMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLQHG 168
DB 61 EYKDELLEARSNGNEKLMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIVQLLQHG 120

QY 169 ADVHAKDGDVLPLNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNVEVCS 228
DB 121 ADVHAKDGGVLPLNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNVEVCS 180

QY 229 LLLSYGADPTLNCNKSALDAPTPOLKRLAYEPKSHLSLQAAAREADVTRIKKLSLE 288
DB 181 LLLSHGADPTLVNCHCKSAVDNAPTELPRLRYTEFKGSHLSLQAAAREADLAKVKTTALE 240

QY 289 MYNFKHPQTHETALHCAASPYKXKQICELLRLKGANINEKTKBPLPLHVAASEKANND 348
DB 241 IINFKQPQSHETALHCAVASLHPKQVTELLRLKGANVNEKNKDFTPLHVAASRAHND 300

QY 349 VVEVVVKEAKVNDNLGOTSILHRAAYCGHLCTCELLLSYCGDPNIIISLOGFTALQWGN 408
DB 301 VMEVLHKGAKVNDLTLGQTHLRAALAGHQTCLLLSYGSDPSIISLOGFTAAQWGN 360

QY 409 ENVQQLLOEGISLGNSEADRLLEAKAGDVETVKLTQVQSVNCRDIEGRSTPLHFAA 468
DB 361 EAVQQLSESTPIRSDVDYRLLEASKAGDLETVQLCSSQNVNCRDIEGRSTPLHFAA 420

QY 469 GYNRVSVVEYLLQHGADVHAKDGGVLPLHNAACSYGHEVABLLVKGAVNVNADLWKT 528
DB 421 GYNRVSVVEYLLHHGADVHAKDGGVLPLHNAACSYGHEVABLLVKGAVNVNADLWKT 480

QY 529 PLHEAAAKGYEICKLLQHGADPTKKNRDGNTPDLVKQDGTDDQLLGRDAALLDAK 588
DB 481 PLHEAAAKGYEICKLLKHGADPTKKNRDGNTPDLVKQDGTDDQLLGRDAALLDAK 540

QY 589 KGLARVKLSLSPDNVNCRDGTGRSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLI 648
DB 541 KGLARVKLSLSPDNVNCRDGTGRSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLI 600

QY 649 PLHNAASYGHVDVAALLIKYNAACVNATDKWATPPLHEAAQKRTQLCALLAHGADPTLK 708
DB 601 PLHNAASYGHVDVAALLIKYNTCVNATDKWATPPLHEAAQKRTQLCALLAHGADPTMK 660

QY 709 NOEGOTPLDVSADDSVALLTAAMPSPALPSYCKPQVLNGVRSFGATADALSSGSSPSS 768
DB 661 NOEGOTPLDVSADDSVALLTAAMPSPALPSYCKPQVLNGVRSFGATADALSSGSSPSS 713

QY 769 LSAASSLDNLGSPFSELSSVSSSGTEGASLEKK--EVPGVDFITQFVRLGLEHMD 826
DB 714 LSAASSIDNLGTPLAELAVGASNAGDGAAGTERKEGEVAGLDNMISQFLKSLGLEHMD 773

QY 827 IFERQITLDVLVEMGHKELKEIGINAYGHRHKLKGVERLISGOGLNPYLTLNTSGS 886
DB 774 IFETEQITLDVLADMGHEELKEIGINAYGHRHKLKGVERLISGOGLNPYLTLNTSGS 833

QY 887 TILDLSPDDKEFOSVEEMOSTVREHRDGGHAGGIFNRYNLIKIQVKCNKKLWERYTHR 946
DB 834 TILLDLAPEDKEYQSVEEMOSTVREHRDGGHAGGIFNRYNLIKIQVKCNKKLWERYTHR 893

QY 947 RKEVSENNHNNRMLPHGSPFVNAILHKGFDERHAYIGMGFAGIYFAENSSKSNQV 1006
DB 894 QKEVSENNHNNRMLPHGSPFVNAILHKGFDERHAYIGMGFAGIYFAENSSKSNQV 953

QY 1007 YGIGGGTCGPVHKDSCYICHRQLLFCRVTGLKSELOFSAMKMAHSPCHHSVTGRPSV 1065
DB 954 YGIGGGTCGPVHKDSCYICHRQLLFCRVTGLKSELOFSAMKMAHSPCHHSVTGRPSV 1012

RESULT 10
Q8BX62_MOUSE
ID Q8BX62_MOUSE PRELIMINARY; PRT; 976 AA.
AC Q8BX62;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 20.
DE 0 day neonate cerebellum cDNA, RIKEN full-length enriched library,
DE clone: C230076123 product: tankyrase, TRF1-interacting ankyrin-related
DE ADP-ribose polymerase, full insert sequence.
GN Name=Tnks;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Murioidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Cerebellum; STRAIN=C57BL/6J;
RX MEDLINE=92729253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Methods Enzymol. 303:19-44(1999).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
Ambesi-Impombato A., Apweiler R., Aurali R.N., Bailey T.L.,
Bansal M.L., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
Crome M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
di Bernardo D., Down T., Engstrom P., Fagioli M., Paulkner G.,
Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
Hill D., Huminecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelson J., Kitamura H.,
Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
Kurochkin I.V., Larsen L.F., Lazarevic D., Lipovich L., Liu J.,
Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,

OKazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavasi G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Rost B., Ruan Y., Salzbeg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugitara K., Sultana R., Takenaka Y., Taki K., Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K., Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S., Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
 "The transcriptional landscape of the mammalian genome.";
 Science 309:1559-1563 (2005).
 [3]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC PubMed=16141073; DOI=10.1126/science.1112009;
 RX RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566 (2005).
 [4]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Ciothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustinchik S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawasava Y., Kedzierka R.M., King B.L., Kanyaga A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Mikl H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
 Nature 420:563-573 (2002).
 [5]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustinchik S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S., Hayashizaki Y.;
 "Functional annotation of a full-length mouse cDNA collection.";
 Nature 409:685-690 (2001).
 [6]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 Genome Res. 10:1617-1630 (2000).
 [7]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 Genome Res. 10:1757-1771 (2000).
 [8]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Kura H., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

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 EMBL; AK048860; BAC33475.1; -; mRNA.
 HSSP; P6157; IN11.
 Ensembl; ENSMUSG00000031529; Mus musculus.
 MGI; MGI:1341087; Tnks.
 GO; GO:0005634; C:nucleus; IEA.
 GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
 GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
 InterPro; IPR02110; ANK.
 InterPro; IPR001290; PARP.
 InterPro; IPR012317; PARP catalytic.
 InterPro; IPR001660; SAM.
 InterPro; IPR011510; SAM_2.
 Pfam; PF00023; Ank; 15.
 Pfam; PF00644; PARP; 1.
 Pfam; PF07647; SAM_2; 1.
 PRINTS; PR01415; ANKYRIN.
 SMART; SM00248; ANK; 12.
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 PROSITE; PS0297; ANK_REPEAT; 1.
 PROSITE; PS0088; ANK_REPEAT; 12.

Db 472 -DTVDLECOLLEAAKAGDLDTRIVRIVLSSPMVNCRLDGRHSTPLHPAAGNRPVVF 530
Qy 479 LLOHGADVHAKDGLVPLHNACSYGHVEVAELIVKHGAVNVNADLMKFTPLHEAAAKG 538
Db 531 LLEHGAEVHASKDGLVPLHNACSYGHVEVTELLVGHGANVNADLMKFTPLHEAAAKG 590
Qy 539 YEICKLLOHGADTKKRDGNTPLDLVKDGTDIODLLRGDAALLDAKKGCLARVKL 598
Db 591 YEIVKLLIKHGADYTKKRDGATPLDLVREGDQDADLLRGNALLDAKKGNTLARVQL 650
Qy 599 SSPDNVCRDQGRHSTPLHLAGVNNLEVAEYLLOHGADVNAODKGLIPLHNAASYGH 658
Db 651 VSDININCRDQGRNSTPLHLAGVNNLEVAEYLLEHGDVNAQDKGLIPLHNAASYGH 710
Qy 659 VDVAALLIKYNACVATDKMAFTPLHEAAQKRGRTQLCALLAHGADPTLKQEGQTPLDL 718
Db 711 LDIAALLIKHNTVNVATDKMGYTPLEHAAQKRGRTQLCSLLLAHGADPPMKQEGQTSLDL 770
Qy 719 VSADVSALLTAAPPSALPSCYKPVOLNGVRSPGATADALSSGSPSSLSAASSLDNL 778
Db 771 ATABDVKCLLDAM-----VASQGTVAGGTAAGAGAGTSGQGILSANGTL--L 816
Qy 779 SGSPSELSSVVS-----SSGTREGASSL-----EKKEVPG 807
Db 817 ATSCSPTEVTLTGASMTLSVPVQPLPVRSCLSPAGCAENVVDGIVDHDDKMPSPS 876
Qy 808 VDFSITQVRLNGLHLMDFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKGVRL 867
Db 877 IESSVSVFLTSQLLEHLIDLFEREQITWDLIAEMGHEDLKQGVSAVYFRHKLKGIATL 936
Qy 868 -ISGQGLNPYLTNTSGSHILDLSPDDKEFQSVSEEMQSTVREHDDGGHAGIFNRY 926
Db 937 RATTGLGLTP-----NPGTLLVDLLPDDKEFLAVEEEMQATIREHDDNGHSGGFNRY 989
Qy 927 NILKIQVCKNKKLWERYTHRRKSEVENHNANERMLPHGSPFFVNAIITHKGFDERHAYIG 986
Db 990 NIVRIQVONRKWLWERYVHRRQEISEEHQASERMLPHGSPFFINAIYQKGFDERHAYIG 1049
Qy 987 GMFGAGIYFAENSSKSNQYVYIGGGTGCPCVHKDKSCYICHRQLLFCRVTLGKSPLOFSA 1046
Db 1050 GMFGAGIYFAEHSKSNQYVYIGGGIGGICPTHKDKSCYQCHRQLLCLVALGKSPLOFSA 1109
Qy 1047 MKMAHSPGHHSVTRGPS 1064
Db 1110 MKMAHAPGHHHSVTRGPS 1127

RESULT 12

Q9VBP3 DROME PRELIMINARY; PRT: 1181 AA.
AC Q9VBP3;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 32.
DE CG4719-PA.
GN Name=tankyrase; ORFNames=Dmel CG4719;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Wandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupek M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnik S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupu J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
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RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
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RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celnik S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]

DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.

DR InterPro; IPR002110; ANK.

DR Pfam; PF00023; Ank; 13.

DR Pfam; PF00644; PARP; 1.

DR PRINTS; PR01415; ANKYRIN.

DR SMART; SMO0248; ANK; 9.

DR PROSITE; PS50297; ANK REP REGION; 1.

DR PROSITE; PS50088; ANK_REPEAT; 10.

DR PROSITE; PS51059; PARP_CATALYTIC; 1.

KW ANK repeat. 1047 1047

FT NON TER

SQ SEQUENCE 1047 AA; 114477 MW; 09E9D3AE198C75E7 CRC64;

Query Match 56.9%; Score 3179; DB 2; Length 1047;

Best Local Similarity 59.1%; Pred No. 3e-179;

Matches 652; Conservative 68; Mismatches 134; Indels 250; Gaps 17;

Qy 108 GEYKDELLESARGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRKIVVOLLQ 167

Db 18 GEYKDELLEAARGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRKIVVOLLQ 77

Qy 168 GADVHAKDGDVPLHNAACSGHYEVTELLVK----- 199

Db 78 GADVHAKDGDVPLHNAACSGHYEVTELLVKVTHHTTHRAQTHTGCVETLARP LLEA 137

Qy 200 -----HGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLNCHNKSALDAPT 253

Db 138 ETVSPQHGACVNMADLWQFTPLHEAASKNRVEVCSLLLSHGADPTLLNCHNKSVDWAPT 197

Qy 254 POLKERLAYEPKSHLSLOAAREADVTRIKKHLSEVMNFKHPQTHETALHCAAAAPYPMR 313

Db 198 PELXERLTYEPKSHLSLOAAREADVAKAKSVLEIINFKHPHTHTAL----- 246

Qy 314 KQICELLURKGANINEKTYEFLPLHVAASEK-----AHNDVVVVVVKHAKVNALDNLQOT 369

Db 247 -----LHDSASRGCGGAHNDIMEVLQKHGAKVNALDNLQOT 282

Qy 370 SLHRAAYCGHLCETLLSYGCDPNIIISLQGTALOMGNENVQQLQESLGNSEADRO 429

Db 283 ALHRAAMAGHLHTCKLLGYGADASLSVQGTAAQMGNEAVQQLSENVPVRSVDVDR 342

Qy 430 LLEAAKAGDVETVKLCVTQSVNCRDIEGROSTPLHFAAGYNNRVSVYLLQHGADVHAK 489

Db 343 LLEAAKAGDLTVKSLCTPQNVNCRDLGSRHSTPLHFAAGYNNRVSVYLLQHGADVHAK 402

Qy 490 DKGLVPLHNAACSGHYEVAELLVKHGVANNVADLWKFTPLHEAAKGYEICKLLQHG 549

Db 403 DKGLVPLHNAACSGHYEVAELLVRHGASVNVADLWKFTPLHEAAKGYEICKLLKHG 462

Qy 550 ADPTKKNPDGNTPLDLVKDGTDIQDLRGDAALLDAAKGLARVKKLSGPDNVNCRDT 609

Db 463 ADPTKKNPDGNTPLDLVKDGTDIQDLRGDAALLDAAKGLARVKKLSGPDNVNCRDT 522

Qy 610 QGRSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGRVDVAALLIKYN 669

Db 523 QGRSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGRVDVAALLIKHN 582

Qy 670 ACVNATDKWFTPLHEAAQKGTQICALLAHGADPTLLKNEGOTPLDLVS----- 720

Db 583 TCVNATDKWFTPLHEAAQKGTQICALLAHGADPTLRNEGOTPLDLATAPVVFDROR 642

Qy 721 -----ADVSALLTAAMPSPALSCYKPOVLNGVRSPGATADALSQSPSPS 767

Db 643 MYDSVSVPPSPQADDIRALLIDAMPDPALESCLPKQ-----ATVWWSG----- 688

Qy 768 SILSAASSLDNLGSPSELSVSSVSSGTGEGASSLEKKEVP-----GVDFSIQT----- 814

Db 689 -----ECQRCRRGRGHIAVPVAVLIPVCGQQHQRPDHPAPRPHGGRGHRISGRDVRVQEGGR 746

Qy 815 -FVRNLGHLMDIFEREQITLDVLVEMGHKEL-KEIGI----- 851

Db 747 RYRRAFAAGH-----DHQPLPEESGAGTPPHLPERADFPSPGRGRH 788

Qy 852 ---NAYGHRHKLINGVERLISGOOGLN-----PYLTNTSGSTILDLSPDKKF 899

Db 789 GARAEGRHQRRLPPAQAQDQGHREAAGRATWKPVDLP LLRPGN----- 834

Qy 900 QSVEEEMQSTVREHRDQGHAGGIFNRNIIKIQVCNKKLWE-----RYTHRRKEYSEE 953

Db 835 -----RPDRPGSRQGV-----PVCGGAAEHHPRAPRWRERRSLQPL 873

Qy 954 NHHANERMLF-----HGSPFVNAIIHKGFDERHAYIGMFGAGI 993

Db 874 QHOGVACGFRAADRDDEPALTKVCFLADSEGSFFINAIHKGFDERHAYIGMFGAGI 933

Qy 994 YFAENSSKSNQYVYGGIGGTCGCPVHKDRSCYIC-----RQLLCFRTVLGKSF 1041

Db 934 YFAENSSKSNQYVYGGIGGTCGCPVHKDRSCYICVCHRSADVNGGCLCARQMLFCRVTLGKSF 993

Qy 1042 LQFSAMKVAHSPGCHSVHTGRPSV 1065

Db 994 LQFSAMKVAHSPGCHSVHTGRPSV 1017

RESULT 15

Q3UES3_MOUSE

ID Q3UES3_MOUSE PRELIMINARY; PRT; 589 AA.

AC Q3UES3;

DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.

DT 11-OCT-2005, sequence version 1.

DT 07-FEB-2006, entry version 6.

DE Adult male liver tumor cDNA, RIKEN full-length enriched library,

DE clone: C730001F05 product: Tankyrase 2 (EC 2.4.2.30) (TANK2) (Tankyrase

DE II) (TNKS-2) (TNF1-interacting ankyrin-related ADP-ribose polymerase

DE 2) (Tankyrase-like protein) (Tankyrase-related protein) homolog

DE (Fragment).

GN Name=Tnk2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Liver;

RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.;"

RL Methods Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Liver;

RC PubMed=16141072; DOI=10.1126/science.1112014;

RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,

RA Oyama R., Ravasi S., Lenhard B., Wells C., Kodzius R., Shimokawa K.,

RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,

RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,

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RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,

RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,

RA Crowe M.L., Datta E., Dalrymple B.P., de Bono B., Della Gatta G.,

RA Di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,

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RA Hill D., Humnicks L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,

RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

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RA Kurochuk I.V., Lazarev L.F., Lazarevic D., Lipovich L., Liu J.,

RA Lium S., McWilliam S., Mader M., Madera M., Marchionni L.,

RA Matsuda H., Matsuzawa S., Miki H., Mignone P., Miyake S., Morris K.,

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RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,

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RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
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RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusis V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kall C., Sasaki D., Tomaru Y.,
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RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
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RA Hayashizaki Y.;
RA "The transcriptional landscape of the mammalian genome.";
RA Science 309:1559-1563(2005).
RA [3]
RN NUCLEOTIDE SEQUENCE
RP STRAIN=C57BL/6J; TISSUE=Liver;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RN NUCLEOTIDE SEQUENCE
RP STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=23254683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saïto R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
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RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
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RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RA "Analysis of the mouse transcriptome based on functional annotation of
RA 60,770 full-length cDNAs.";
RA Nature 420:563-573(2002).
RA [5]
RN NUCLEOTIDE SEQUENCE
RP STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RA Nature 409:685-690(2001).
RA [6]
RN NUCLEOTIDE SEQUENCE
RP STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RA "Normalization and subtraction of cap-trapper-selected cDNAs to
RA prepare full-length cDNA libraries for rapid discovery of new genes.";
RA Genome Res. 10:1617-1630(2000).
RA [7]
RN NUCLEOTIDE SEQUENCE
RP STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20530913; PubMed=11076961; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RA sequencing pipeline with 384 multicapillary sequencer.";
RA Genome Res. 10:1757-1771(2000).
RA [8]
RN NUCLEOTIDE SEQUENCE
RP STRAIN=C57BL/6J; TISSUE=Liver;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AK149368; BAE28838.1; -; mRNA.
CC MGI: MGI:1921743; Tnkg2.
CC GO: GO:0005634; C:nucleus; IEA.
CC GO: GO:0003950; P:NAD+ ADP-ribosyltransferase activity; IEA.
CC GO: GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
CC InterPro: IPR002110; ANK.
CC InterPro: IPR012317; P:PARP_catalytic.
CC InterPro: IPR01660; SAM_2.
CC InterPro: IPR011510; SAM_2.
CC Pfam: PF00023; Ank; 5.
CC Pfam: PF00644; PARP; 1.
CC Pfam: PF07647; SAM_2; 1.
CC PRINTS: PR01415; ANKYRIN.
CC SMART: SM00248; ANK; 4.
CC SMART: SM00454; SAM; 1.
CC PROSITE: PSS0297; ANK_REPEAT; 1.
CC PROSITE: PSS0088; ANK_REPEAT; 4.
CC PROSITE: PSS1059; PARP_CATALYTIC; 1.
CC PROSITE: PSS0105; SAM_DOMAIN; 1.
CC KW ANK repeat.
CC FT NON_TER 1 1
CC SQ SS_SEQUENCE 589 AA; 64051 MW; AF630275E3C75124 CRC64;
CC Query Match 50.7%; Score 2833; DB 2; Length 589;
CC Best Local Similarity 96.8%; Pred. No. 4e-159;
CC Matches 536; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy	512	LVKHGAVNVADLWKFTPLHEAAAKGKYEICKLLQHGADPTKKORDGNTPLDLVKDGT	571
Db	1	LVKHGAVNVADLWKFTPLHEAAAKGKYEICKLLQHGADPTKKORDGNTPLDLVKDGT	60
Qy	572	DIQDLRGDAALLDAAKGLARVKLSPPDNVNCRDTCGRHSTPLHLAAGYNNLEVAEY	631
Db	61	DIQDLRGDAALLDAAKGLARVKLSPPDNVNCRDTCGRHSTPLHLAAGYNNLEVAEY	120
Qy	632	LLQHGADVNAODKGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAOKGR	691
Db	121	LLQHGADVNAODKGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTPLHEAAOKGR	180
Qy	692	TOLCALLAHGADPTLKNQEGQTPLDLVSADVSALLTAAMPSPALPCYKQVNLGVRS	751
Db	181	TOLCALLAHGADPTLKNQEGQTPLDLVSADVSALLTAAMPSPALPCYKQVNLGVRS	240
Qy	752	PGATADALSSGPPSSSLSAASSLNLGSPSELSSVSSSGTEGASLEKEVPCVDPS	811
Db	241	PGATADALSSGPPSSSLSAASSLNLGSPSELSSVSSSGTEGASLEKEVPCVDPS	300
Qy	812	ITQFVRNLGLEHLMDFEREQITLQVEMGHKELKEIGINAYGHRHKLKIGVERLISGQ	871
Db	301	ITQFVRNLGLEHLMDFEREQITLQVEMGHKELKEIGINAYGHRHKLKIGVERLISGQ	360
Qy	872	QGLNPYLTLNTSGSCTILIDLSPDDKBFQSVEEEMQSTVREHRDGHAGGIFNRYNILKI	931
Db	361	QGLNPYLTLNTSGSCTILIDLSPDDKBFQSVEEEMQSTVREHRDGHAGGIFNRYNILKI	420
Qy	932	QKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFVNAILHKGFDERHAYIGGMFGA	991
Db	421	QKVCNKKLWERYTHRRKEVSEENHNHANERMLFHGSPFVNAILHKGFDERHAYIGGMFGA	480
Qy	992	GIYFAENSSKSNQYVYIGGGTGCPCVHKDRSCYICHRQLLCRVTLGKSFQFSAMKWAH	1051
Db	481	GIYFAENSSKSNQYVYIGGGTGCPCVHKDRSCYICHRQLLCRVTLGKSFQFSAMKWAH	540
Qy	1052	SPPGHHSVTGRPSV	1065
Db	541	SPPGHHSVTGRPSV	554

Search completed: December 18, 2006, 17:34:40
Job time : 217 secs

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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:55:21 ; Search time 34.6529 Seconds
(without alignments)
2975.278 Million cell updates/sec

Title: US-10-616-101-3

Perfect score: 5585

Sequence: 1 GFGKDVVYLLQNGASVQA.....AMKMAHSPGHHVSGRPSV 1065

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 381649 seqs, 96809478 residues

Total number of hits satisfying chosen parameters: 381649

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

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- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
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- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	860.5	15.4	1330	7	US-11-293-697-3237
2	842	15.1	1880	7	US-11-050-875-628
3	842	15.1	1881	7	US-11-050-875-629
4	678	12.1	919	7	US-11-293-697-4122
5	527	9.4	743	7	US-11-371-354-56501
6	483.5	8.7	685	6	US-10-533-519-1308
7	465	8.3	765	7	US-11-317-329-3
8	465	8.3	765	7	US-11-317-329-34
9	465	8.3	765	7	US-11-317-329-35
10	465	8.3	765	7	US-11-317-329-36
11	465	8.3	765	7	US-11-317-329-37
12	465	8.3	765	7	US-11-317-329-38
13	465	8.3	765	7	US-11-317-329-39
14	465	8.3	765	7	US-11-317-329-40
15	465	8.3	765	7	US-11-317-329-41
16	465	8.3	765	7	US-11-317-329-42
17	465	8.3	765	7	US-11-317-329-43
18	465	8.3	765	7	US-11-317-329-44
19	465	8.2	765	7	US-11-375-615-56
20	451	8.1	1061	7	US-11-397-222-4
21	420	7.5	616	7	US-11-371-354-59433
22	408.5	7.3	435	7	US-11-371-354-13702
23	408.5	7.3	435	7	US-11-371-354-78380
24	394	7.1	1050	7	US-11-371-354-65355
25	391	7.0	784	7	US-11-317-329-12

26	391	7.0	832	7	US-11-320-072-96	Sequence 96, Appl
27	390.5	7.0	786	7	US-11-317-329-13	Sequence 13, Appl
28	390.5	7.0	786	7	US-11-317-329-31	Sequence 31, Appl
29	390.5	7.0	786	7	US-11-317-329-32	Sequence 32, Appl
30	390.5	7.0	786	7	US-11-317-329-33	Sequence 33, Appl
31	382	6.8	1762	6	US-10-502-394-94	Sequence 94, Appl
32	380.5	6.8	1715	6	US-10-502-394-93	Sequence 93, Appl
33	379.5	6.8	1719	7	US-11-344-932-378	Sequence 378, App
34	371.5	6.7	347	7	US-11-317-329-30	Sequence 30, Appl
35	365	6.5	1184	6	US-10-502-394-90	Sequence 90, Appl
36	365	6.5	1771	6	US-10-502-394-91	Sequence 91, Appl
37	365	6.5	1777	6	US-10-570-909-17	Sequence 107, Appl
38	365	6.5	1777	6	US-10-570-909-107	Sequence 107, App
39	363.5	6.5	1715	6	US-10-502-394-89	Sequence 89, Appl
40	363.5	6.5	1753	6	US-10-504-973-30	Sequence 30, Appl
41	350	6.3	587	7	US-11-371-354-61877	Sequence 61877, A
42	341	6.1	727	6	US-10-449-902-54192	Sequence 54192, A
43	337	6.0	2278	6	US-10-374-780A-1842	Sequence 1842, Ap
44	332.5	6.0	835	7	US-11-377-316-202	Sequence 202, App
45	326.5	5.8	456	7	US-11-056-355B-39159	Sequence 39159, A

ALIGNMENTS

RESULT 1

US-11-293-697-3237
; Sequence 3237, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cdNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3237
; LENGTH: 1330
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-293-697-3237

Query Match	15.4%	Score	860.5	DB	7	Length	1330
Best Local Similarity	29.8%	Pred. No.	1.2e-46				
Matches	283	Conservative	127	Mismatches	386	Indels	153
Gaps	21						
Qy	3	GRKDVVYLLQNGASVQARDGGGLPLHNACSGHAEVWVWVLLRHGADPNARDNNWYTPL	62				
Db	54	GHVGLVQELLGRGSSVDSATKGNLTALHSLAQAEVVKVKEGANINAQSQNGFTPL	113				
Qy	63	HEAAIKGIDVICVILLOHGAETPTINTDGR-----ALDLADPSAKAVLTGYKDEL---	115				
Db	114	YMAQENHIDVVKYLLLENGANQSTATEDGFTPLAVALQOQHQAVALLENDTKGVRLP	173				
Qy	116	LESARGNEKEMALLTPLNVNCHASDGRKS-----TPHLAAGNVRKIVQL	163				
Db	174	ALHTAARKDPTKSAALLQ-----NDHNADVQSKMNVNRTTESGFTPLHAAHYGNVATL	230				
Qy	164	LLOHGADVHAKDKGLVPLHNACSGHYEVTELLVKEGACVNMADLWQFTPLHEASKNR	223				
Db	231	LLNKGAAVDFTRANGITPLHVASKRGVNNVWVLLDRGGQIDAKTRDGLTPLHCAARGH	290				
Qy	224	VEVCSLLSYGADPTLLNCHNKSADLAPTQLKERLAYEFKHSLLQAAREADVTRIKK	283				
Db	291	DQVVELLIERGA-PLLARTKN-----GLSPLHMAAQGDHVECVK	328				
Qy	284	HLSEUMNFKHP-----QTHETALHCAASPYPKRQICELLRLKGANINEKTEFLTPL	338				
Db	329	HL-----LQHKAPVDVDTLVLTALHVA-----HCGHYRVTKLLDKRANPNARALNGFTPL	381				

339	QY	HVASEKAHNDVVEVVKHEAKVNALDNLGOTSLHRAAYCGHLOTCRLLLSYGCDDPNIIISL	399
382	DB	HIACKNRIRKVMELLVKYGASIQAITESGLTPIHVAAFMGHLNVLLLLQNGASPDVTNI	441
399	QY	QGFALOMGN-----ENVQQLLQEGI-----SIGNSEADROLLE-----	432
442	DB	RGETALHMAARAGQVEVVRCLLRNGALVDARAREEQTPLHTIASLKGKTEIVQLLQHMWH	501
433	QY	-----AAKAGDVETVKKLTQVSNCRDIEGRQSTPLHFAAGVNRVSVVEY	478
502	DB	PDAATNRYTPLHISAREGOVDVASVLELGAAGHSLATK-KGFTPLHVAAKYGSLDVAKL	560
479	QY	LLQHGADVHAKDKGGLVPLHNACSYGHEVVAELVKGAVNVNADLMKFTPLHEAAAKGK	538
561	DB	LLQRRAAADSAGKNGLTPLHVAHYDNQKVALLLLEKASPHATAKNGYTPLHIAAKKNQ	620
539	QY	YETCKLLQHGADPTKKNRGDNTPLDLV-KDGDITDIQDLLRGDAALLDAAKKGCLARVKK	597
621	DB	MQIASTLLNYGAETNIYTKQGVTPHLASQBSGHTDMVTLLDKGANIHMSTKSGL-----	675
598	QY	LSSPDNVNCRTQGRHSTPLHLAAGYNLEVAEVLQHGADVNAQDKGLIPLHNAASVG	657
676	DB	-----TSLHLLAQEDKVNVDILITKHGAQODDHTKLGUYTPLIVACHYG	718
658	QY	HVDVAALLIKYNACVNATDKWAFPLHEAAQKGRITQLCALLLAHGADPTLKNQEGOTPLD	717
719	DB	NVRKVNFLKQGANVNAKTNGYTPLHQAQOQGHTHIINVLLQHGAKPNATTANGNTALA	778
718	QY	L-----VSADDVSALITAAAPPSPALPSCYKQPVUNGVRSPGATADALSSGSPSSLSA	771
779	DB	IAKRLGIVSVVDTLKVVTEEVTTTTTITEK-----HKLNVPETMTVEVL-----DVSD	826
772	QY	ASSLDNLGSFSEL-----SSVSSSGTEGASSLEKKEVPGVDFTSQFV--RN	818
827	DB	EEGDNTWTDGGEYLRPEDLKBGDLSLPFSQFLDGMNLYRYSLEGGRSDSURSFSSRS	886
819	QY	LGLEHLMDIPIREQITLDVLVEMGHKELKEIGINAYGHRHKLIKQVERL	867
887	DB	HTLSHAS--YLRDSAVMDDSVVIPSQVSTLAKAERNYSRLSWGTENL	933
RESULT 2			
US-11-050-875-628			
; Sequence 628, Application US/11050875			
; Publication No. US20060263786A1			
; GENERAL INFORMATION:			
; APPLICANT: Comugen Ltd			
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS A			
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF COLON CANCER			
; FILE REFERENCE: 1947.1001			
; CURRENT APPLICATION NUMBER: US/11/050,875			
; CURRENT FILING DATE: 2005-01-27			
; NUMBER OF SEQ ID NOS: 1583			
; SEQ ID NO 628			
; LENGTH: 1880			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-11-050-875-628			
Query Match			
Best Local Similarity 15.1%; Score 842; DB 7; Length 1880;			
Matches 279; Conservative 152; Mismatches 356; Indels 306; Gaps 27			
3	QY	GRKDVVEYLLQNGASVQARDGGLIPLHNACSFGEHAEVNVLLRHGADPNARDNWNYPYL	62
88	DB	QDVEVRLVNYGANVNAQSQKGFPLYMAAQENHLEVVKFLLIENGANQVATEDGFTPL	147
63	QY	HEAAIKGIDYCVILLOHGAETPI-----RNTDGRALTDLADPSAKAVLTGEYKD	113
148	DB	AVALQOQGHENVVAHLINVTGKVRPLPALHIAARNDDTRTA-----AVLLQNDPNP	198
114	QY	ELLESARGNBEKMMALLTPLNVNCHASDGRKS-----TPHLHAAGY	155

199	DVL--SKTG-----	-FTPLHIAAHYENLVNAQALLNARGASVNFPTQNGITITPLHIASRR	248	
156	NRVKIYVOLLQHGADVHADKGDVLPLHNACSYGHYEVTELLVKGACVNMADLWQFPL	215		
249	GNVIVRLLLDRGAIETKTQDELTPLHCAARNGHVRITSEILLDHGAPIQAKTNGLSPI	308		
216	HEAASKNRVENCSSILLSYGADPTLLNCHNKSAIDLAPTQPKERLAYEFKGHSLQAARE	275		
309	HMAAQGDHLDCVRLLLQVDAE-----ID-----	331		
276	ADVTRIKGHLSLEWNFVXHPQTHETALHCAASPYPKRKQICELLRLRGANINEKTEPL	335		
332	-DIT-----	LDHLTPLVAA---HCGHHRVAKVLLDKGAKPNSRALNGF	371	
336	TPLHVASEKAHNDVVEVVKHBAKNALDNLGOTSLHRAAYCGHLOCTCELLLSYGDPMI	395		
372	TPLHIACKGNHVRVMEILLKTGASDAVTESGLTPLHVASFMGHFLPVKNLLQRGASPNV	431		
396	ISLQFTALOMG-----NENVQOOLQE-----	GISLGNSEADROLLE-	432	
432	SNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKAKDDOTPLHCAARIQHTNMVKLLLEN	491		
433	-----	AAKAGDVETVKKLCITVQ--SVNCRDIEGRQSTPELHPAAGYNNRVS	474	
492	NANPNLATTAGHTPLHIAAREGHVEITVALLLEKEASQACMTKKG--	FTPLHVAAKYGVKR	549	
475	VVEYLLQHGADVHADKGDGVLPLHNACSYGHYEVTELLVKGACVNVADLWK--	FTPLHHEA	533	
550	VAELLERDAHFAAGKNGLTPLHVAVHHNNDIVKLLLPGRGSPH--	SPAWNRYTEPLHIA	608	
534	AAKGKYEICKLLOHGADPTKKNRQDNTPLDI--VKDGDTDIODLLRGDAALLDAAKKGCL	592		
609	AKONQVEVARSLLQYGGSANASSVQGVTPHLHAAQEGHAEWALL-----	653		
593	ARVKLSSPDNVNCRDQTGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHN	652		
654	-----	LKQANGNLGNKSG--LTPLHLVAQEGHVPVADVLKHGVMDATTRMGYTPLHV	706	
653	AASYGHVDVAAALIKYNACVNAWDKAWFTPLHHEAAQKGTQLCALLANGADPTLKNQEG	712		
707	ASHYGNIKLVKFLLQHQADVNAKTKLGYSPHQAAQOQGHTDIVTLLLLKNGASPNVSSDG	766		
713	QTPLDL-----	VSADDDYALLTAMPSPALPSC-----	740	
767	TTPLATAKRLGYSVTEVVLKVTDFTSFVLVSDKHRMSFPEVDEILDVSEDEGEELISF	826		
741	-----	YKPOVLNGVRSPGATADALSQSPSPSSL-----	AASLDN	777
827	KAERDRSDVBEKELLDFVKLDQVVESPA-----	PRIPCAMPETVIVRSEBEQ	878	
778	LSGSFBEELSSVWSSGTEGASSLEKKEVPGVDFSIITQFVRNLGLEHLMIDIFEREQITLDV	837		
879	ASKEYDEDSLIPSPATETSDNISPVASPVHTGFLVSFM-----	917		
838	LVEMGHKELKEIGINAYGHRHKLKGYE-----	RLISGOQGLNPYLTLMTSG	884	
918	-----	VDARGSGRSGRHNGLRVVIIPRTCAAPTRICRLVKQKULSTPPPLAEEEG	969	
885	SGTILIDLSP-----	DDKEFQSVEEENQOSTVREHRDGHAGGIF	923	
970	LASRIIALGFTGAQFLSPVIVEIPHFAHGGRGRELVLVLRSENGSVWKEHR-----	1020		
924	NRYNLIKQKVCN	936		
1021	SRYGESYLDQILN	1033		

RESULT 3
US-11-050-875-629
; Sequence 629, Application US/11050875
; Publication No. US20060263786A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd

;
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;

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; FILE REFERENCE: 1847.1001
; CURRENT APPLICATION NUMBER: US/11/050.875
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1583
; SEQ ID NO 629
; LENGTH: 1881
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-050-875-629

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Query Match	Score 842;	DB 7;	Length 1981;
Best Local Similarity	25.5%;	Pred. No. 3.3e-45;	
Matches 279;	Conservative	152;	Mismatches 356;
			Indels 306;
			Gaps 27;

Qy	3	GRKDVVYLLQNGASVOARDGGGLPLHNACSFGEAEVVVULLRHGADPNARDWNWYTPL	62
Db	89	GODEVRELNYGANNVAQSQGTPLYMAAQENHLEVVVFKLENGANQNVATEDGFTPL	148
Qy	63	HEAAIKGIDVICVILLOHGAEPTI-----RNTDQRTALDLPASKAVLTGEYKDD	113
Db	149	AVALOQGHENVVAHLINYTGKVRPLPALHIAARNDTRTA-----AVLQNDENP	199
Qy	114	ELLESARGNEEKMMALLTPLNVNCHASDGRKS-----TPLHLAAGY	155
Db	200	DVL--SKTG-----FTPLHIAAHYENLNVQALLNRGASVNFPTPONGITPLHIAARR	249
Qy	156	NRVKIVOLLQHGADVHAKOGDVLVPLHNACSYGHYEVTELLVKGACVNAWMLWQFTPL	215
Db	250	GNVIMVRELLDRGQAQIETTKQDELTPLHCAARNGHVRISETLLDHGAPQIAKTRNGLSPI	309
Qy	216	HEAASKNRVECSLLLSYGADPTLLNCHNKSAILDAPTPQLKERLAYEFKGHSLLQAARE	275
Db	310	HMAAQGDHLCVRLQLQYDAE-----ID-----	332
Qy	276	ADVTRIKGHLSELMVNFKHPOTHETALHCAAASPYPKKQICEILLRKGANINEKTEFL	335
Db	333	-DIT-----LDHLLTPLHVAA---HCGHRRYAKVLLDKGAKPNRSALNGF	372
Qy	336	TPLHVASEKAHNDVVEVVKHEAKVNALDNIGOTSLHRAACVGHLOTCELLLSYGCDDNI	395
Db	373	TPLHIACKKNHVRWELLTKTGASIDAVTESGLTPLHAVSPWGHLPVKNLLQRGASENV	432
Qy	396	ISLQGFALQMG-----NENVQQLQE-----GISGNSEADQRLLE-	432
Db	433	SNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKAKADQDTPHCAARTGHTNMVKLLLEN	492
Qy	433	-----AAKAGDVETVKKLCCTVQ--SYNCRDIEGRQSTPLHFAAGYNRVS	474
Db	493	NAMPNLATTAGHTPLHIAAREGHVETVLAALLEKASQACMTKKG--FTPLHVAAKYIGVR	550
Qy	475	VVEYLLQHGADVHAKDGGVLVPLHNACSYGHYEAEVLVKGAVVNVADLWK--FTPLHEA	533
Db	551	VAELLERDAHAPNAAGKNGLTPLHAVVHHNLDIVKLLPRGSGPH--SPAMNGYTPLHIA	609
Qy	534	AAKGKYEIKLLOLQHGADPTKKNRDGNTPLDL-VKDGDTDIQDLRGDAALLDRAKGCCL	592
Db	610	AKQONQVARSLLLYGGSANAESVQGVTPPLHAAQEGHAENVALL-----	654
Qy	593	ARVKKLSSPDNVNCRDTQGRHSTPLHIAAGVNNLEVAEYLLQHGADVNAQDKGLIPLHN	652
Db	655	-----LSKQANGNLGNKSG--LTPHLVVAQEGHPVADVLIKHGVWVDATTRMGYTPLHV	707
Qy	653	AASYGHVDVVAALLIKYNA CVNATDKWAFTPLHEAAQKGRTOQLCALLLAHGADPTLKNQEG	712
Db	708	ASHYGNIKLVKFLLOHQADVNAKTKLGYSPHLHQAAQOQHTDITVTLLLKNGASPNVESSDG	767
Qy	713	QTPLDL-----VSADDVSALLTAAMPSPALPSC-----	740
Db	768	TTPLAIAKRILGYISVTDVLKVVTDTETGFVLVSKHRMVSFFETVDEILDVSBDEGELISF	827
Qy	741	-----YKPOVLNGVRSPCATADALSSGSPSSPSLS--AASSLDN	777

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828 KAERDRSDVDEKELLDVFVKLDQVVESPA I-----PRIPCAMPTVWIRSEEQ 879
778 LSGSFSELVSVSSSGTEGASSLEKKEVPGVDFSIITQFVRNLGLEHLMDFIREQITLDV 837
880 ASKEYEDSLIPSPATESTDNISPVASPVHTGFLVFM----- 918
838 LVEMGHKELKEIGINAYGHRHKLKIGVE-----RLISGOQGLNPYLTLTNSG 884
919 -----VDARGSGMRGSRHNLGRVIPPRTCAAPTRITCRVLVKPKLSTPPPLAEEG 970
885 SGTILIDLSP-----DKEFQSVSEEMQSTVREHRDGHAGGIF 923
971 LASRIIALGPTGAQFLSPVIVEIPHFASHGRGDELVLRLSENGSVWKEHR----- 1021
924 NRYNILKIQVCN 936
1022 SRYGESYLDQILN 1034

RESULT 4
US-11-293-697-4122
; Sequence 4122, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4122
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-293-697-4122

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Query Match	12.1%;	Score 678;	DB 7;	Length 919;
Best Local Similarity	28.5%;	Pred. No. 3.7e-35;		
Matches	235;	Conservative 109;	Mismatches 304;	Indels 178; Gaps 24;
QY	11	LLQNGASVQARDGG	LIPLHNACSF	GHAENVNLLLRHGADPNARDNNWYTPLHEAAIKGK 70
DB	2	LIHKEDVNTLSEK	ETPLHVAFLGDAE	IEILLSGARVNAKDNWMLTPLHRAVASRS 61
QY	71	IDVCI VILQHGABPT	RTNTDGR	TALDLPASAKAVITGEYKDBELLESARSGNEEKOMAL 130
DB	62	EEAVQVLLIKHSAD	VNARDKNWQ	TPLHVA-AANKAV-----KCAEV 100
QY	131	LTPLNVNCHASGR	KETPLHLAAGY	NKVIQVLLLOHGADVDAKDGIVPLHNCASYGH 190
DB	101	IIPLSSVNVSDRG	RTALHHAALNG	HVEVMVLLLAGANINAFDKDRRALHWAAYMGH 160
QY	191	YEVTELLVKHGAC	NAMDLMQFTPL	HEAASKNRVVCVCSLLLSYGDPTLNCNHNKSAIDL 250
DB	161	LDVVALLINHGA	EVCTCKDKGYT	PLHAASNGQINVVKHLLINLGVETDEINVYGNLTALHI 220
QY	251	APTPTQKERLAYE	FKGHSLLQAARE	ADVTRI KKHLSLEWMVNFKHQTHE--TALHCAAASP 309
DB	221	A-----CYN-----	QGDVVN	ELIDY-----GANVNPQNNNGTTPHLFAAAS 258
QY	310	YPKRKQIC-ELL	LRKGANINEK	TKEFTPLPHVAASEKAHNDVVEVVKHEAKVNALDNLGQ 368
DB	259	H--GALCIELLV	NNGADVNIQSK	DGKSPHLMTAVHGRFTRSQTLIQNGEIDCVDKDN 315
QY	369	TSIHRAYCCHLT	CRILLSYGCD	PNIIISLGFTALOMGNENVQQLLOEGISLGNSEADR 428
DB	316	TPLHVAARYGHE	LLINTLSGAD	TACKGTHSFWPPLHAAIN-----AHSDCR 364
QY	429	QLLEAAKAGADV	ETVKKLCTVQ	SNCNRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHA 488


```

; TYPE: PRT
; ORGANISM: Homo sapien
US-10-533-519-1308

Query Match      8.7%; Score 483.5; DB 6; Length 685;
Best Local Similarity 25.4%; Pred. No. 7.1e-23;
Matches 196; Conservative 93; Mismatches 259; Indels 225; Gaps 22;

QY 3 GRKDVVYLQNGASVQARDGGLIPLHNACSGHAEVNVNLLRHGADPNARDNNYTP 62
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 7 GHLELVKYLASGANVHATTATGDTALTACBNGHTDADVLLQAGADLDKQE----- 59
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 HAAIKGIDVICVILQHGAEPTIRNTDGTALDLPSSAKAVLTGKYKDELLESARSG 122
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 -----DMKTILEGIDPA-----KHQE----- 75
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 NEEKWALLTPLNVNCHASDRKSTPLHLAAGYNRKIVQLLQHGADVH-AKOKGDLVP 181
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 76 -----HSEGGGR-TPLMKAARAGHLCTVQFLISKGANVNVRATANNHTV 118
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 LHNACSYGHYEVTELLVKGACVNAWDLWQFTPLH-----EAASKNRVEVCSSL 231
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 VSLACAGGLHVAVELLALHGA-----DPTRLKDGSTMLTEAAKGHTNVVSYLL 168
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 SYGADPTLLNCHNKSAIDLAPT-----QLKERLAYEFKSHSLLOAAREADVTRIK--KH 284
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 169 DY---PNNVLSVPTTDVQLPPPSODQSEPDRTSQE---NSPALLGVOKAVSTRVPTGSN 223
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 285 LSEMVNFKHPQT-----HETALHCAASPYPKRKQ 315
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 224 SSSQTECLTPBSCSQTTSNVASQSMPPVYPSVDVDAHTESNHDALTALACAGGH---EE 280
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 316 ICELLLRKGANINEKTEFLPLHVASEKANDNVVVVVKHAKYNA-LDNLGQTSLHRA 374
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 281 LVSVLIAARDAKIEHRDKGFTPLILAATAGHVGVEIILLDKGDIQAQSERKDTPLSLA 340
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 375 AVCGHLOTCLLLSYGCDPNIIISLOGFTALQW-----GNENVQOLL-----QEGISL 421
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 341 CSGGQEVVDLLLAGANKEHNRVSDYTPLSLAASGGYVNIKIILLNAGAEINSTGSKL 400
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 422 GNSEADROLLEAAKAGDVETVKKLTQVSNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQ 481
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 401 GIS-----PLMLAAMNGHVPVAVKLLDMGSDINAQIETNRNTALTALACFGRAEVVSLLD 456
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 482 HGADVHAKDKGLVPLHNACSYGHYEVAELLVKHGAVNVNADL---WKFTPLHAAAKGY 539
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 457 RKANVEHRAKTGLTPLMEEAASGGYAEVGRVLLDKGADVNAPEVPSRDTALTIAADKGYH 516
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 540 EICKLLLOHGADPTKKNRDGNTPLDVKDGDITDIDLLRGDAALLDAAKGCCLARVKKLS 599
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 517 KPCELLIHRGAHIDVRNKKGNTPMLASNG----- 546
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 600 SPDVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHV 659
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 547 -----GHEDVQLLVQAGADVDAADNRKITPLMSAFRKGHV 582
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 660 DVAALLIK-----YNACVNATDKWAFPLHAAQ---KGRTOICA 696
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 583 KVVQYLVKEVNPSPDIECMRYIATI--TDKELLKKCHQCQVETIVKAKDQQA 633
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-11-317-329-3
; Sequence 3, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 34
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-34

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

QY 245 KSAIDLAP-----TPOLKERLAYEFKSHSLLOAAREADVTRIKHLSLEMVNFKHPQTHET 300
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 KRALQLSDRKNLVPRDEELCIYENKVTPLQPLVAQGSVEQVRLLLA-----HEV 386
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 301 ALHCAASPYPKRKQICELLLRKGANINEKTEFLPLHVASEKANDNVVVVVKHAKV 360
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 387 DVDCTASGY-----TPLLIAAQDQPPDLCAALLAHGADA 421
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 361 NALDNLGQTSLHRAAYCCHLOTCELLLSYGCDPNIIISLOGFTALQMGNNVQOLLQEGIS 420
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 422 NRVEDGWAFLHFAAQNGDDRTARLLLDHGCACVDAQREBGTPLHLAAQN----- 471
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 421 LGNSEADROLLEAAKAGDVETVKKLTQVSNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 472 --NFENVARLLVSQA-----DPLREAEKG--TPLHVAAYFGHVSIVKLLT 514
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 481 QHGADVHAKDKGLVPLHNACSYGHYEVAELLVKHGAVNVNADLWKFTPLHAAAKGYE 540
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 515 SOGAELDAQORNLRTPLHLAVERGKVRAIQHLKSGAVPDALDQSGYGPLHTAAARGKYL 574
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 541 ICKLLLOHGADPTKKNRDGNTPLDVKDGDITDIDLLRGDAALLDAAKGCCLARVKKLS 600
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 575 ICKMLRYGASLELPTHQGTPLHL-----AAYKGHLE-ETIHLA 613
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 601 PDVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 614 ESHANMGALGAVNWTPLHLAARHGEEAVVSALQCGADPNAAEQSGWTPLHLAVQSTFL 673
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 661 VAALLIKYNACVNATDKWAFPLHAAQKGRTOICALLAHGADPTLKNQEGOTPLDL 718
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 674 SVINLEHHANVHARNKVGWTPAHLAALKGNITAILKVLVEAGAQLDVQDGVSCPTQL 731
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-11-317-329-34
; Sequence 34, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 34
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-34

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

QY 245 KSAIDLAP-----TPOLKERLAYEFKSHSLLOAAREADVTRIKHLSLEMVNFKHPQTHET 300
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

; TYPE: PRT
; ORGANISM: Homo sapien
US-10-533-519-1308

Query Match      8.7%; Score 483.5; DB 6; Length 685;
Best Local Similarity 25.4%; Pred. No. 7.1e-23;
Matches 196; Conservative 93; Mismatches 259; Indels 225; Gaps 22;

QY 3 GRKDVVYLQNGASVQARDGGLIPLHNACSGHAEVNVNLLRHGADPNARDNNYTP 62
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 7 GHLELVKYLASGANVHATTATGDTALTACBNGHTDADVLLQAGADLDKQE----- 59
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 HAAIKGIDVICVILQHGAEPTIRNTDGTALDLPSSAKAVLTGKYKDELLESARSG 122
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 -----DMKTILEGIDPA-----KHQE----- 75
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 NEEKWALLTPLNVNCHASDRKSTPLHLAAGYNRKIVQLLQHGADVH-AKOKGDLVP 181
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 76 -----HSEGGGR-TPLMKAARAGHLCTVQFLISKGANVNVRATANNHTV 118
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 LHNACSYGHYEVTELLVKGACVNAWDLWQFTPLH-----EAASKNRVEVCSSL 231
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 VSLACAGGLHVAVELLALHGA-----DPTRLKDGSTMLTEAAKGHTNVVSYLL 168
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 SYGADPTLLNCHNKSAIDLAPT-----QLKERLAYEFKSHSLLOAAREADVTRIK--KH 284
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 169 DY---PNNVLSVPTTDVQLPPPSODQSEPDRTSQE---NSPALLGVOKAVSTRVPTGSN 223
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 285 LSEMVNFKHPQT-----HETALHCAASPYPKRKQ 315
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 224 SSSQTECLTPBSCSQTTSNVASQSMPPVYPSVDVDAHTESNHDALTALACAGGH---EE 280
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 316 ICELLLRKGANINEKTEFLPLHVASEKANDNVVVVVKHAKYNA-LDNLGQTSLHRA 374
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 281 LVSVLIAARDAKIEHRDKGFTPLILAATAGHVGVEIILLDKGDIQAQSERKDTPLSLA 340
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 375 AVCGHLOTCLLLSYGCDPNIIISLOGFTALQW-----GNENVQOLL-----QEGISL 421
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 341 CSGGQEVVDLLLAGANKEHNRVSDYTPLSLAASGGYVNIKIILLNAGAEINSTGSKL 400
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 422 GNSEADROLLEAAKAGDVETVKKLTQVSNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQ 481
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 401 GIS-----PLMLAAMNGHVPVAVKLLDMGSDINAQIETNRNTALTALACFGRAEVVSLLD 456
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 482 HGADVHAKDKGLVPLHNACSYGHYEVAELLVKHGAVNVNADL---WKFTPLHAAAKGY 539
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 457 RKANVEHRAKTGLTPLMEEAASGGYAEVGRVLLDKGADVNAPEVPSRDTALTIAADKGYH 516
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 540 EICKLLLOHGADPTKKNRDGNTPLDVKDGDITDIDLLRGDAALLDAAKGCCLARVKKLS 599
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 517 KPCELLIHRGAHIDVRNKKGNTPMLASNG----- 546
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 600 SPDVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHV 659
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 547 -----GHEDVQLLVQAGADVDAADNRKITPLMSAFRKGHV 582
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 660 DVAALLIK-----YNACVNATDKWAFPLHAAQ---KGRTOICA 696
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 583 KVVQYLVKEVNPSPDIECMRYIATI--TDKELLKKCHQCQVETIVKAKDQQA 633
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-11-317-329-3
; Sequence 3, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174

```

Db 338 KRALQSDRKNLVPRDEELCIYENKVTPLQFLVAQSGVEQVRLLLA-----HEV 386
Qy 301 ALHCAAAAPYKPKRQICELLRLKRGANINEKTEFPLPLHVAEKAHNDVVEVVVKEAKV 360
Db 387 DVDCCQTASGY-----TPLLIAAQDQPDLCALLAHGADA 421
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISLOGFTALONGNENVOQLQEGIS 420
Db 422 NRVDGDMAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 421 LGNSADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNVSVVEYLL 480
Db 472 --NFENVARLLVSRQA-----DPNLRABEGK--TPLHVAAYFGHVSIVKLIT 514
Qy 481 OHGADVHAQDKGGLVPLHNACSYGHYEVAELLVKGGAVNVADLWKFTPLHEAAAKGKYE 540
Db 515 SOGAELDAQORNLRTPLHLAVERGKVAIQHLKSGAVPDALDQSGYGPLHTAAARGKYL 574
Qy 541 ICKLLLOHGADPTKKNRDGNTPLDLVKDGDTDIQLLRGDAALLDAKKGCLARVKKLSS 600
Db 575 ICKMLLRYGASLELPTHQGWTPHL-----AAYKGHL-EIHLHA 613
Qy 601 PDVNCRDITQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGANVWTPHLAARHGEAVVSALLQCGADPNAAEQSGWTPHLAVQORSTFL 673
Qy 661 VAALLIKYNACVNATDKWAFPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDL 718
Db 731 SVINLEHHANVHARNKVGWTPAHLAALKGNTAILKVLVEAGAQLDVQDGVSCSTPLQL 731

RESULT 9
US-11-317-329-35
; Sequence 35, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-35

Query Match 8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 245 KSAIDLAP-----TPQKERLAYEFKGHSLLQAAREADVTRIKKHSLEMVNFKHPQTHET 300
Db 338 KRALQSDRKNLVPRDEELCIYENKVTPLQFLVAQSGVEQVRLLLA-----HEV 386
Qy 301 ALHCAAAAPYKPKRQICELLRLKRGANINEKTEFPLPLHVAEKAHNDVVEVVVKEAKV 360
Db 387 DVDCCQTASGY-----TPLLIAAQDQPDLCALLAHGADA 421
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISLOGFTALONGNENVOQLQEGIS 420
Db 422 NRVDGDMAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 421 LGNSADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNVSVVEYLL 480
Db 472 --NFENVARLLVSRQA-----DPNLRABEGK--TPLHVAAYFGHVSIVKLIT 514
Qy 481 OHGADVHAQDKGGLVPLHNACSYGHYEVAELLVKGGAVNVADLWKFTPLHEAAAKGKYE 540
Db 515 SOGAELDAQORNLRTPLHLAVERGKVAIQHLKSGAVPDALDQSGYGPLHTAAARGKYL 574
Qy 541 ICKLLLOHGADPTKKNRDGNTPLDLVKDGDTDIQLLRGDAALLDAKKGCLARVKKLSS 600
Db 575 ICKMLLRYGASLELPTHQGWTPHL-----AAYKGHL-EIHLHA 613
Qy 601 PDVNCRDITQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGANVWTPHLAARHGEAVVSALLQCGADPNAAEQSGWTPHLAVQORSTFL 673
Qy 661 VAALLIKYNACVNATDKWAFPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDL 718
Db 731 SVINLEHHANVHARNKVGWTPAHLAALKGNTAILKVLVEAGAQLDVQDGVSCSTPLQL 731

Db 515 SOGAELDAQORNLRTPLHLAVERGKVAIQHLKSGAVPDALDQSGYGPLHTAAARGKYL 574
Qy 541 ICKLLLOHGADPTKKNRDGNTPLDLVKDGDTDIQLLRGDAALLDAKKGCLARVKKLSS 600
Db 575 ICKMLLRYGASLELPTHQGWTPHL-----AAYKGHL-EIHLHA 613
Qy 601 PDVNCRDITQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGANVWTPHLAARHGEAVVSALLQCGADPNAAEQSGWTPHLAVQORSTFL 673
Qy 661 VAALLIKYNACVNATDKWAFPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDL 718
Db 731 SVINLEHHANVHARNKVGWTPAHLAALKGNTAILKVLVEAGAQLDVQDGVSCSTPLQL 731

RESULT 10
US-11-317-329-36
; Sequence 36, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-36

Query Match 8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 245 KSAIDLAP-----TPQKERLAYEFKGHSLLQAAREADVTRIKKHSLEMVNFKHPQTHET 300
Db 338 KRALQSDRKNLVPRDEELCIYENKVTPLQFLVAQSGVEQVRLLLA-----HEV 386
Qy 301 ALHCAAAAPYKPKRQICELLRLKRGANINEKTEFPLPLHVAEKAHNDVVEVVVKEAKV 360
Db 387 DVDCCQTASGY-----TPLLIAAQDQPDLCALLAHGADA 421
Qy 361 NALDNLGQTSLHRAAYCGHLQTCRLLSYGCDPNIIISLOGFTALONGNENVOQLQEGIS 420
Db 422 NRVDGDMAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 421 LGNSADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNVSVVEYLL 480
Db 472 --NFENVARLLVSRQA-----DPNLRABEGK--TPLHVAAYFGHVSIVKLIT 514
Qy 481 OHGADVHAQDKGGLVPLHNACSYGHYEVAELLVKGGAVNVADLWKFTPLHEAAAKGKYE 540
Db 515 SOGAELDAQORNLRTPLHLAVERGKVAIQHLKSGAVPDALDQSGYGPLHTAAARGKYL 574
Qy 541 ICKLLLOHGADPTKKNRDGNTPLDLVKDGDTDIQLLRGDAALLDAKKGCLARVKKLSS 600
Db 575 ICKMLLRYGASLELPTHQGWTPHL-----AAYKGHL-EIHLHA 613
Qy 601 PDVNCRDITQGRHSTPLHAAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGANVWTPHLAARHGEAVVSALLQCGADPNAAEQSGWTPHLAVQORSTFL 673
Qy 661 VAALLIKYNACVNATDKWAFPLHEAAQKGRTOCALLLAHGADPTLKNQEGOTPLDL 718
Db 731 SVINLEHHANVHARNKVGWTPAHLAALKGNTAILKVLVEAGAQLDVQDGVSCSTPLQL 731


```
RESULT 11
US-11-317-329-37
; Sequence 37, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-37

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy      245 KSAIDLAP-----TPOLKERLAYEPKGHSLQQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Db      338 KRALQLSDRKNLVRDELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386

Qy      301 ALHCAASPYPKRKQICELLRLKGANINEKTEFTPLHVASERKAHNDVVEVVKHEAKV 360
Db      387 DVDCQTASGY-----TPLLIAAQDQDPLCALLAHGADA 421

Qy      361 NALDNLGQTSILHRAAYCGHLQTCRLLLSYGCDPNIIISLQGFALTQMGNNVQQLLQEGIS 420
Db      422 NRVEDGWAPLHFAAQNGDDRTARILLDHGACVDAQEREGWTPHLAAQN-----471

Qy      421 LGNSEADRLLEAAKAGDVETVKKLTQVSNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db      472 --NFENVARLLVSRQA-----DPLREAEKG--TPLHVAAYFGHVSIVKLLT 514

Qy      481 OHGADVHAKRGGLVPLHNACSYGHYEVAELLVKGAVNVVADLWKFTPLHEAAKGYE 540
Db      515 SQGAELDAQQRNLRTPLHLAVERGKVRAIQHLKSGAVPDALDQSGYGLPHTAAARGKYL 574

Qy      541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQLLLRGDAALLDAAKKGCLARVKKLSS 600
Db      575 ICKMLLYGASLELPTHQGWTPHL-----AAYKGHL-EIHLA 613

Qy      601 PDVNCRTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db      614 ESHANMGALGAVNWTPLHLAARGHEEVVSALLQCGADPNAAEQSGWTPHLHVAQVSTFL 673

Qy      661 VAALLIKYNACVNATDKWAFPLHEAAQKGTQLCALLAHGADPTLKNQSGQTPDL 718
Db      674 SVINLLEHANVHARNKVGWTPAHLAALKGNNTAILKVLVEAGAQLDVQDGVSCPTPLQ 731

RESULT 12
US-11-317-329-38
; Sequence 38, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-38

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy      245 KSAIDLAP-----TPOLKERLAYEPKGHSLQQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Db      338 KRALQLSDRKNLVRDELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386

Qy      301 ALHCAASPYPKRKQICELLRLKGANINEKTEFTPLHVASERKAHNDVVEVVKHEAKV 360
Db      387 DVDCQTASGY-----TPLLIAAQDQDPLCALLAHGADA 421

Qy      361 NALDNLGQTSILHRAAYCGHLQTCRLLLSYGCDPNIIISLQGFALTQMGNNVQQLLQEGIS 420
Db      422 NRVEDGWAPLHFAAQNGDDRTARILLDHGACVDAQEREGWTPHLAAQN-----471

Qy      421 LGNSEADRLLEAAKAGDVETVKKLTQVSNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Db      472 --NFENVARLLVSRQA-----DPLREAEKG--TPLHVAAYFGHVSIVKLLT 514

Qy      481 OHGADVHAKRGGLVPLHNACSYGHYEVAELLVKGAVNVVADLWKFTPLHEAAKGYE 540
Db      515 SQGAELDAQQRNLRTPLHLAVERGKVRAIQHLKSGAVPDALDQSGYGLPHTAAARGKYL 574

Qy      541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQLLLRGDAALLDAAKKGCLARVKKLSS 600
Db      575 ICKMLLYGASLELPTHQGWTPHL-----AAYKGHL-EIHLA 613

Qy      601 PDVNCRTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVD 660
Db      614 ESHANMGALGAVNWTPLHLAARGHEEVVSALLQCGADPNAAEQSGWTPHLHVAQVSTFL 673

Qy      661 VAALLIKYNACVNATDKWAFPLHEAAQKGTQLCALLAHGADPTLKNQSGQTPDL 718
Db      674 SVINLLEHANVHARNKVGWTPAHLAALKGNNTAILKVLVEAGAQLDVQDGVSCPTPLQ 731

RESULT 13
US-11-317-329-39
; Sequence 39, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-39

Query Match      8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy      245 KSAIDLAP-----TPOLKERLAYEPKGHSLQQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Db      338 KRALQLSDRKNLVRDELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386
```

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Qy 301 ALHCAASPYPKQKQICELLRKGNINEKTEFLTPLVASEKAKNDVVEVVVKHEAKV 360
Db 387 DVDCQTASGY-----TPLLIAAQDQDPDLCAALLAHGADA 421
Qy 361 NALDNLGOTSLHRAAYCGHLOTCRLLSYGCDPNIIISLQGFALQMGNNVQQLQEGIS 420
Db 422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 421 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVBYLL 480
Db 472 --NFENVARLLVSRQA-----DNLREAEKG--TPLHVAAYFGHVSLLVLLT 514
Qy 481 QHGADVHAKDGGVLPLHNACSYGHEVAELLVKGAVNVVADLWKFTPLHHEAAKGYE 540
Db 515 SQGAELDAQORNLRTPHLAVERGVKRAIQHLLKSGAVPDALDQSGYGLPHTAAARGYL 574
Qy 541 ICKLLOHGADPTKKNRDGNTPLDLVKDGDITDQLLLRGAALLDAARKGCLARVKKLSS 600
Db 575 ICKMLLYRGASLELPTHQGWTPHL-----AAYKGHL-EIIHLLA 613
Qy 601 PDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGAVNWTPLHLAARHGEAAVVSALLQCGADPNAAEQSGWTPHLAVQSTFL 673
Qy 661 VAALLIKYNACVNATDKWAFTPHLHEAAKQRTQLCALLAHGADPTLKNQEGQTPDL 718
Db 674 SVINLEHHANVHARNKVGTWTPAHLAALKGNITAILKVLVEAGAQLDVQDQVGSCTPLQL 731

RESULT 14
US-11-317-329-40
; Sequence 40, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-40

Query Match 8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 245 KSAIDLAP----TPQKERLAYEFKSHLSLQAAREADVTRIKKHLSEMNFKHPQTHET 300
Db 338 KRALQLSDRKNLVPRDEELCIYENKVTPLOFLVAQGSVEQVRLLLA-----HEV 386
Qy 301 ALHCAASPYPKQKQICELLRKGNINEKTEFLTPLVASEKAKNDVVEVVVKHEAKV 360
Db 387 DVDCQTASGY-----TPLLIAAQDQDPDLCAALLAHGADA 421
Qy 361 NALDNLGOTSLHRAAYCGHLOTCRLLSYGCDPNIIISLQGFALQMGNNVQQLQEGIS 420
Db 422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 421 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVBYLL 480
Db 472 --NFENVARLLVSRQA-----DNLREAEKG--TPLHVAAYFGHVSLLVLLT 514
Qy 481 QHGADVHAKDGGVLPLHNACSYGHEVAELLVKGAVNVVADLWKFTPLHHEAAKGYE 540
Db 515 SQGAELDAQORNLRTPHLAVERGVKRAIQHLLKSGAVPDALDQSGYGLPHTAAARGYL 574
Qy 541 ICKLLOHGADPTKKNRDGNTPLDLVKDGDITDQLLLRGAALLDAARKGCLARVKKLSS 600
Db 575 ICKMLLYRGASLELPTHQGWTPHL-----AAYKGHL-EIIHLLA 613
Qy 601 PDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGAVNWTPLHLAARHGEAAVVSALLQCGADPNAAEQSGWTPHLAVQSTFL 673
Qy 661 VAALLIKYNACVNATDKWAFTPHLHEAAKQRTQLCALLAHGADPTLKNQEGQTPDL 718
Db 674 SVINLEHHANVHARNKVGTWTPAHLAALKGNITAILKVLVEAGAQLDVQDQVGSCTPLQL 731

RESULT 15
US-11-317-329-41
; Sequence 41, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-41

Query Match 8.3%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 245 KSAIDLAP----TPQKERLAYEFKSHLSLQAAREADVTRIKKHLSEMNFKHPQTHET 300
Db 338 KRALQLSDRKNLVPRDEELCIYENKVTPLOFLVAQGSVEQVRLLLA-----HEV 386
Qy 301 ALHCAASPYPKQKQICELLRKGNINEKTEFLTPLVASEKAKNDVVEVVVKHEAKV 360
Db 387 DVDCQTASGY-----TPLLIAAQDQDPDLCAALLAHGADA 421
Qy 361 NALDNLGOTSLHRAAYCGHLOTCRLLSYGCDPNIIISLQGFALQMGNNVQQLQEGIS 420
Db 422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 421 LGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVBYLL 480
Db 472 --NFENVARLLVSRQA-----DNLREAEKG--TPLHVAAYFGHVSLLVLLT 514
Qy 481 QHGADVHAKDGGVLPLHNACSYGHEVAELLVKGAVNVVADLWKFTPLHHEAAKGYE 540
Db 515 SQGAELDAQORNLRTPHLAVERGVKRAIQHLLKSGAVPDALDQSGYGLPHTAAARGYL 574
Qy 541 ICKLLOHGADPTKKNRDGNTPLDLVKDGDITDQLLLRGAALLDAARKGCLARVKKLSS 600
Db 575 ICKMLLYRGASLELPTHQGWTPHL-----AAYKGHL-EIIHLLA 613
Qy 601 PDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Db 614 ESHANMGALGAVNWTPLHLAARHGEAAVVSALLQCGADPNAAEQSGWTPHLAVQSTFL 673
Qy 661 VAALLIKYNACVNATDKWAFTPHLHEAAKQRTQLCALLAHGADPTLKNQEGQTPDL 718
Db 674 SVINLEHHANVHARNKVGTWTPAHLAALKGNITAILKVLVEAGAQLDVQDQVGSCTPLQL 731
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Search completed: December 18, 2006, 18:01:20

Job time : 39.6529 secs

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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:21:00 ; Search time 162.464 Seconds
(without alignments)
3489.682 Million cell updates/sec

Title: US-10-616-101-4
Perfect score: 6464
Sequence: 1 RCSARRGAAGGGAQGRGV.....AYPEYLITYQIMRPGMVDG 1240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6464	100.0	1240	4 AAY97749	Tankyrase
2	6464	100.0	1240	6 ABG73731	Tankyrase
3	6464	100.0	1240	7 ADH69406	Human tan
4	6464	100.0	1240	9 ADY97762	Human tan
5	6375.5	98.6	1262	4 AAB66290	Human tan
6	6375.5	98.6	1287	8 ADR66429	Human pro
7	6375.5	98.6	1287	8 ADR66087	Human pro
8	6375.5	98.6	1385	4 AAB66294	Human tan
9	6121	94.7	1169	4 AAB66288	Human tan
10	6121	94.7	1169	4 AAB66278	Human tan
11	6108	94.5	1166	4 AAB66295	Human tan
12	6108	94.5	1166	8 ADR14792	Amino aci
13	6092	94.2	1166	3 AAB27211	Human tan
14	6088	94.2	1166	5 ABP69457	Human pol
15	6053	93.6	1166	4 AAY72589	Human tan
16	5766	89.2	1100	4 AAY97748	Tankyrase
17	5766	89.2	1100	6 ABG73732	Tankyrase
18	5766	89.2	1100	6 ABG73730	Tankyrase
19	5766	89.2	1100	7 ADR69405	Human tan
20	5766	89.2	1100	9 ADY97766	Human tan
21	5760	89.1	1100	6 ABG73735	Tankyrase
22	5760	89.1	1100	9 ADY97769	Human tan
23	5658	87.5	1084	6 ABG73736	Tankyrase

24	5656	87.5	1083	9	ADY97770	Human tan
25	5605	86.7	1074	2	AAY05734	Human tan
26	5582	86.4	1065	2	ADY97761	Human tan
27	5543	85.8	1166	4	AAB47022	Human SPA
28	5474	84.7	1431	3	AAB27210	Human tan
29	5303.5	82.0	1083	6	AAE35352	Human col
30	5103.5	79.0	1327	3	AAY44402	Human tan
31	5103.5	79.0	1327	3	AAB27212	Human tan
32	5103.5	79.0	1327	4	AAB66279	Human tan
33	5103.5	79.0	1327	5	AAU79537	Human tan
34	5103.5	79.0	1327	8	ADR14791	Amino aci
35	5040.5	78.0	1333	3	AAB27209	Human tan
36	5038.5	77.9	991	4	AAB47023	Mouse SPA
37	4624.5	71.5	907	4	AAB48574	Human bre
38	4102	63.5	784	4	AAB66285	Human tan
39	4005	62.0	1181	4	ABB60894	Drosophil
40	3997	61.8	1181	4	AAB66297	Human tan
41	3959	61.2	756	4	AAB66286	Human tan
42	3938	60.9	802	5	AAO20512	Protein o
43	3307	51.2	949	3	RAY44404	Human tru
44	3307	51.2	949	5	AAU79539	Truncated
45	2913	45.1	583	9	ADY97768	Human tan

ALIGNMENTS

RESULT 1
AAY97749
ID AAY97749 standard; protein; 1240 AA.
XX AAY97749;
XX
DT 06-AUG-2001 (first entry)
XX
DE Tankyrase homologue isotype 2 protein sequence.

XX Tankyrase homologue isotype 2; TaHo-1; TaHo-2; cell proliferation;
KW cell cycle protein; cell cycle associated disorder; cancer; gene mapping;
KW chromosome mapping; gene therapy; vaccine.
XX Unidentified.
XX
PN WO200130987-A2.
XX
PD 03-MAY-2001.
XX
PF 25-OCT-2000; 2000WO-US041528.
XX
PR 25-OCT-1999; 99US-00427154.
XX
PA (RIGE-) RIGEL PHARM INC.

XX Luo Y, Chan E, Xu X, Huang B;
WPI; 2001-300503/31.
XX N-PSDB; AAA91488.

XX Novel recombinant cell cycle polypeptide, tankyrase H useful for inducing
or preventing cell proliferation in cells, and for diagnosing, treating
or preventing cell cycle associated disorders such as cancer.

XX Claim 22; Fig 4; 63pp; English.

XX This sequence is the Tankyrase homologue isotype 2 (TaHo-2) protein of
the invention. The invention also relates to the TaHo-2 protein. The TaHo
proteins are useful for inducing or preventing cell proliferation in
cells, and in the study or treatment of conditions mediated by the cell
cycle proteins, such as to diagnose, treat or prevent cell cycle
associated disorders, preferably cancer. The TaHo coding sequences are
useful as hybridisation probes, in chromosome and gene mapping and in the
generation of anti-sense DNA and RNA. The coding sequences are also
useful for the preparation of TaHo, for generating either transgenic

CC	animals or knock out animals which, in turn, are useful in a development
CC	and screening of therapeutically useful agents, in gene therapy, as
CC	vaccine, and for construction of hybridisation probes for mapping the
CC	gene which encodes TaHo and for the genetic analysis of individuals with
CC	genetic disorders. The TaHo proteins, and their coding sequences are
CC	useful in screening assays
XX	
XX	
SQ	Sequence 1240 AA;
	Query Match
	Best Local Similarity 100.0%; Score 6464; DB 4; Length 1240;
	Matches 1240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RCSARRGAGGCGAQRGARVGAAGHCTADPDTAGSQAARALASASSPGGLALLAGPGLLL 60
DB	1 RCSARRGAGGCGAQRGARVGAAGHCTADPDTAGSQAARALASASSPGGLALLAGPGLLL 60
QY	61 RLLALLAVAAARIMSGRRACAGGGAACAASAAEAVEPAARELFEACRNGDVERVKRLVTP 120
DB	61 RLLALLAVAAARIMSGRRACAGGGAACAASAAEAVEPAARELFEACRNGDVERVKRLVTP 120
QY	121 EKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSPGHAEV 180
DB	121 EKVNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSPGHAEV 180
QY	181 VNLLRHGADPNARDNWNYPPLHEAAIKGKIDVCIVLLOHGAEPTRINTDGTALDLADP 240
DB	181 VNLLRHGADPNARDNWNYPPLHEAAIKGKIDVCIVLLOHGAEPTRINTDGTALDLADP 240
QY	241 SAKAVLTGEYKDELESARSNGEKMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKI 300
DB	241 SAKAVLTGEYKDELESARSNGEKMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKI 300
QY	301 VQLLQHGADVHAKDGLVPLHNACSYGHYEVTELLVKHGACVNMALMQPTPLHEAAS 360
DB	301 VQLLQHGADVHAKDGLVPLHNACSYGHYEVTELLVKHGACVNMALMQPTPLHEAAS 360
QY	361 KNRVEVCSLLSYGADPTLLNCHNKSADLAPTPQIKERLAYEFKGHSLLOQAREADVTR 420
DB	361 KNRVEVCSLLSYGADPTLLNCHNKSADLAPTPQIKERLAYEFKGHSLLOQAREADVTR 420
QY	421 IKKHLSLEWNVFKPQTHETALHCAASPYPRKQICELLIRKGANINEKTEFTPLHV 480
DB	421 IKKHLSLEWNVFKPQTHETALHCAASPYPRKQICELLIRKGANINEKTEFTPLHV 480
QY	481 ASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQ 540
DB	481 ASEKAHNDVVEVVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQ 540
QY	541 FTALQNGHENVQQLLOEGISLGNSEADROLLEAAKAGDVETVKCLTVQSVNCRDIEGRQ 600
DB	541 FTALQNGHENVQQLLOEGISLGNSEADROLLEAAKAGDVETVKCLTVQSVNCRDIEGRQ 600
QY	601 STPLHFAAGYNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHYEVAEVLVKHGAENV 660
DB	601 STPLHFAAGYNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHYEVAEVLVKHGAENV 660
QY	661 VADLWKFTPLHEAAAKGYEICKLLQHGADPTKKNRDNQNTPLDLVKGDGTDIDQLLRGD 720
DB	661 VADLWKFTPLHEAAAKGYEICKLLQHGADPTKKNRDNQNTPLDLVKGDGTDIDQLLRGD 720
QY	721 AALLDAAKKGLARVKKLSPPNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADYN 780
DB	721 AALLDAAKKGLARVKKLSPPNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADYN 780
QY	781 AQDKGGLIPLHNAASVGHVDVAALLIKYNACVNAATDKWAFTPLHEAAQKGRQTCALLLA 840
DB	781 AQDKGGLIPLHNAASVGHVDVAALLIKYNACVNAATDKWAFTPLHEAAQKGRQTCALLLA 840
QY	841 HGADPTLKNQEGQTPLDLVASDDVSALLTAAMPSPALPSCYKQVNLNVRSPGATADALS 900
DB	841 HGADPTLKNQEGQTPLDLVASDDVSALLTAAMPSPALPSCYKQVNLNVRSPGATADALS 900

QY	901 SGPSPSSLSAASSLDNLSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSTITQFVRNLG 960
DB	901 SGPSPSSLSAASSLDNLSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSTITQFVRNLG 960
QY	961 LEHLMDFERSQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLT 1020
DB	961 LEHLMDFERSQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLT 1020
QY	1021 NTSGSGTILIDLSPDDKEFQSVVEEEMQSTVRHRDGGHAGGIFNRYNLIKIOKVCNKKLW 1080
DB	1021 NTSGSGTILIDLSPDDKEFQSVVEEEMQSTVRHRDGGHAGGIFNRYNLIKIOKVCNKKLW 1080
QY	1081 ERYTHRRKEVSEENHNHANERMLFHGSPFVNAIHKGFDERHAYICGMFGAGIYFAENSS 1140
DB	1081 ERYTHRRKEVSEENHNHANERMLFHGSPFVNAIHKGFDERHAYICGMFGAGIYFAENSS 1140
QY	1141 KSNQVYVIGGGTGCPVHKDRSCYICHRQLLPCRVTLTKHSFLOFSAMKMAHSPPGHHSVT 1200
DB	1141 KSNQVYVIGGGTGCPVHKDRSCYICHRQLLPCRVTLTKHSFLOFSAMKMAHSPPGHHSVT 1200
QY	1201 GRPSVNGLALAEYVYRGEQAYPEYLITYQIMRPEGMVDG 1240
DB	1201 GRPSVNGLALAEYVYRGEQAYPEYLITYQIMRPEGMVDG 1240
RESULT 2	
ID	ABG73731 standard; protein; 1240 AA.
XX	ABG73731;
XX	08-APR-2003 (first entry)
DE	Tankyrase H isotype 2 TaHo-2 fragment from clone K23.
KW	Tankyrase; tankyrase H; cell cycle protein; growth inhibitor; TaHo-2;
KW	TaHo; cytostatic; immunostimulant; gene therapy; vaccine; cancer; tumour;
XX	cell cycle related disorder; poly ADP-ribose polymerase; PARP.
OS	Unidentified.
XX	WO200286170-A1.
PN	31-OCT-2002.
PD	
XX	25-APR-2002; 2002WO-US013185.
XX	
PR	25-APR-2001; 2001US-00843159.
XX	(RIGE-) RIGEL PHARM INC.
PI	Luo Y, Chan E, Xu X, Huang B, Ossovskaya V;
XX	
DR	WPI; 2003-093158/08.
DR	N-PSDB; ABQ77067.
XX	
PT	New recombinant nucleic acid encoding a cell cycle protein, useful for
PT	diagnosing and treating a cell cycle related disorder, e.g. cancer.
XX	
PS	Claim 14; Fig 4; 90pp; English.
CC	This invention describes a novel recombinant nucleic acid encoding the
CC	cell cycle protein TaHo, a tankyrase H isoform. The products of the
CC	invention have cytostatic and immunostimulant activity and can be used
CC	for gene therapy and in vaccines. The cell cycle protein TaHo and the
CC	nucleic acid encoding the protein are useful for diagnosing and treating
CC	a cell cycle related disorder, e.g. cancer, or for inhibiting growth of a
CC	tumour cell. The methods are useful for screening for a bioactive agent
CC	capable of binding to a cell cycle protein tankyrase H, or a bioactive
CC	agent capable of modulating a cell cycle protein tankyrase H or PARP
CC	(poly ADP-ribose polymerase) activity. The antibodies are useful for
CC	inducing an immune response against the cell cycle proteins. This
CC	sequence represents the tankyrase H isoform 2, TaHo-2, isolated from

CC clone K23 which is described in the disclosure of the invention

XX SQ Sequence 1240 AA;

Query Match 100.0%; Score 6464; DB 6; Length 1240;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCSARRGAAGGCGAORGARVGAAGTADPDVPTAGSOAARALSASSPGGLALLAGPGLLL 60
DB 1 RCSARRGAAGGCGAORGARVGAAGTADPDVPTAGSOAARALSASSPGGLALLAGPGLLL 60
QY 61 RLLALLLAVAAARIMSGRRACGGGACASAAAEVPAARELFEACRNGDVERVRLVTP 120
DB 61 RLLALLLAVAAARIMSGRRACGGGACASAAAEVPAARELFEACRNGDVERVRLVTP 120
QY 121 EKNSRDTAGRKSTPLHFAAGFRKDVVEYLLQNGANVOARDGGLIPLHNACSFHAEV 180
DB 121 EKNSRDTAGRKSTPLHFAAGFRKDVVEYLLQNGANVOARDGGLIPLHNACSFHAEV 180
QY 181 VNLRLRHGADPNARDNNWNTPLHAAIKGKIDVCIVLLQHGAEPTIRNDGRTALDLADP 240
DB 181 VNLRLRHGADPNARDNNWNTPLHAAIKGKIDVCIVLLQHGAEPTIRNDGRTALDLADP 240
QY 241 SAKAVLTGEYKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHAAAGYNNVKI 300
DB 241 SAKAVLTGEYKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHAAAGYNNVKI 300
QY 301 VOLLOHGADVHAKDGBLPLHNAACSYGHEVTELLVKGACVNMADLQFTPLHEAAS 360
DB 301 VOLLOHGADVHAKDGBLPLHNAACSYGHEVTELLVKGACVNMADLQFTPLHEAAS 360
QY 361 KNRVEVCSLLSYGADPTLLNCHNKAIDLAPTPOLKERLAYEPKHSILOAAREADVTR 420
DB 361 KNRVEVCSLLSYGADPTLLNCHNKAIDLAPTPOLKERLAYEPKHSILOAAREADVTR 420
QY 421 IKKHLSEWVNFKHPQTHETALHCAAAPYKPKQICELLRLKGANINEKTEFTPLHV 480
DB 421 IKKHLSEWVNFKHPQTHETALHCAAAPYKPKQICELLRLKGANINEKTEFTPLHV 480
QY 481 ASEKAHNDVVEVVKHEAKVNALDNLGQTSLHRAAYCGHLOTCLRLLSYGCDDPNIISLQ 540
DB 481 ASEKAHNDVVEVVKHEAKVNALDNLGQTSLHRAAYCGHLOTCLRLLSYGCDDPNIISLQ 540
QY 541 FTALOMGNENVOQLLOEGISLGNSEADQLLEAAKAGDVETVKKLTCTVQSVNCRDIEGR 600
DB 541 FTALOMGNENVOQLLOEGISLGNSEADQLLEAAKAGDVETVKKLTCTVQSVNCRDIEGR 600
QY 601 STPLHFAAGYNNRVSVEYLLQHGADVHAKDGLVPLHNACSYGHEVVAELLVKHGAVVN 660
DB 601 STPLHFAAGYNNRVSVEYLLQHGADVHAKDGLVPLHNACSYGHEVVAELLVKHGAVVN 660
QY 661 VADLWKFTPLHAAAKGYEICKLLOHGADPTKKNRDGNTPLDVKDGDGTDIDQLLRGD 720
DB 661 VADLWKFTPLHAAAKGYEICKLLOHGADPTKKNRDGNTPLDVKDGDGTDIDQLLRGD 720
QY 721 AALLDAKKGCLARVKKLSPPDNVNCRTQGRHSTPLHAGYNNLEVAEYLLQHGADV 780
DB 721 AALLDAKKGCLARVKKLSPPDNVNCRTQGRHSTPLHAGYNNLEVAEYLLQHGADV 780
QY 781 AQDKGGLIPLHNAASGYHVDVAALLIKYNACVNDKWAFTPLHAAOKGRTOLCALLA 840
DB 781 AQDKGGLIPLHNAASGYHVDVAALLIKYNACVNDKWAFTPLHAAOKGRTOLCALLA 840
QY 841 HGADPTLKNQEGQTPDLVSDADDVSALLTAAMPSPALPSCYKQVNLGVRSPGATADALS 900
DB 841 HGADPTLKNQEGQTPDLVSDADDVSALLTAAMPSPALPSCYKQVNLGVRSPGATADALS 900
QY 901 SGPSPSSLSAASSLDNLSGFSFSELSSVVSSSGTEGASLEKKEVPGVDFSIQTVRNIG 960
DB 901 SGPSPSSLSAASSLDNLSGFSFSELSSVVSSSGTEGASLEKKEVPGVDFSIQTVRNIG 960
QY 961 LEHLMDFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTL 1020

DB 961 LEHLMDFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTL 1020
QY 1021 NTSGSGTILIDLSDDKEFQSVBEEMOSTVREHDDGGHAGGIFNRYNLIKQKVCNKKLW 1080
DB 1021 NTSGSGTILIDLSDDKEFQSVBEEMOSTVREHDDGGHAGGIFNRYNLIKQKVCNKKLW 1080
QY 1081 ERYTHRRKEVSEENHNHANERMLPHGSPFNVAIIHKGFDERHAYIGGMFGAGIYFAENSS 1140
DB 1081 ERYTHRRKEVSEENHNHANERMLPHGSPFNVAIIHKGFDERHAYIGGMFGAGIYFAENSS 1140
QY 1141 KSNQVYVIGGCGTGPCVHKDRSCYVCHROLLFCRVTLTKSFLQFSAMQVAHSPPGHHSVT 1200
DB 1141 KSNQVYVIGGCGTGPCVHKDRSCYVCHROLLFCRVTLTKSFLQFSAMQVAHSPPGHHSVT 1200
QY 1201 GRPSVNGLALAEYVYRGEQAYPEYLITYQIMRPEGMDG 1240
DB 1201 GRPSVNGLALAEYVYRGEQAYPEYLITYQIMRPEGMDG 1240

RESULT 3

ID ADH69406 standard; protein; 1240 AA.

AC ADH69406;

DT 25-MAR-2004 (first entry)

XX Human tankyrase homologue isotype 2 (TaHo-2).

DE Tankyrase H cell cycle protein; p21; gene therapy;
KW bioactive agent screening; cancer; cytostatic; human.

XX Homo sapiens.

XX US6617102-B1.

XX 09-SEP-2003.

XX 25-OCT-2000; 2000US-00696668.

XX 25-OCT-1999; 99US-00427154.

XX (RIGE-) RIGEL PHARM INC.

XX Luo Y, Chan E, Xu X, Huang B, Ososovskaya V;

XX WPI; 2003-895391/82.

XX N-PSDB; ADH69415.

XX Screening for a bioactive agent capable of interfering with the binding
PT of a tankyrase H cell cycle protein and p21 for diagnosing or treating
PT cancer by combining a tankyrase H cell cycle protein, a candidate
PT bioactive agent and p21.

XX Claim 1; SEQ ID NO 4; 39pp; English.

XX The invention relates to a method for screening a bioactive agent capable
CC of interfering with the binding of a tankyrase H cell cycle protein and
CC p21. The invention is useful in gene therapy. The method is useful for
CC screening for a bioactive agent capable of interfering with the binding
CC of a tankyrase H cell cycle protein and p21 for preparing a composition
CC for diagnosing or treating cancer. the present sequence is human
CC tankyrase homologue isotype 2 (TaHo-2).

XX Sequence 1240 AA;

Query Match 100.0%; Score 6464; DB 7; Length 1240;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCSARRGAAGGCGAORGARVGAAGTADPDVPTAGSOAARALSASSPGGLALLAGPGLLL 60

Db 1 RCSARRGAGGOGAQRGARVGAAGTAPDPVTVTAGSQAARALSSAPGGALLALLGPGCLLL 60
QY 61 RLLALLLAVAAARIMSGRCAGGGAA CASAAAEAVEPAARELFEACRNGDVERVKRLVTP 120
Db 61 RLLALLLAVAAARIMSGRCAGGGAA CASAAAEAVEPAARELFEACRNGDVERVKRLVTP 120
QY 121 EKVNSRDTAGRKSTPLHFAAGGRKDVVEYLLQNGANVOARDGGILPLHNACSPGHAEB 180
Db 121 EKVNSRDTAGRKSTPLHFAAGGRKDVVEYLLQNGANVOARDGGILPLHNACSPGHAEB 180
QY 181 VNLLLRHGADPNARDNWNVTPLHEAAIKGIDVICIVLLQHGAEPTIRNTDGR TALDLADP 240
Db 181 VNLLLRHGADPNARDNWNVTPLHEAAIKGIDVICIVLLQHGAEPTIRNTDGR TALDLADP 240
QY 241 SAKAVLTGEYKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI 300
Db 241 SAKAVLTGEYKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI 300
QY 301 VOLLLOHGADVHAKDKGDLVPLHNACSYGHEVTELLVKGHACVNMADLWQFTPLHEAAS 360
Db 301 VOLLLOHGADVHAKDKGDLVPLHNACSYGHEVTELLVKGHACVNMADLWQFTPLHEAAS 360
QY 361 KNRVECSLLLSYGADPTLLNCHNKSADLPTPOLKERLAYEFKGHSLLOAAREADVTR 420
Db 361 KNRVECSLLLSYGADPTLLNCHNKSADLPTPOLKERLAYEFKGHSLLOAAREADVTR 420
QY 421 IKKHLSELMVNFPGHPTHTALHCAAAASYPKPKQICELLLRKGANINBKTEFTPLHV 480
Db 421 IKKHLSELMVNFPGHPTHTALHCAAAASYPKPKQICELLLRKGANINBKTEFTPLHV 480
QY 481 ASEKAHNDVVEVVKHAKVNALDNLGQTSLSHRAAYCGHLQTCRLLLSYCGDPNIIISLQ 540
Db 481 ASEKAHNDVVEVVKHAKVNALDNLGQTSLSHRAAYCGHLQTCRLLLSYCGDPNIIISLQ 540
QY 541 FTALQNGENVQOLLQEGISLGNSEADROLLBAAKAGDVETVKLCTVQSVNCRDIEGRQ 600
Db 541 FTALQNGENVQOLLQEGISLGNSEADROLLBAAKAGDVETVKLCTVQSVNCRDIEGRQ 600
QY 601 STPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVAELLVKGAVVN 660
Db 601 STPLHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVAELLVKGAVVN 660
QY 661 VADLWKFTPLHEAAAKGKYEICKLLOHGADPTKKNRDGNTPLDLVKDGDTDIQLLRGD 720
Db 661 VADLWKFTPLHEAAAKGKYEICKLLOHGADPTKKNRDGNTPLDLVKDGDTDIQLLRGD 720
QY 721 AALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVN 780
Db 721 AALLDAAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVN 780
QY 781 AQDKGGLIPLHNAASVGHVDVAALLIKYNACVNAATDKWAFTPLHEAAQKGRTOLCALLLA 840
Db 781 AQDKGGLIPLHNAASVGHVDVAALLIKYNACVNAATDKWAFTPLHEAAQKGRTOLCALLLA 840
QY 841 HGADPTLNQEGQTPLDLVASDVSALLTAAMPSPALPCYKPOVLNGVRSFGATADALS 900
Db 841 HGADPTLNQEGQTPLDLVASDVSALLTAAMPSPALPCYKPOVLNGVRSFGATADALS 900
QY 901 SGFSPSSLSAASLDNLGSGFSELSVSVSSGTEGASLEKKEVPGVDFSIQFVRNLG 960
Db 901 SGFSPSSLSAASLDNLGSGFSELSVSVSSGTEGASLEKKEVPGVDFSIQFVRNLG 960
QY 961 LEHLMDFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQQLNPYLTL 1020
Db 961 LEHLMDFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQQLNPYLTL 1020
QY 1021 NTSGSGTLLIDLSPDDKEFQSEVEEMQSTVREHRDGGHAGGIFNRYNIIKIQKVCNKKLW 1080
Db 1021 NTSGSGTLLIDLSPDDKEFQSEVEEMQSTVREHRDGGHAGGIFNRYNIIKIQKVCNKKLW 1080
QY 1081 ERYTHRRKEVSENNHNANERMLFHGSPFVNAI IHKGFDERHAYIGGMFGAGIYFAENSS 1140
Db 1081 ERYTHRRKEVSENNHNANERMLFHGSPFVNAI IHKGFDERHAYIGGMFGAGIYFAENSS 1140

QY 1141 KSNQYVYIGGGTGCPVHKDRSCYICHRQLLCFRTVLGKSFLOFSAMKMAHSPGHHSVT 1200
Db 1141 KSNQYVYIGGGTGCPVHKDRSCYICHRQLLCFRTVLGKSFLOFSAMKMAHSPGHHSVT 1200
QY 1201 GRPSVNGLALAEVVIYRGFOAYPEYLITYQIMRPEGMVDG 1240
Db 1201 GRPSVNGLALAEVVIYRGFOAYPEYLITYQIMRPEGMVDG 1240
RESULT 4
ADY97762
ID ADY97762 standard; protein; 1240 AA.
XX
AC ADY97762;
XX
XX
DT 16-JUN-2005 (first entry)
XX
DE Human tankyrase homologue isotype 2 protein SEQ ID NO:4.
XX
KW cell cycle; cancer; cytostatic; tankyrase homologue isotype 2.
XX
OS Homo sapiens.
XX
PN US2005074825-A1.
XX
PD 07-APR-2005.
XX
XX
PF 08-JUL-2003; 2003US-00616101.
XX
PR 25-OCT-1999; 99US-00427154.
PR 25-OCT-2000; 2000US-00696668.
PR 25-APR-2001; 2001US-00843159.
XX
XX (LUOY/) LUO Y.
PA (CHAN/) CHAN E.
PA (XUXX/) XU X.
PA (HUAN/) HUANG B.
PA (OSSO/) OSSOVSKAYA V.
XX
XX
PI Luo Y, Chan E, Xu X, Huang B, Ossovskaya V;
XX
XX WPI; 2005-294737/30.
DR N-PSDB; ADY97760.
XX
XX
PT Novel recombinant polypeptide such as cell cycle protein e.g. tankyrase
XX homolog, useful for screening its modulator.
XX
XX Claim 21; SEQ ID NO 4; 75pp; English.
XX
CC The invention relates to a recombinant polypeptide (I) such as cell cycle
CC protein e.g. tankyrase homologue (TaHo), comprising an amino acid
CC sequence having 85% or more sequence identity to the 1065 amino acid
CC sequence of ADY97761 or the 1240 amino acid sequence of ADY97762. Also
CC described: (1) diagnosing cancer, which involves determining the activity
CC of (I) from a test sample of an individual and comparing the level with a
CC control with a control; (2) treating (M1) an individual with a cell cycle
CC related disorder, which involves administering to the individual an
CC inhibitor of TaHo; (3) a recombinant nucleic acid (II) encoding (I),
CC comprising a nucleic acid that hybridizes under high stringent conditions
CC to a sequence complementary to the 3797 base pair sequence of ADY97760,
CC the 3816 base pair sequence of ADY97760, or a nucleic acid having 85% or
CC more sequence identity to ADY97759 or ADY97760; (4) an expression vector
CC (III) comprising (II) operably linked to regulatory sequences recognized
CC by a host cell (IV) transformed with the nucleic acid; (5) a host cell
CC comprising (II) or (III); (6) producing (I); (7) a polypeptide that
CC specifically binds to (I); and (8) inhibiting (M2) growth of a tumor
CC cell, involves contacting the tumor with a bioactive agent capable of
CC inhibiting TaHo activity. (I) is useful for screening a bioactive agent
CC capable of modulating (I), or screening for agents capable of interfering
CC with the binding of (I) and P21. (M1) is useful for treating an
CC individual with a cell cycle related disorder. (M2) is useful for
CC inhibiting growth of a tumor cell by a bioactive agent e.g. antisense

CC oligonucleotide. The present sequence represents the human tankyrase
CC homologue isotype 2.
XX
SQ Sequence 1240 AA;

Query Match 100.0%; Score 6464; DB 9; Length 1240;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RCSARRAGGCGGAGRGARVCAAGTAPDPVTAGSQAARALSASSPGGLALLAGPGLL 60
DB 1 RCSARRAGGCGGAGRGARVCAAGTAPDPVTAGSQAARALSASSPGGLALLAGPGLL 60
QY 61 RLLALLAVALAARIMSGRRACAGGGAACASAAAEAVEPAARELFACRNGDVERVKRLVTP 120
DB 61 RLLALLAVALAARIMSGRRACAGGGAACASAAAEAVEPAARELFACRNGDVERVKRLVTP 120
QY 121 EKNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEV 180
DB 121 EKNSRDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEV 180
QY 181 VNLRLRGADPNARDNNYTPHAAIKGKIDVICIVLLOHGAETIRNTDGTALDLADP 240
DB 181 VNLRLRGADPNARDNNYTPHAAIKGKIDVICIVLLOHGAETIRNTDGTALDLADP 240
QY 241 SAKAVLTGEYKDELLSARGSEKEMKALLTPLNVNCHASDGRKSTPLHLAGVNRVKI 300
DB 241 SAKAVLTGEYKDELLSARGSEKEMKALLTPLNVNCHASDGRKSTPLHLAGVNRVKI 300
QY 301 VQLLQHGADVHAKDGDVPLHNACSYGHEVTELLVKGACVNMADLWQTFPLHEAAS 360
DB 301 VQLLQHGADVHAKDGDVPLHNACSYGHEVTELLVKGACVNMADLWQTFPLHEAAS 360
QY 361 KNRVECSLLSYGADPTLLCHNKSALDAPTQLKRLAYEPKSHLLOAAREADVTR 420
DB 361 KNRVECSLLSYGADPTLLCHNKSALDAPTQLKRLAYEPKSHLLOAAREADVTR 420
QY 421 IKHLSLEWVNFHPOTHETALHCAASPYPRKQICELLURKGANINEKTEFLTPH 480
DB 421 IKHLSLEWVNFHPOTHETALHCAASPYPRKQICELLURKGANINEKTEFLTPH 480
QY 481 ASEKAHNDVVEVVKHAKVNALNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQ 540
DB 481 ASEKAHNDVVEVVKHAKVNALNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIISLQ 540
QY 541 FTALQMGNEVQQLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQ 600
DB 541 FTALQMGNEVQQLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQ 600
QY 601 STPLHFAAGVNRVSVVEYLLQHGADVHAKDGGVPLHNACSYGHEVVAELLVKGAVVN 660
DB 601 STPLHFAAGVNRVSVVEYLLQHGADVHAKDGGVPLHNACSYGHEVVAELLVKGAVVN 660
QY 661 VADLWKTPTLHFAAGKYEIKCLLQHGADPTKKNRDGNTPDLVKDGDITDIQLLRGD 720
DB 661 VADLWKTPTLHFAAGKYEIKCLLQHGADPTKKNRDGNTPDLVKDGDITDIQLLRGD 720
QY 721 AALLDAKKGCLARVKLSSPDNNVNCRDTPQGRHSTPLHLAGYNNLEVAEYLLQHGADV 780
DB 721 AALLDAKKGCLARVKLSSPDNNVNCRDTPQGRHSTPLHLAGYNNLEVAEYLLQHGADV 780
QY 781 AODKGGIPLHNAASYGHVDVAALLIKYNACVNATDKWAFPLHFAAKGRTQICALLA 840
DB 781 AODKGGIPLHNAASYGHVDVAALLIKYNACVNATDKWAFPLHFAAKGRTQICALLA 840
QY 841 HGADPTLKNQEGOTPLDLSADDDVALLTAAMPSPALPSCYKQVNLGVRSPGATADALS 900
DB 841 HGADPTLKNQEGOTPLDLSADDDVALLTAAMPSPALPSCYKQVNLGVRSPGATADALS 900
QY 901 SGPSPPSSLSAASLDNLGSGFSLSVSSSGTEGASSLEKKEVPVDFSIQFVRNLG 960
DB 901 SGPSPPSSLSAASLDNLGSGFSLSVSSSGTEGASSLEKKEVPVDFSIQFVRNLG 960

QY 961 LEHLMDFIEREQITLDVLVEMGHKELKEIGINAYCHRHKLKIGVERLISGQGLNPYLTL 1020
DB 961 LEHLMDFIEREQITLDVLVEMGHKELKEIGINAYCHRHKLKIGVERLISGQGLNPYLTL 1020
QY 1021 NTSSGGLTILDLSPDDKEFQSVVEEMQSTVREHRDGGHAGGIFNRYNLIKTKQVCNKKLW 1080
DB 1021 NTSSGGLTILDLSPDDKEFQSVVEEMQSTVREHRDGGHAGGIFNRYNLIKTKQVCNKKLW 1080
QY 1081 ERYTHRRKEVSEENHNHANERMLPHGSPFVNAILTHKGFDERHAYIGMGFAGIYFAENSS 1140
DB 1081 ERYTHRRKEVSEENHNHANERMLPHGSPFVNAILTHKGFDERHAYIGMGFAGIYFAENSS 1140
QY 1141 KSNQYVYGIGGGTGCPVHKDRSCYICHQRLFCRVTLGKSLQFSAMKMAHSPPGHHSVT 1200
DB 1141 KSNQYVYGIGGGTGCPVHKDRSCYICHQRLFCRVTLGKSLQFSAMKMAHSPPGHHSVT 1200
QY 1201 GRPSVNGLALAEYVYRGEQAYPEYLITYQIMRPEGWVDG 1240
DB 1201 GRPSVNGLALAEYVYRGEQAYPEYLITYQIMRPEGWVDG 1240

RESULT 5

AAB66290
ID AAB66290 standard; protein; 1262 AA.

XX AAB66290;

XX AC

DT 05-APR-2001 (first entry)

XX Human tankyrase2 clone consensus protein SEQ ID NO: 107.

XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;

XX inflammatory disorder.

XX Homo sapiens.

XX WO200100849-A1.

XX 04-JAN-2001.

XX 28-JUN-2000; 2000WO-US017827.

XX 29-JUN-1999; 99US-0141582P.

XX (ICOS-) ICOS CORP.

XX Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;

XX WPI; 2001-102896/11.

XX N-PSDB; AAF63930.

XX New tankyrase2 polypeptides, useful for treating conditions mediated by poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers, inflammatory and autoimmune disorders.

XX Example 2; Page 173-176; 242pp; English.

XX The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRF1, which is a telomere-specific binding protein. The regulation of telomere length, in which TRF1 has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory disorders

XX Sequence 1262 AA;

Query Match 98.6%; Score 6375.5; DB 4; Length 1262;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1225; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 6 RGAAGGCGAGRGARVCAAGTAPDPVTAGSQAARALSASSPGGLALLAGPGLLRLAL 65

Db 29 RGRGAGSPARGAR-GRGHGTAPDPVTAGSQARALASSFGGLALLAGFGLLRLLAL 87
Qy 66 LLAAVAARIMSGRRGAGGAAACASAAABEPAARELFEACRNGDVERKRLVTPKVS 125
Db 88 LLAAVAARIMSGRRGAGGAAACASAAABEPAARELFEACRNGDVERKRLVTPKVS 147
Qy 126 RDTAGRKSTPLHFAAGFGKDVVEYLLQNGANVQARDGGGLPLHNACSFGEAEVNNLL 185
Db 148 RDTAGRKSTPLHFAAGFGKDVVEYLLQNGANVQARDGGGLPLHNACSFGEAEVNNLL 207
Qy 186 RHGADPNARDNNWYTPLEHAAIKGKIDVICIVLLQHGAEPTIRNTDGTALDLDAPSAXV 245
Db 208 RHGADPNARDNNWYTPLEHAAIKGKIDVICIVLLQHGAEPTIRNTDGTALDLDAPSAXV 267
Qy 246 LTGEYKDDLEESARSGNEEKOMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 305
Db 268 LTGEYKDDLEESARSGNEEKOMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 327
Qy 306 QHGADVHAKDGDIVPLHNACSYGHEVTELLVKGACVNAWMDLWQFTPLHEAASKRVE 365
Db 328 QHGADVHAKDGDIVPLHNACSYGHEVTELLVKGACVNAWMDLWQFTPLHEAASKRVE 387
Qy 366 VCSLLSYGADPTLLNCHNKSAIDLAPTQPKERLAYEFKGHSLQAAAREADVTRIKKHL 425
Db 388 VCSLLSYGADPTLLNCHNKSAIDLAPTQPKERLAYEFKGHSLQAAAREADVTRIKKHL 447
Qy 426 SLEMVNFKHPTHTALHCAAAAPYKPKQICELLRKGANINEKTEFLTPLHVASEKA 485
Db 448 SLEMVNFKHPTHTALHCAAAAPYKPKQICELLRKGANINEKTEFLTPLHVASEKA 507
Qy 486 HNDVVVVVKEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYCGDPIISLQFTALQ 545
Db 508 HNDVVVVVKEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYCGDPIISLQFTALQ 567
Qy 546 MGENVQQLQEGISLGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDTEGRSTPLH 605
Db 568 MGENVQQLQEGISLGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDTEGRSTPLH 627
Qy 606 FAAGYNRVSVVEYLLQHGADVHAKDGGVLPLHNACSYGHEVTELLVKGAVVNVADLW 665
Db 628 FAAGYNRVSVVEYLLQHGADVHAKDGGVLPLHNACSYGHEVTELLVKGAVVNVADLW 687
Qy 666 KFTPLHEAAAKGYEICKLLQHGADPDKKRDGNTPLDLVKDGTDTQDLRGDAALLD 725
Db 688 KFTPLHEAAAKGYEICKLLQHGADPDKKRDGNTPLDLVKDGTDTQDLRGDAALLD 747
Qy 726 AAKGCLARVKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 785
Db 748 AAKGCLARVKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 807
Qy 786 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFPTPLHEAAKQRTQLCALLAHGADP 845
Db 808 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFPTPLHEAAKQRTQLCALLAHGADP 867
Qy 846 TLKQEGQTPDLVSADDSALLTAMPSPALPCYKQVNLNVGSPGATDALSGSPSS 905
Db 868 TLKQEGQTPDLVSADDSALLTAMPSPALPCYKQVNLNVGSPGATDALSGSPSS 927
Qy 906 PSSLSAASLNLGSGFSELSSVSSGTEGASSLEKKEKVPDPSITQFVNLGLHELM 965
Db 928 PSSLSAASLNLGSGFSELSSVSSGTEGASSLEKKEKVPDPSITQFVNLGLHELM 987
Qy 966 DIFEREQITDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISQOQGLNPLYTLNTSGS 1025
Db 988 DIFEREQITDVLVEMGHKELKEIGINAYGHRHKLIKGVERLISQOQGLNPLYTLNTSGS 1047
Qy 1026 GTILIDLSPDDKEFQSVSEEMQSTVREHRDGGHAGGINRNYNLIKQVCKNKKLWERYTH 1085
Db 1048 GTILIDLSPDDKEFQSVSEEMQSTVREHRDGGHAGGINRNYNLIKQVCKNKKLWERYTH 1107
Qy 1086 RRKEYSEENHNHANERMLPHGSPFVNAIHKGFDERHAYIGMGAGIYFAENSCKSNQY 1145

Db 1108 RRKEYSEENHNHANERMLPHGSPFVNAIHKGFDERHAYIGMGAGIYFAENSCKSNQY 1167
Qy 1146 VYIGGGTGCPCPHKDRSCYICHRQLLFCRVTLTKGSLQFSAMKMAHSPGHHSVTGRPSV 1205
Db 1168 VYIGGGTGCPCPHKDRSCYICHRQLLFCRVTLTKGSLQFSAMKMAHSPGHHSVTGRPSV 1227
Qy 1206 NGLALAEVYVYGEQAYPEYLITYQIMRPEGMVDG 1240
Db 1228 NGLALAEVYVYGEQAYPEYLITYQIMRPEGMVDG 1262
RESULT 6
ADR66429
ID ADR66429 standard; protein; 1287 AA.
XX ADR66429;
XX
XX 02-DEC-2004 (first entry)
XX Human prostatic carcinoma derived protein SEQ ID 283 #2.
DE human; cytostatic; diagnosis; prostatic cancer;
XX differential expression analysis.
KW Homo sapiens.
OS
XX
XX WO2004076614-A2.
PN
XX
PD 10-SEP-2004.
XX
XX 22-FEB-2004; 2004WO-DE000433.
PF
XX 27-FEB-2003; 2003DE-01009985.
PR 14-MAY-2003; 2003DE-01022134.
XX
XX (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
XX
XX Hinzmann B, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
PI Xinzhang L, Staub E;
XX
XX WPI; 2004-653386/63.
DR
XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
agents.
PT
XX
PS Claim 2; Page 1266; 1607pp; German.
XX
XX This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from

Qy	846	TLKNQGGTPLD	LVSA	DDVS	ADDS	VALL	TAAMP	PSAL	PS	CYK	PQV	LVNG	VRS	FGA	TAD	ALSS	GPSS	905	
Db	893	TLKNQGGTPLD	LVSA	DDVS	ADDS	VALL	TAAMP	PSAL	PS	CYK	PQV	LVNG	VRS	FGA	TAD	ALSS	GPSS	952	
Qy	906	PSLSAAS	SLDNL	SGSF	SEL	SSV	VSS	SGT	EGAS	LEK	KEV	GP	VD	FSIT	QFVR	NLGL	SHLM	965	
Db	953	PSLSAAS	SLDNL	SGSF	SEL	SSV	VSS	SGT	EGAS	LEK	KEV	GP	VD	FSIT	QFVR	NLGL	SHLM	1012	
Qy	966	DI	FERE	QITL	DV	LV	ENG	KEL	KE	IG	INAY	GHR	HKL	ING	VER	LIS	GGQGL	NPLYLT	1025

Qy	1026	GTTLIDLPDDKEFQSVVEERQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTH	10855
Db	1073	GTTLIDLPDDKEFQSVVEERQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTH	11323

1132	RRKEVSEENHNHANERMLFHGSPFVNAIHKGFDERHAYICGMFGAGIYFAENSSKSNQY	1192
1133	VYIGGGTGCPCVHKDRSCYICHRQLLFCRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV	1205
1146	VYIGGGTGCPCVHKDRSCYICHRQLLFCRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV	1205
1193	VYIGGGTGCPCVHKDRSCYICHRQLLFCRVTLGKSLQFSAMKWAHSPPGHHSVTGRPSV	1252
1206	NGLALAEYVIYRGEQAYPEYLITQIMRPEGVDG	1240
1253	NGLALAEYVIYRGEQAYPEYLITQIMRPEGVDG	1287
RESULT 7		
ADR66087	ADR66087 standard; protein; 1287 AA.	
XX	AC	ADR66087;
XX	AC	
DT	02-DEC-2004	(first entry)
XX	Human prostatic carcinoma derived protein SEQ ID 283 #1.	
DE	human; cytostatic; diagnosis; prostatic cancer;	
XX	differential expression analysis.	
KW	Homo sapiens.	
XX	WO2004076614-A2.	
XX	10-SEP-2004.	
XX	22-FEB-2004; 2004WO-DE000433.	
XX	27-FEB-2003; 2003DE-01009985.	
PR	14-MAY-2003; 2003DE-01022134.	
XX	(HINZ/) HINZMANN B.	
PA	(DAHL/) DAHL E.	
PA	(ROSE/) ROSENTHAL A.	
PA	(HERM/) HERMANN K.	
PA	(PILA/) PILARSKY C.	
XX	Hinzmann B, Rosenthal A, Hermann K, Pilarczyk C, Specht T;	
PI	Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;	
PI	Xinzhong L, Staub E;	
XX	WPI; 2004-653386/63.	
DR	New nucleic acids, and encoded proteins, from prostatic cancer tissue,	
XX	useful for diagnosis, treatment and in screening for specific binding	
PT	agents.	
PT	Claim 2; Page 764; 1607pp; German.	
XX	This invention describes novel cytostatic polynucleotide and polypeptide	

Claim 2; Page 764; 1607pp; German.

CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of a
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65803-ADR6954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.
XX
SQ Sequence 1287 AA;

Query Match 98.6%; Score 6375.5; DB 8; Length 1287;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1225; Conservative 1; Mismatches 8; Indels 1; Gaps 1;
QY 6 RGAAGGCGAAGRVGAAGTADPVTAGQAARALSASSPGGLALLLAGPGLLLRLLAL 65
DB 54 RGRGAGSPARGAR-GRGHGTADPVTAGQAARALSASSPGGLALLLAGPGLLLRLLAL 112
QY 66 LLAVAAARIMSGRRACGGGAACASAAEAPEAPARELFACRNGDVERVKRLVTPKVN 125
DB 113 LLAVAAARIMSGRRACGGGAACASAAEAPEAPARELFACRNGDVERVKRLVTPKVN 172
QY 126 RDTAGRKSTPLHPFAAGGRKDVVEYLLQNGANVOARDGGLIPLHNACSGFHAENVNLL 185
DB 173 RDTAGRKSTPLHPFAAGGRKDVVEYLLQNGANVOARDGGLIPLHNACSGFHAENVNLL 232
QY 186 RHGADPNARDNNVYPLHEAAIKGIDVCTVLLQHGAEPTIRNTDGTALDLADPSAKAV 245
DB 233 RHGADPNARDNNVYPLHEAAIKGIDVCTVLLQHGAEPTIRNTDGTALDLADPSAKAV 292
QY 246 LTGEYKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 305
DB 293 LTGEYKDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLL 352
QY 306 QHGADVHAKDKGLVPLHNACSGHYEVTELLVKGACVNMADLWQPTPLHBAASKNRVE 365
DB 353 QHGADVHAKDKGLVPLHNACSGHYEVTELLVKGACVNMADLWQPTPLHBAASKNRVE 412
QY 366 VCSLLLSYGADPTLLNCHNKAIDLATPTPKERLAYEPKGSLLQAAAREADVTRIKKHL 425
DB 413 VCSLLLSYGADPTLLNCHNKAIDLATPTPKERLAYEPKGSLLQAAAREADVTRIKKHL 472
QY 426 SLEWVNFKHPQTHETALHCAAAASPYPRKKQICELLRLKGANINEKTEFLTPLHVASEKA 485
DB 473 SLEWVNFKHPQTHETALHCAAAASPYPRKKQICELLRLKGANINEKTEFLTPLHVASEKA 532
QY 486 HNDVVEVVHGAEKVNDLNGQTSLSHRAAYCGHLQTCRLLLSYGCDDPNIISLQGFALQ 545
DB 533 HNDVVEVVHGAEKVNDLNGQTSLSHRAAYCGHLQTCRLLLSYGCDDPNIISLQGFALQ 592
QY 546 MGNENVQQLLEQISLGNSEADQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLH 605
DB 605 MGNENVQQLLEQISLGNSEADQLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLH 652
QY 606 FAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSGHYEVAELLVKHGAVVNVADLW 665
DB 653 FAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSGHYEVAELLVKHGAVVNVADLW 712
QY 666 KFTPLHEAAKAGKYEICKLLLOHGADPTTKNRDGNTPDLVKDGDTDIQLLLRGDAALLD 725
DB 713 KFTPLHEAAKAGKYEICKLLLOHGADPTTKNRDGNTPDLVKDGDTDIQLLLRGDAALLD 772
QY 726 AAKKGCLARVKKLSLSPDNVNCRTQGRHSTPLHLAAGYNLNLEVAEYLLQHGADVNAQDKG 785
DB 773 AAKKGCLARVKKLSLSPDNVNCRTQGRHSTPLHLAAGYNLNLEVAEYLLQHGADVNAQDKG 832
QY 786 GLIPLHNAASGYHVDVAALLIKYNACVNATDKWAFPLHBAASKGRTOCALLLAHGAADP 845
DB 833 GLIPLHNAASGYHVDVAALLIKYNACVNATDKWAFPLHBAASKGRTOCALLLAHGAADP 892
QY 846 TLKNQSGOTPLDLVSAADDYSALLTAAMPSPALSCYKQVLNGLVRSFGATADALSSGSS 905
DB 893 TLKNQSGOTPLDLVSAADDYSALLTAAMPSPALSCYKQVLNGLVRSFGATADALSSGSS 952
QY 906 PSSLSAASSLDNLSSGSELSVSSSGTEGASSLEKKEVPGVDFSIQTFVRNLGLEHLM 965
DB 953 PSSLSAASSLDNLSSGSELSVSSSGTEGASSLEKKEVPGVDFSIQTFVRNLGLEHLM 1012
QY 966 DIPERQITLDVLVEMGHKELKEIGINAYGHRHKLKGVVERLISGQGLNPYLTNTSGS 1025
DB 1013 DIPERQITLDVLVEMGHKELKEIGINAYGHRHKLKGVVERLISGQGLNPYLTNTSGS 1072
QY 1026 GTTILIDLSPDKEFQSVVEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTH 1085
DB 1073 GTTILIDLSPDKEFQSVVEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTH 1132
QY 1086 RRKEVSEENHNHANERMLFHGSPFVNALIHKGFDERHAYITGGMFGAGIYFAENSSKSNQY 1145
DB 1133 RRKEVSEENHNHANERMLFHGSPFVNALIHKGFDERHAYITGGMFGAGIYFAENSSKSNQY 1192
QY 1146 VYIGGGTGCVPVHKRSCYICHRQLLPFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1205
DB 1193 VYIGGGTGCVPVHKRSCYICHRQLLPFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSV 1252
QY 1206 NGLALAEYVIYRGEQAYPEYLIITYQIMRPEGMYDG 1240
DB 1253 NGLALAEYVIYRGEQAYPEYLIITYQIMRPEGMYDG 1287
RESULT 8
AAB66294
ID AAB66294 standard; protein; 1385 AA.
XX AAB66294;
XX AC AC
XX XX XX
DT 05-APR-2001 (first entry)
XX
DB Human tankyrase2 TANK2-LONG SEQ ID NO: 133.
XX
XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
XX inflammatory disorder.
XX Homo sapiens.
XX OS
XX WO200100849-A1.
PN
XX 04-JAN-2001.
XX
XX 28-JUN-2000; 2000WO-US017827.
PF
XX
XX 29-JUN-1999; 99US-0141582P.
PR
XX
XX (ICOS-) ICOS CORP.
PA
XX
XX Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;

XX WPI; 2001-102896/11.
DR N-PSDB; AAF63952.
XX
PT New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
PT inflammatory and autoimmune disorders.
XX
PS Claim 2; Page 191-194; 242pp; English.
XX
CC The present invention provides the protein and coding sequence for the
CC human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
CC ribosylation activity and is involved in the modification of TRF1, which
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders
XX
SQ Sequence 1385 AA;

Query Match 98.6%; Score 6375.5; DB 4; Length 1385;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1225; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

6 RGAAGGCAQAGARVGAAGHTAPDPVTAGSQAARALSASSPGGLALLIAGPGLLRLLAL 65
152 RSGRGASPGARG-GRGHTGAPDPVTAGSQAARALSASSPGGLALLIAGPGLLRLLAL 210
66 LLAVAAARIMSGRCAGGAAACASAAAEVPAARELFEACRNGDVERVKRLVTPKVN 125
211 LLAVAAARIMSGRCAGGAAACASAAAEVPAARELFEACRNGDVERVKRLVTPKVN 270
126 RDTAGRKSTPLHFAAGFRKDVVEYLLQNGANVQARDGGIPLHNACSPGHAENVLL 185
271 RDTAGRKSTPLHFAAGFRKDVVEYLLQNGANVQARDGGIPLHNACSPGHAENVLL 330
186 RHGADPNARDNNTPLHAAIKGIDVICVILQHGAEPTIRNTDGR TALDLADPSAKAV 245
331 RHGADPNARDNNTPLHAAIKGIDVICVILQHGAEPTIRNTDGR TALDLADPSAKAV 390
246 LTGEYKDDLELESARSNGNEERKMALLTPLNVNCHASDGRKSTPLHLAGYNRKIVQL 305
391 LTGEYKDDLELESARSNGNEERKMALLTPLNVNCHASDGRKSTPLHLAGYNRKIVQL 450
306 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNDLWQFTPLHAAASKRVE 365
451 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNDLWQFTPLHAAASKRVE 510
366 VCSLLSYGADPTLLNCHNKSAIDLAPTPQKRLAYEFKSHLSLQAAAREADVTRIKKHL 425
511 VCSLLSYGADPTLLNCHNKSAIDLAPTPQKRLAYEFKSHLSLQAAAREADVTRIKKHL 570
426 SLEWVNFKHPQTHETALHCAASPYPKRQICELLLRKGANINEKTEFLTPHVASEKA 485
571 SLEWVNFKHPQTHETALHCAASPYPKRQICELLLRKGANINEKTEFLTPHVASEKA 630
486 HNDVVVVVHKAHVNALDNIQOTSLHRAAYCGHLQTCRLLLSYGCDDNIIISLQGFALQ 545
631 HNDVVVVVHKAHVNALDNIQOTSLHRAAYCGHLQTCRLLLSYGCDDNIIISLQGFALQ 690
546 MGENVVOQLLOGLISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDTEGRQSTPLH 605
691 MGENVVOQLLOGLISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDTEGRQSTPLH 750
606 FAAGYNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNDLW 665
751 FAAGYNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNDLW 810
666 KFTPLHAAAKGKVEICKLLQHGADPTKKNRDGNTPLDLVKGDDTDIDQLLRGDAALLD 725
811 KFTPLHAAAKGKVEICKLLQHGADPTKKNRDGNTPLDLVKGDDTDIDQLLRGDAALLD 870

Qy 726 AAKGCLARVKLSSPDNVNCRDTQGRHSHTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 785
Db 871 AAKGCLARVKLSSPDNVNCRDTQGRHSHTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 930
Qy 786 GLIPLHNAASYGHVDVAALLIKYNACVNDKWAFTPLHAAQKGRTOQLCALLAHGADP 845
Db 931 GLIPLHNAASYGHVDVAALLIKYNACVNDKWAFTPLHAAQKGRTOQLCALLAHGADP 990
Qy 846 TLKNOEGQTPDLVSDADDVSALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSS 905
Db 991 TLKNOEGQTPDLVSDADDVSALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSS 1050
Qy 906 PSSLSAASSLDNLGSPSELSVVSSSGTGEASLEKEKVEPGVDFSIQTFVRNLGLEHLM 965
Db 1051 PSSLSAASSLDNLGSPSELSVVSSSGTGEASLEKEKVEPGVDFSIQTFVRNLGLEHLM 1110
Qy 966 DIFEREQITDLVLEMGHKEKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGS 1025
Db 1111 DIFEREQITDLVLEMGHKEKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGS 1170
Qy 1026 GTILIDLSPPDKBQSFQSVEEEMOSTVREHRDGHAGGIFNRYNLIKIOKVCNKKLWERYTH 1085
Db 1171 GTILIDLSPPDKBQSFQSVEEEMOSTVREHRDGHAGGIFNRYNLIKIOKVCNKKLWERYTH 1230
Qy 1086 RRKEVSEENHNANERMLFHGSPFVNAIHHKGFDERHAYIGMFGAGIYFAENSCKSNQY 1145
Db 1231 RRKEVSEENHNANERMLFHGSPFVNAIHHKGFDERHAYIGMFGAGIYFAENSCKSNQY 1290
Qy 1146 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1205
Db 1291 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1350
Qy 1206 NGLALAEVLYIRGEQAYPEYLITVQIMRPSGWDG 1240
Db 1351 NGLALAEVLYIRGEQAYPEYLITVQIMRPSGWDG 1385

RESULT 9
AAB66288
ID AAB66288 standard; protein; 1169 AA.
XX AAB66288;
AC
XX
DT 05-APR-2001 (first entry)
XX
DE Human tankyrase2 clone consensus protein SEQ ID NO: 101.
XX
KW Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
KW inflammatory disorder.
XX
OS Homo sapiens.
XX
FN WO200100849-A1.
XX
PD 04-JAN-2001.
XX
PF 28-JUN-2000; 2000WO-US017827.
XX
PR 29-JUN-1999; 99US-0141582P.
XX
PA (ICOS-) ICOS CORP.
XX
PI Christenson E, Denaggio AJ, Goldman PS, Mcelligott DL;
XX WPI; 2001-102896/11.
DR N-PSDB; AAF63952.
XX
PT New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
XX inflammatory and autoimmune disorders.
XX
XX Example 1; Page 162-1665; 242pp; English.
XX

CC The present invention provides the protein and coding sequence for the
CC human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
CC ribosylation activity and is involved in the modification of TRF1, which
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders
XX
SQ Sequence 1169 AA;
Query Match 94.7%; Score 6121; DB 4; Length 1169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 72 ARMSGRCAGGGGAACASAAAEVPAARELFELACRNGDVERVKRLVTPKVNSTRDTAGR 131
Db 1 ARMSGRCAGGGGAACASAAAEVPAARELFELACRNGDVERVKRLVTPKVNSTRDTAGR 60
Qy 132 KSTPLHPAAGFGRKDVVEYLLONGANVQARDGGGLIPLHNACSFHAEVNVNLLRHGADP 191
Db 61 KSTPLHPAAGFGRKDVVEYLLONGANVQARDGGGLIPLHNACSFHAEVNVNLLRHGADP 120
Qy 192 NARDNNWYTPLHEAAIKGKIDVCTVLLQHGAEPTIRNTDGTALDADPSAKAVLTGEYK 251
Db 121 NARDNNWYTPLHEAAIKGKIDVCTVLLQHGAEPTIRNTDGTALDADPSAKAVLTGEYK 180
Qy 252 KDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADV 311
Db 181 KDELLESARSNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLQHGADV 240
Qy 312 HAKDKGLVPLHNACSYGHVEVTELLVKHGACVNAMDWQFTPLHAEASKNRVEVCSSL 371
Db 241 HAKDKGLVPLHNACSYGHVEVTELLVKHGACVNAMDWQFTPLHAEASKNRVEVCSSL 300
Qy 372 SYGADPTLLCHNKSAIDLAFTPOLKERLAYEFKHSLLQAAAEADVTRIKHLSLEWVN 431
Db 301 SYGADPTLLCHNKSAIDLAFTPOLKERLAYEFKHSLLQAAAEADVTRIKHLSLEWVN 360
Qy 432 FKHPQTHETALHCAASAPYKPKKQICELLRLKGANINEKTEFLTPHLVASEKAHNDVVE 491
Db 361 FKHPQTHETALHCAASAPYKPKKQICELLRLKGANINEKTEFLTPHLVASEKAHNDVVE 420
Qy 492 VVYHKAQNALDNLGQTSLHRAAYCGHLOTCLRLLSYGCDPNIIISLQGTALOMGNENV 551
Db 421 VVYHKAQNALDNLGQTSLHRAAYCGHLOTCLRLLSYGCDPNIIISLQGTALOMGNENV 480
Qy 552 QOLLQEGISLGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYN 611
Db 481 QOLLQEGISLGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYN 540
Qy 612 RVSVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVNADLWKFTPLH 671
Db 541 RVSVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVNADLWKFTPLH 600
Qy 672 EAAAKGYEICKLLQHGADPTKKNRGNTPLDLVKDGDITDIQDLRGDAALLDAKKGC 731
Db 601 EAAAKGYEICKLLQHGADPTKKNRGNTPLDLVKDGDITDIQDLRGDAALLDAKKGC 660
Qy 732 LARVKLSSPDNNVNCRTQGRHSTPLHLAAGYNLEVAEYLLQHGADVNAQDKGLIPLH 791
Db 661 LARVKLSSPDNNVNCRTQGRHSTPLHLAAGYNLEVAEYLLQHGADVNAQDKGLIPLH 720
Qy 792 NAASGYHVDVAALLIKYNACVNATDKWAFPLHAEAAQKRTQLCALLLAHGAADPTLKNQE 851
Db 721 NAASGYHVDVAALLIKYNACVNATDKWAFPLHAEAAQKRTQLCALLLAHGAADPTLKNQE 780
Qy 852 GQTPDLVSDVDSALLTAAAPPSPALPSCKYKQVINGVRSPGATADALSSGPPSPSSLSA 911
Db 781 GQTPDLVSDVDSALLTAAAPPSPALPSCKYKQVINGVRSPGATADALSSGPPSPSSLSA 840
Qy 912 ASSLDNLGSGSFSELSSVSSSGTEGASLEKKEVPGVDFPSITQFVRNLGLEHLMDFERE 971

Db 841 ASSLDNLGSGSFSELSSVSSSGTEGASLEKKEVPGVDFPSITQFVRNLGLEHLMDFERE 900
Qy 972 QITLDVLVEMGHKELKEIGINAYGHRHKLKGVVERLISGOOGLNPYLTNTSGSGTILID 1031
Db 901 QITLDVLVEMGHKELKEIGINAYGHRHKLKGVVERLISGOOGLNPYLTNTSGSGTILID 960
Qy 1032 LSPDDKEFQSVSEEMOSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVS 1091
Db 961 LSPDDKEFQSVSEEMOSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVS 1020
Qy 1092 EENHNHANERMLFHGSPFVNALIIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGG 1151
Db 1021 EENHNHANERMLFHGSPFVNALIIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGG 1080
Qy 1152 GTGCPVHKORSVCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSVNGLALA 1211
Db 1081 GTGCPVHKORSVCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSVNGLALA 1140
Qy 1212 EYVIYRGEQAYPEYLITYQIMRPEGWVG 1240
Db 1141 EYVIYRGEQAYPEYLITYQIMRPEGWVG 1169
RESULT 10
AAB66278
ID AAB66278 standard; protein; 1169 AA.
XX
AC AAB66278;
DT 05-APR-2001 (first entry)
DE Human tankyrase2 related protein sequence SEQ ID NO: 2.
XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
KW inflammatory disorder.
XX Homo sapiens.
XX WO200100849-A1.
PN 04-JAN-2001.
XX 28-JUN-2000; 2000WO-US017827.
PF 29-JUN-1999; 99US-0141582P.
PR (ICOS-) ICOS CORP.
XX Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
PI WPI; 2001-102896/11.
DR N-PSDB; AAF63837.
XX New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
PT inflammatory and autoimmune disorders.
XX Disclosure; Page 109-113; 242pp; English.
PS The present invention provides the protein and coding sequence for the
XX human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
CC ribosylation activity and is involved in the modification of TRF1, which
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders
XX SQ Sequence 1169 AA;
Query Match 94.7%; Score 6121; DB 4; Length 1169;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 ARIMSGRCAGGAAACACAAAAEVEPAARELFEACRNGDVERVKRLVTPKVNRSRDTAGR 131
Db 1 ARIMSGRCAGGAAACACAAAAEVEPAARELFEACRNGDVERVKRLVTPKVNRSRDTAGR 60
Qy 132 KSTPLHPAAGFGRKDVVYLLQNGANVQARDGGGLPLHNACSFHGAHVNNLLRHGADP 191
Db 61 KSTPLHPAAGFGRKDVVYLLQNGANVQARDGGGLPLHNACSFHGAHVNNLLRHGADP 120
Qy 192 NARDNNWYTPLHEAAIKGKIDVICVLLQHGAEPTIRNTDGRDALTADPSAKAVLTGEYK 251
Db 121 NARDNNWYTPLHEAAIKGKIDVICVLLQHGAEPTIRNTDGRDALTADPSAKAVLTGEYK 180
Qy 252 KDELLESARSNGEKNMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADV 311
Db 181 KDELLESARSNGEKNMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADV 240
Qy 312 HAKOKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLL 371
Db 241 HAKOKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCSLLL 300
Qy 372 SYGADPTLLNCHNSAIDLATPOLKERLAYEFKGHSLLQAREADVTRIKKHSLEMVN 431
Db 301 SYGADPTLLNCHNSAIDLATPOLKERLAYEFKGHSLLQAREADVTRIKKHSLEMVN 360
Qy 432 FKHPQTHETALHCAAASYPKPKKOICELLRRKGANINEKTEFLTPLHVASEKAHNDVVE 491
Db 361 FKHPQTHETALHCAAASYPKPKKOICELLRRKGANINEKTEFLTPLHVASEKAHNDVVE 420
Qy 492 VVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLSYGCDFNIIISLQGTALQNGENV 551
Db 421 VVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLSYGCDFNIIISLQGTALQNGENV 480
Qy 552 QQLQEGISLGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGROSTPLHPAAGYN 611
Db 481 QQLQEGISLGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGROSTPLHPAAGYN 540
Qy 612 RVSVVEYLQHGADVHAKDGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLH 671
Db 541 RVSVVEYLQHGADVHAKDGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLH 600
Qy 672 EAAAKGKYEICKLLQHGADPTKKNRQDPTPLDLVKQDGTIDQLLRGDAALLDAKKG 731
Db 601 EAAAKGKYEICKLLQHGADPTKKNRQDPTPLDLVKQDGTIDQLLRGDAALLDAKKG 660
Qy 732 LARVKLSSPDVNCVCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLH 791
Db 661 LARVKLSSPDVNCVCRDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLH 720
Qy 792 NAASVGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRQOLCALLAHGADPTLKNQE 851
Db 721 NAASVGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRQOLCALLAHGADPTLKNQE 780
Qy 852 GQTPDLVSDVSDVALLTAAMPSPALPCYKQVNLGVRSFGATADALSSGSPSPSLSA 911
Db 781 GQTPDLVSDVSDVALLTAAMPSPALPCYKQVNLGVRSFGATADALSSGSPSPSLSA 840
Qy 912 ASSLDNLSSGSPSELSSVSSSGTEGASSLEKKEVPGVDFSTQFVRNIGLHLMIDIPERE 971
Db 841 ASSLDNLSSGSPSELSSVSSSGTEGASSLEKKEVPGVDFSTQFVRNIGLHLMIDIPERE 900
Qy 972 QITLDLVEMGHKELKEIGINAYGHRHKLKGVVERLISGQGLNPYLTNTSGSTILID 1031
Db 901 QITLDLVEMGHKELKEIGINAYGHRHKLKGVVERLISGQGLNPYLTNTSGSTILID 960
Qy 1032 LSPDDKEFSVEEEMQSTVREHRDGGHAGGIFNRYNIIKIQKCNKCLWERYTHRRKEVS 1091
Db 961 LSPDDKEFSVEEEMQSTVREHRDGGHAGGIFNRYNIIKIQKCNKCLWERYTHRRKEVS 1020
Qy 1092 BENNHANERMLFHGSPFNVAIIHKGFDERHAYTGMFGAGIYFAENSCKSNQVYVIGIG 1151
Db 1021 BENNHANERMLFHGSPFNVAIIHKGFDERHAYTGMFGAGIYFAENSCKSNQVYVIGIG 1080

Qy 1152 GTGCPVHKDRSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSVNGLALA 1211
Db 1081 GTGCPVHKDRSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTGRPSVNGLALA 1140
Qy 1212 EYVIYRGEQAYPEYLITTYQIMRPEGWVDG 1240
Db 1141 EYVIYRGEQAYPEYLITTYQIMRPEGWVDG 1169
RESULT 11
AAB66295
ID AAB66295 standard; protein; 1166 AA.
XX AAB66295;
XX AC
XX 05-APR-2001 (first entry)
DT
XX Human tankyrase2 TANK2-SHORT SEQ ID NO: 135.
DE Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasia; aging;
KW inflammatory disorder.
KW Homo sapiens.
XX OS
XX WO200100849-A1.
FN
XX 04-JAN-2001.
PD
XX 28-JUN-2000; 2000WO-US017827.
XX PF
XX 29-JUN-1999; 99US-0141582P.
PR
XX (ICOS-) ICOS CORP.
PA
XX Christenson E, Demaggio AJ, Goldman PS, Mcelligott DL;
PI WPI; 2001-102896/11.
DR N-PSDB; AAF63953.
XX
XX New tankyrase2 polypeptides, useful for treating conditions mediated by
PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
PT inflammatory and autoimmune disorders.
XX
XX Claim 3; Page 200-203; 242pp; English.
XX
XX The present invention provides the protein and coding sequence for the
CC human tankyrase2 protein. This is found in two different versions,
CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-
CC ribosylation activity and is involved in the regulation of telomere
CC is a telomere-specific binding protein. The regulation of telomere
CC length, in which TRF1 has a role, is linked to ageing and cancer. The
CC sequences are useful in the treatment of cancers and inflammatory
CC disorders
CC
SQ Sequence 1166 AA;
Query Match 94.5%; Score 6108; DB 4; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 75 MSGRCAGGAGGAAACAAAAEVEPAARELFEACRNGDVERVKRLVTPKVNRSRDTAGRST 134
Db 1 MSGRCAGGAGGAAACAAAAEVEPAARELFEACRNGDVERVKRLVTPKVNRSRDTAGRST 60
Qy 135 PLHPAAGFGRKDVVYLLQNGANVQARDGGGLPLHNACSFHGAHVNNLLRHGADPNAR 194
Db 61 PLHPAAGFGRKDVVYLLQNGANVQARDGGGLPLHNACSFHGAHVNNLLRHGADPNAR 120
Qy 195 DNWNTYTPLHEAAIKGKIDVICVLLQHGAEPTIRNTDGRDALTADPSAKAVLTGEYKDE 254
Db 121 DNWNTYTPLHEAAIKGKIDVICVLLQHGAEPTIRNTDGRDALTADPSAKAVLTGEYKDE 180
Qy 255 LLESARSNGEKNMALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAK 314

Db 181 LLESARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAK 240
Qy 315 DKGLVPLHNACSYGHEVTELLVKGACVAMDLWQFTPLHEAASKNRVEVCSSLISYG 374
Db 241 DKGLVPLHNACSYGHEVTELLVKGACVAMDLWQFTPLHEAASKNRVEVCSSLISYG 300
Qy 375 ADPTLLCHNKSAIDLAPTOLKRLAYEFKSHLSLQAAREADVTRIKKHLSELMVNFKH 434
Db 301 ADPTLLCHNKSAIDLAPTOLKRLAYEFKSHLSLQAAREADVTRIKKHLSELMVNFKH 360
Qy 435 POTHETALHCAASAPYPRKQICELLRLKGNINKEKTFPLTHVASEKAHNDVVEVV 494
Db 361 POTHETALHCAASAPYPRKQICELLRLKGNINKEKTFPLTHVASEKAHNDVVEVV 420
Qy 495 KHEAKVNALDNLGQTSLHRAAYCCHLOTCLRLLSYGCDPNIIISLQGTALQMGNEVQOL 554
Db 421 KHEAKVNALDNLGQTSLHRAAYCCHLOTCLRLLSYGCDPNIIISLQGTALQMGNEVQOL 480
Qy 555 LQEGISLGNSEADQLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRV 614
Db 481 LQEGISLGNSEADQLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNRV 540
Qy 615 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGVVNVADLWKFTPLHEAA 674
Db 541 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGVVNVADLWKFTPLHEAA 600
Qy 675 AKGYEICKLLQHGADPTKKNRDNPTPLDVLKDGDDTDIQLLGRDAALLDAKKGCLAR 734
Db 601 AKGYEICKLLQHGADPTKKNRDNPTPLDVLKDGDDTDIQLLGRDAALLDAKKGCLAR 660
Qy 735 VKLSSPDNVNCRDTQGRHSTPLHAGYNNLVAEYLLQHGADVNAQDGGLIPLHNA 794
Db 661 VKLSSPDNVNCRDTQGRHSTPLHAGYNNLVAEYLLQHGADVNAQDGGLIPLHNA 720
Qy 795 SYGHVDVAALLIKYNACVNATDKWFTPLHAAQKGRTOCLCALLAHGADPTLKNQEGQT 854
Db 721 SYGHVDVAALLIKYNACVNATDKWFTPLHAAQKGRTOCLCALLAHGADPTLKNQEGQT 780
Qy 855 PLDLVSADDDVSALLTAAMPSPALPCYKQVINGVRSPGATADALSSGSPSSLSAASS 914
Db 781 PLDLVSADDDVSALLTAAMPSPALPCYKQVINGVRSPGATADALSSGSPSSLSAASS 840
Qy 915 LDNLGSGFSELSVSSSGTEGASLEKKEVPGVDPSITQVRNLGLEHLMDFPERQIT 974
Db 841 LDNLGSGFSELSVSSSGTEGASLEKKEVPGVDPSITQVRNLGLEHLMDFPERQIT 900
Qy 975 LDVLVEMGHKELKEIGINAYGHRHKLKGVBERLISGQGLNPYLTLNTSGGTLIDLSP 1034
Db 901 LDVLVEMGHKELKEIGINAYGHRHKLKGVBERLISGQGLNPYLTLNTSGGTLIDLSP 960
Qy 1035 DDKEFQSVSEEMQSTVREHRDGHAGGIFNRYNLIKIKQVCNKKLWERYTHRRKEVSEEN 1094
Db 961 DDKEFQSVSEEMQSTVREHRDGHAGGIFNRYNLIKIKQVCNKKLWERYTHRRKEVSEEN 1020
Qy 1095 HNANERMLFHGSPFVNAILHKGFDERHAYITGFMFGAGIYPAENSXSNQVYIGGGTG 1154
Db 1021 HNANERMLFHGSPFVNAILHKGFDERHAYITGFMFGAGIYPAENSXSNQVYIGGGTG 1080
Qy 1155 CPVHKDRSCYICHRQLLFCRVTLGKSLFQPSAMKWAHSPRGHSHVGTGSPVNGLALAEYV 1214
Db 1081 CPVHKDRSCYICHRQLLFCRVTLGKSLFQPSAMKWAHSPRGHSHVGTGSPVNGLALAEYV 1140
Qy 1215 IYRGEQAYPEYLITYQIMRPEGMDG 1240
Db 1141 IYRGEQAYPEYLITYQIMRPEGMDG 1166

RESULT 12
ADRI4792
ID ADRI4792 standard; protein; 1166 AA.
XX
AC ADRI4792;

XX 04-NOV-2004 (first entry)
XX Amino acid sequence of human MAPCAX orthologue #24.
XX adenomatous polyposis coli protein; APC; axin pathway;
XX modifier of APC and axin; MAPCAX; cancer; human.
XX Homo sapiens.
XX WO2004066948-A2.
XX 12-AUG-2004.
XX 28-JAN-2004; 2004WO-US002338.
XX 29-JAN-2003; 2003US-0443484P.
XX 11-FEB-2003; 2003US-0447358P.
XX 10-APR-2003; 2003US-0461789P.
XX 14-MAY-2003; 2003US-0470684P.
XX 19-JUN-2003; 2003US-0479650P.
XX (EXEL-) EXELIXIS INC.
XX Gendreau SB, Morablanco EL, Lickteig K, Zhang H;
XX WPI; 2004-580849/56.
XX N-PSDB; ADRI4766.
XX Identifying a candidate adenomatous polyposis coli protein (APC) and axin
XX pathways modulating agent for treating cancer by contacting an assay
XX system comprising a modifier of APC and axin polypeptide or nucleic acid
XX with a test agent.
XX Example 1; SEQ ID NO 50; 199pp; English.
XX The specification describes a method for identifying a candidate
XX adenomatous polyposis coli protein (APC) and axin pathways modulating
XX agents. The method comprises providing an assay system comprising a
XX modifier of APC and axin (MAPCAX) polypeptide or nucleic acid, contacting
XX the assay system with a test agent under conditions where, except for the
XX presence of the test agent, the system provides a reference activity, and
XX detecting a test agent-biased activity of the assay system, where a
XX difference between the test agent-biased activity and the reference
XX activity identifies the test agent as a candidate APC and axin pathways
XX modulating agent. The method is useful in identifying a candidate
XX adenomatous polyposis coli protein (APC) and a pathways modulating agent,
XX which are useful for preparing a composition for diagnosing or treating
XX cancer. The present sequence represents a human orthologue of a
XX Caenorhabditis elegans MAPCAX polypeptide. The sequence was identified
XX using BLAST analysis.
XX Sequence 1166 AA;
XX Query Match 94.5%; Score 6108; DB 8; Length 1166;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 75 MSGRRACAGGGAACASAAAEEAVEPAARELFEACRNGDVERVKRLVTPKVNSTRDTAGRKST 134
Db 1 MSGRRACAGGGAACASAAAEEAVEPAARELFEACRNGDVERVKRLVTPKVNSTRDTAGRKST 60
Qy 135 PLHPAAGFGKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVLLRHGADPNAR 194
Db 61 PLHPAAGFGKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVLLRHGADPNAR 120
Qy 195 DNWNYTPLHEAAIKGKIDVCIVLLOHCAEPTIRNTDGTALDPSAKAVLTGEYKDE 254
Db 121 DNWNYTPLHEAAIKGKIDVCIVLLOHCAEPTIRNTDGTALDPSAKAVLTGEYKDE 180
Qy 255 LLESARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAK 314
Db 181 LLESARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAK 240

QY 315 DKGLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLSYG 374
DB 241 DKGLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLSYG 300
QY 375 ADPTLLCHNKSAIDLAPTQPKERLAYEFKSHSLQAAREADVTRIKKHLSEMVNPKH 434
DB 301 ADPTLLCHNKSAIDLAPTQPKERLAYEFKSHSLQAAREADVTRIKKHLSEMVNPKH 360
QY 435 PQTHTALHCAASPYPRKQICELLARKGANINEKTEFLTPLHVASEKAHNDVVEVV 494
DB 361 PQTHTALHCAASPYPRKQICELLARKGANINEKTEFLTPLHVASEKAHNDVVEVV 420
QY 495 KHEAKVNADNLGQTSLHRAAYCGHLCRLLLSYGCDPNIISLQGTALQWGNENVOQL 554
DB 421 KHEAKVNADNLGQTSLHRAAYCGHLCRLLLSYGCDPNIISLQGTALQWGNENVOQL 480
QY 555 LOEGISLGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRV 614
DB 481 LOEGISLGNSEADROLLEAAKAGDVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNRV 540
QY 615 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVAEILLVKHGVNVDLWKFTPLHEAA 674
DB 541 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVAEILLVKHGVNVDLWKFTPLHEAA 600
QY 675 AKGYEICKLLQHGADPTKKNRDNQNTPLDLVKDGTDIQDLRGDAALLDAKKGCLAR 734
DB 601 AKGYEICKLLQHGADPTKKNRDNQNTPLDLVKDGTDIQDLRGDAALLDAKKGCLAR 660
QY 735 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNA 794
DB 661 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNA 720
QY 795 SYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTOICALLIAGADPTLKNQEGOT 854
DB 721 SYGHVDVAALLIKYNACVNATDKWAFTPLHEAAQKGRTOICALLIAGADPTLKNQEGOT 780
QY 855 PLDIVSADVDVALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSPSSLSAASS 914
DB 781 PLDIVSADVDVALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSPSSLSAASS 840
QY 915 LDNLGSGFSELSVVSSSGTEGASLEKKEVPGVDFSTITQFVRNLGLEHLMDFPEREQIT 974
DB 841 LDNLGSGFSELSVVSSSGTEGASLEKKEVPGVDFSTITQFVRNLGLEHLMDFPEREQIT 900
QY 975 LDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTINTSGGTILIDLSP 1034
DB 901 LDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTINTSGGTILIDLSP 960
QY 1035 DKKEFQSVVEEMQSVREHRDGHAGGIFNRYNLIKIOKNCNKILWERYTHRRKEVSEEN 1094
DB 961 DKKEFQSVVEEMQSVREHRDGHAGGIFNRYNLIKIOKNCNKILWERYTHRRKEVSEEN 1020
QY 1095 HNHNAMRLFHGSPFVNAI IHKGFDERHAYIGGMFAGIYFAENSSKSNQYVYIGGGTG 1154
DB 1021 HNHNAMRLFHGSPFVNAI IHKGFDERHAYIGGMFAGIYFAENSSKSNQYVYIGGGTG 1080
QY 1155 CPVHKDRSCYICHRQLLCRVTLGKSFLOFSAMKMAHSPPGHSHSVTGRPSVNGLALBYV 1214
DB 1081 CPVHKDRSCYICHRQLLCRVTLGKSFLOFSAMKMAHSPPGHSHSVTGRPSVNGLALBYV 1140
QY 1215 IYRGEQAYPEVILITYQIMRPEGWDG 1240
DB 1141 IYRGEQAYPEVILITYQIMRPEGWDG 1166

RESULT 13
ID AAB27211 standard; protein; 1166 AA.
XX
AC AAB27211;
XX
DT 27-FEB-2001 (first entry)

XX Human tankyrase II protein sequence SEQ ID NO: 6.
DE Human; tankyrase II; telomere length; signal transduction.
KW Homo sapiens.
OS
FH Key Location/Qualifiers
FT Misc-difference 124 /note= "encoded by TTA"
FT Misc-difference 125 /note= "encoded by TAC"
FT
XX WO200061813-A1.
PN 19-OCT-2000.
PD
XX 10-APR-2000; 2000WO-US009558.
PF 09-APR-1999; 99US-0128577P.
PR 13-APR-1999; 99US-0129123P.
XX (GERO-) GERON CORP.
PA Morin GB, Funk WD, Piatyszek MA;
XX WPI; 2000-679503/66.
XX N-PSDB; AAC66825.
XX Novel mammalian Tankyrase II polypeptide and the polynucleotide encoding the polypeptide useful for modulating or maintaining telomere length, replicative capacity, apoptosis, chromosome packing or gene expression.
XX Claim 4; Fig 4; 52pp; English.
XX The present sequence is a version of the human tankyrase II protein sequence. The protein is thought to be involved in signal transduction in the cell, and to have binding activity for other telomere-associated proteins. It is possible that it plays a role in the regulation of telomere length, thus affecting the replicative ability of the cell. The protein is useful for ribosylating target proteins, for determining tankyrase II binding activity in a sample, and for modulating telomere length in a cell
XX Sequence 1166 AA;

Query Match 94.2%; Score 6092; DB 3; Length 1166;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1164; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 75 MSGRCAGGGAACASAAAEVPAARELFEACRNGDVERVKRLVTPKVNSRDTAGRKST 134
DB 1 MSGRCAGGGAACASAAAEVPAARELFEACRNGDVERVKRLVTPKVNSRDTAGRKST 60
QY 135 PLHFAAGFGRKDVVEYLLQNGANYQARDGGLIPLHNACSFHAEVNNLLRHGADPNAR 194
DB 61 PLHFAAGFGRKDVVEYLLQNGANYQARDGGLIPLHNACSFHAEVNNLLRHGADPNAR 120
QY 195 DNWNTYPLHEAAIKGKIDVCIVLLQHGAEPIRNTDGRALTDLADPSAKAVLTGEYKDE 254
DB 121 DNWNTYPLHEAAIKGKIDVCIVLLQHGAEPIRNTDGRALTDLADPSAKAVLTGEYKDE 180
QY 255 LLESARSGNEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIKIVOLLQHGADVHAK 314
DB 181 LLESARSGNEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIKIVOLLQHGADVHAK 240
QY 315 DKGLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLSYG 374
DB 241 DKGLVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSLLSYG 300
QY 375 ADPTLLCHNKSAIDLAPTQPKERLAYEFKSHSLQAAREADVTRIKKHLSEMVNPKH 434
DB 301 ADPTLLCHNKSAIDLAPTQPKERLAYEFKSHSLQAAREADVTRIKKHLSEMVNPKH 360

Qy 435 PQTHTALHCAAAAPYPRKQICELLIRKKGANINKEKTEFLTPHLHVASEKAHNDVVEVV 494
Db 361 PQTHTALHCAAAAPYPRKQICELLIRKKGANINKEKTEFLTPHLHVASEKAHNDVVEVV 420
Qy 495 KHEAKVALDNLGQTSLHRAAYCGHLOTCTLLLSYGCDPNIIISLOGFTALQMGNEVQOL 554
Db 421 KHEAKVALDNLGQTSLHRAAYCGHLOTCTLLLSYGCDPNIIISLOGFTALQMGNEVQOL 480
Qy 555 LQEGISLGNSEADQLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRV 614
Db 481 LQEGISLGNSEADQLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRV 540
Qy 615 VVEYLLQHGADVHAKDGGGLVPLHNACSYGHEVVAELLVKHGAVNVADLWKFTPLHEAA 674
Db 541 VWEYLLQHGADVHAKDGGGLVPLHNACSYGHEVVAELLVKHGAVNVADLWKFTPLHEAA 600
Qy 675 AKGYEICKLLQHGADPTKQNRDGNTPDLVDKGDGTDIQLLRGDAALLDAKKGCLAR 734
Db 601 AKGYEICKLLQHGADPTKQNRDGNTPDLVDKGDGTDIQLLRGDAALLDAKKGCLAR 660
Qy 735 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNA 794
Db 661 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNA 720
Qy 795 SYGHVDVAALLIKYNACVNATDKWAFPLHEAAQKGTQLCALLLAHGAADPTLKNQEGQT 854
Db 721 SYGHVDVAALLIKYNACVNATDKWAFPLHEAAQKGTQLCALLLAHGAADPTLKNQEGQT 780
Qy 855 PLDLVSADDSVALLTAAMPSPALSCYKQVINGVRSPGATADALSSGSPSSLSAAS 914
Db 781 PLDLVSADDSVALLTAAMPSPALSCYKQVINGVRSPGATADALSSGSPSSLSAAS 840
Qy 915 LDNLSGSFSELSVVSSSGTGASLSKEVPGVDFTQVRNLGLEHLMIDIFEREQIT 974
Db 841 LDNLSGSFSELSVVSSSGTGASLSKEVPGVDFTQVRNLGLEHLMIDIFEREQIT 900
Qy 975 LDVLVEMGHKELKIGINAYGHRHLKGVVERLISGQGLNPYTLTNTSGSTLIDLSP 1034
Db 901 LDVLVEMGHKELKIGINAYGHRHLKGVVERLISGQGLNPYTLTNTSGSTLIDLSP 960
Qy 1035 DDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLTIKQVCKKWLERYTHRRKEVSEEN 1094
Db 961 DDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLTIKQVCKKWLERYTHRRKEVSEEN 1020
Qy 1095 HNANERMLFHGSPFVNAIHKGFDERHAYTIGMGFAGIYPAENSCKSNQVYVYGGG 1154
Db 1021 HNANERMLFHGSPFVNAIHKGFDERHAYTIGMGFAGIYPAENSCKSNQVYVYGGG 1080
Qy 1155 CPVHKRSCYIYCHQRLFCRVTLGKSLQFSAMKVAHSPGHHVTCRPSVNGLALAEYV 1214
Db 1081 CPVHKRSCYIYCHQRLFCRVTLGKSLQFSAMKVAHSPGHHVTCRPSVNGLALAEYV 1140
Qy 1215 IYRGEQAYPEYLIYQIMRPEGVDG 1240
Db 1141 IYRGEQAYPEYLIYQIMRPEGVDG 1166
ESULT 14
BP69457
D ABP69457 standard; protein, 1166 AA.
X
C ABP69457;
X
T 20-JAN-2003 (first entry)
X Human polypeptide SEQ ID NO 1504.
X Human; genome mapping; gene therapy; food supplement; virus; fungus;
cell-proliferative disorder; neurodegenerative disease; bacterial;
Parkinson's disease; Alzheimer's disease; autoimmune disease;
multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;

KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
OS Homo sapiens.
PN W0200270539-A2.
XX 12-SEP-2002.
XX 05-MAR-2002; 2002WO-US005095.
XX 05-MAR-2001; 2001US-00799451.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Zhou P, Goodrich RW, Auundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX WPI; 2002-759812/82.
DR N-PSDB; ABZ11674.
DR New polynucleotides comprising sequences assembled from expressed
sequence tags (ESTs), useful for treating cell-proliferative, or platelet
neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
or coagulation disorders.
PS Claim 9; SEQ ID NO 1504; 1012pp + Sequence Listing; English.
XX The invention relates to an isolated polynucleotide (I) comprising a
nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burn, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1166 AA;

Query Match 94.2%; Score 6088; DB 5; Length 1166;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 75 MSGRRCAGGAGCAACAAAAEVEPAARELFEACRNGDVERVKRLVTPEKNSRDTAGRKST 134
Db 1 MSGRRCAGGAGCAACAAAAEVEPAARELFEACRNGDVERVKRLVTPEKNSRDTAGRKIH 60
Qy 135 PLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHGAEEVNNLLRHGADPNAR 194
Db 61 PLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHGAEEVNNLLRHGADPNAR 120
Qy 195 DNWNTPLHEAAIKGKIDVCIVLLOHGAETIRNTDGTALDPSAKAVLTGEYKDE 254
Db 121 DNWNTPLHEAAIKGKIDVCIVLLOHGAETIRNTDGTALDPSAKAVLTGEYKDE 180
Qy 255 LLESARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLOHGAADVHAK 314
Db 181 LLESARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLLOHGAADVHAK 240
Qy 315 DKGDVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSELLLSYG 374
Db 241 DKGDVPLHNACSYGHEVTELLVKHGACVNMADLWQFTPLHEAASKNRVEVCSELLLSYG 300

Qy	255	LLSARSGNBEKMWALLTPTLVNWNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAK	314
Db	181	LLSARSGNBEKMWALLTPTLVNWNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAK	240
Qy	315	DKGDLVPLHNACS YGHYEVTELLVKGHCAGVNMDLWQFTPLHEAASKNRVEVCSLLLSYG	374
Db	241	DKGDLVPLHNACS YGHYEVTELLVKGHCAGVNMDLWQFTPLHEAASKNRVEVCSLLLSYG	300
Qy	375	ADPTLLNCHNKS AIDLAPTPOLKERLAYEPKSHSLQAAREADVTRI KKHLSLEWVNFKH	434
Db	301	ADPTLLNCHNKS AIDLAPTPOLKERLAYEPKSHSLQAAREADVTRI KKHLSLEWVNFKH	360
Qy	435	POTHETALHCAAAS PYPKRQIICELLIRKGANINEKTKFPLTPLHVASEKAHNDVVEVVV	494
Db	361	POTHETAXHCAAAS PYPKRQIICELLIRKGAIXNEKTKFPLTPLHVASEKAHNDVVEVVV	420
Qy	495	KHEAKVNALNLGOTS LHRAA YCGHLQTCRLLSYGCDPNIISLQGF TALQMGNEVQOL	554
Db	421	KHEAKVNALNLGOTS LHRAA YCGHLQTCRLLSYGCDPNIISLQGF TALQMGNEVQOL	480
Qy	555	LQEGISLGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRV	614
Db	481	LQEGISLGNSEADROLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRV	540
Qy	615	VVEYLLQHGADVHAKDKGGLVPLHNACS YGHYEVAEILLVKGAVNVNADLWKETPLHEAA	674
Db	541	VVEYLLQHGADVHAKDKXLLVPLHNACS YGHYEVAEILLVKGAVNVNADLWKETPLHEAA	600
Qy	675	AKGYEYICKULLQHGADPTKKNRDNPTPLDVKDGDDTDIQLLRGDAALLDAAKKGCLAR	734
Db	601	AKGYEYICKULLQHGADPTKKNRDNPTPLDVKDGDDTDIQLLRGDAALLDAAKKGCLAR	660
Qy	735	VKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAA	794
Db	661	VKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAA	720
Qy	795	SYGHVDVVAALLIKYNACVNATDKWAFPLHEAAQKGRTOLCALLLAHAGDPTLKNQEGQT	854
Db	721	SYGHVDVVAALLIKYNACVNATDKWAFPLHEAAQKGRTOLCALLLAHAGDPTLKNQEGQT	780
Qy	855	PLDLVSADDSALLTAAMPSPALPSCYKQVPLNGVRSPGATADALSGSPSPSSLSAASS	914
Db	781	PLDLVSADDSALLTAAMPSPALPSCYKQVPLNGVRSPGATADALSGSPSPSSLSAASS	840
Qy	915	LDNLSSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSI TOFVRNLGLEHLMDFPEREQIT	974
Db	841	LDNLSSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSI TOFVRXLGLEHLMDFPEREQIT	900
Qy	975	LDVLVEMGHKELKEIGINAYGHRHKLKGYVERLISGOQGLNPYLTNTSGSGTILIDLSP	1034
Db	901	LDVLVEMGHKELKEIGINAYGHRHKLKGYVERLISGOQGLNPYLTNTSGSGTILIDLSP	960
Qy	1035	DDKEFQSVBEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLMERYTHRRKEYSEEN	1094
Db	961	DDKEFQSVBEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLMERYTHRRKEYSEEN	1020
Qy	1095	HNHANERMLPHGSPFVNAAI THKGDFERHAYTGMFGAGIYPAENSSKSNQYVYIGGGTG	1154
Db	1021	HNHANERMLPHGSPFVNAAI THKGDFERHAYTGMFGAGIYPAENSSKSNQYVYIGGGTG	1080
Qy	1155	CPVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPPGHHSVTGRPSVNGLA LAEYV	1214
Db	1081	CPVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPPGHHSVTGRPSVNGLA LAEYV	1140
Qy	1215	IYRGEQAYPEYLITYQIMRPEGWVDG	1240
Db	1141	IYRGEQAYPEYLITYQIMRPEGWVDG	1166

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:51:56 ; Search time 153.857 Seconds
(without alignments)
3733.253 Million call updates/sec

Title: US-10-616-101-4

Perfect score: 6464

Sequence: 1 RCSARRGAAGGQAGRGARV.....AYPEYLITYQIMRPGMVDG 1240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pcp:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pcp:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pcp:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pcp:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pcp:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6464	100.0	1240	5	US-10-616-101-4 Sequence 4, Appli
2	6375.5	98.6	1262	4	US-10-199-937-107 Sequence 107, App
3	6375.5	98.6	1385	4	US-10-199-937-133 Sequence 133, App
4	6121	94.7	1169	4	US-10-199-937-2 Sequence 2, Appli
5	6121	94.7	1169	4	US-10-199-937-101 Sequence 101, App
6	6108	94.5	1166	3	US-09-972-115A-6 Sequence 6, Appli
7	6108	94.5	1166	4	US-10-163-587A-15 Sequence 15, Appl
8	6108	94.5	1166	4	US-10-199-937-135 Sequence 135, App
9	5877	90.9	1227	3	US-09-849-602-26 Sequence 26, Appl
10	5766	89.2	1100	5	US-10-616-101-8 Sequence 8, Appli
11	5760	89.1	1100	5	US-10-616-101-11 Sequence 11, Appl
12	5656	87.5	1083	5	US-10-616-101-12 Sequence 12, Appli
13	5602	86.7	1074	3	US-09-509-196A-2 Sequence 2, Appli
14	5582	86.4	1065	5	US-10-616-101-3 Sequence 3, Appli
15	5452	84.3	1267	3	US-09-972-115A-4 Sequence 4, Appli
16	5103.5	79.0	1327	3	US-09-841-835-2 Sequence 2, Appli
17	5103.5	79.0	1327	3	US-09-972-115A-8 Sequence 8, Appli
18	5103.5	79.0	1327	4	US-10-199-937-4 Sequence 4, Appli
19	5031.5	77.8	1333	3	US-09-972-115A-2 Sequence 2, Appli
20	4102	63.5	784	4	US-10-199-937-89 Sequence 89, Appl
21	4005	62.0	1181	6	US-11-097-143-9474 Sequence 9474, Ap
22	3997	61.8	1181	4	US-10-199-937-139 Sequence 139, App
23	3959	61.2	756	4	US-10-199-937-91 Sequence 91, Appl
24	3938	60.9	802	3	US-09-964-899-41 Sequence 41, Appl
25	3938	60.9	802	5	US-10-975-523-41 Sequence 41, Appl
26	3307	51.2	949	3	US-09-841-835-10 Sequence 10, Appl
27	2913	45.1	583	5	US-10-616-101-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-10-616-101-4
; Sequence 4, Application US/10616101
; Publication No. US20050074825A1

; GENERAL INFORMATION:

; APPLICANT: Luo, Ying

; APPLICANT: Chan, Eva

; APPLICANT: Xu, Xiang

; APPLICANT: Huang, Betty

; APPLICANT: Ossoskaya, Valeria

; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods c

; FILE REFERENCE: RIGL-010CIP3

; CURRENT APPLICATION NUMBER: US/10/616.101

; CURRENT FILING DATE: 2003-07-08

; PRIOR APPLICATION NUMBER: US 09/843,159

; PRIOR FILING DATE: 2001-04-25

; PRIOR APPLICATION NUMBER: US 09/696,668

; PRIOR FILING DATE: 2000-10-25

; PRIOR APPLICATION NUMBER: US 09/427,154

; PRIOR FILING DATE: 1999-10-25

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 1240

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-616-101-4

Query Match	100.0%;	Score	6464;	DB	5;	Length	1240;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	1240;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	RCSARRGAAGGQAGRGARVGAAGTAPDPVTAGSQAARALSASSPGGLALLAGPGLLL	60				
Db	1	RCSARRGAAGGQAGRGARVGAAGTAPDPVTAGSQAARALSASSPGGLALLAGPGLLL	60				
Qy	61	RLALLLAVAAARTMSGRRCCAGGGAACASAAAEEVEPAARELFACRNGDVERVKRLVTP	120				
Db	61	RLALLLAVAAARTMSGRRCCAGGGAACASAAAEEVEPAARELFACRNGDVERVKRLVTP	120				
Qy	121	EKNSRDTAGRKSTPLHFAAGFGKDVVEYLLQNGANVQARDGGLIPLHNACSGFHAEV	180				
Db	121	EKNSRDTAGRKSTPLHFAAGFGKDVVEYLLQNGANVQARDGGLIPLHNACSGFHAEV	180				
Qy	181	VNLLRHGADPNARDNNWNTPLHAAATKGKIDVCIVLQHGAEPTIRNTDGTALDLADP	240				
Db	181	VNLLRHGADPNARDNNWNTPLHAAATKGKIDVCIVLQHGAEPTIRNTDGTALDLADP	240				
Qy	241	SAKAVLTGEYKKDBLLSARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI	300				
Db	241	SAKAVLTGEYKKDBLLSARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI	300				

Db 241 SAKAVITGEYKDELLESARSNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKI 300
Qy 301 VOLLQHGADVHAKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAAS 360
Db 301 VOLLQHGADVHAKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAAS 360
Qy 361 KNRVEVCSLLSYGADPTLLNCHNSAIDLAPTOLKERLAYEFKGHSLLOAAREADVTR 420
Db 361 KNRVEVCSLLSYGADPTLLNCHNSAIDLAPTOLKERLAYEFKGHSLLOAAREADVTR 420
Qy 421 IKGHLSEWVNFKHPQTHETALHCAASAPYPRKQICELLRKGANINEKTEFTPLHV 480
Db 421 IKGHLSEWVNFKHPQTHETALHCAASAPYPRKQICELLRKGANINEKTEFTPLHV 480
Qy 481 ASEKAHNDVVEVVKHAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNISLQ 540
Db 481 ASEKAHNDVVEVVKHAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNISLQ 540
Qy 541 FTALQMGNEVQOLLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGR 600
Db 541 FTALQMGNEVQOLLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGR 600
Qy 601 STPLHFAAGYNRVSVEVYLLQHGADVHAKGDLVPLHNACSYGHEVVAELLVKHGAVN 660
Db 601 STPLHFAAGYNRVSVEVYLLQHGADVHAKGDLVPLHNACSYGHEVVAELLVKHGAVN 660
Qy 661 VADLWKFTPLHEAAKGYEICKLLQHGADPTKKNRDGNTPLDLVKQDGTDIQDLRGD 720
Db 661 VADLWKFTPLHEAAKGYEICKLLQHGADPTKKNRDGNTPLDLVKQDGTDIQDLRGD 720
Qy 721 AALLDAKGGCLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVN 780
Db 721 AALLDAKGGCLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVN 780
Qy 781 AADKGGGLPLHNAASYGHVDVAALLIKYNACVNAATDKWAFPLHEAAQKGTQOLCALLIA 840
Db 781 AADKGGGLPLHNAASYGHVDVAALLIKYNACVNAATDKWAFPLHEAAQKGTQOLCALLIA 840
Qy 841 HGADPTLNQEGQTPDLVSDVDSALLITAMPSPALPSCYKQVNLGVRSPGATADALS 900
Db 841 HGADPTLNQEGQTPDLVSDVDSALLITAMPSPALPSCYKQVNLGVRSPGATADALS 900
Qy 901 SGSPSSLSAASLDNLGSGFSELSSVSSSGTEGASLEKKEVPGVDFSTQFVRNLG 960
Db 901 SGSPSSLSAASLDNLGSGFSELSSVSSSGTEGASLEKKEVPGVDFSTQFVRNLG 960
Qy 961 LEHLMDIFEREQITLDVLVEVGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTL 1020
Db 961 LEHLMDIFEREQITLDVLVEVGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYLTL 1020
Qy 1021 NTSGGTTLIDLSDDKBFQSVVEEMQSTVREHRRDGGHAGGIFNRYNLIKIQKVCNKKLW 1080
Db 1021 NTSGGTTLIDLSDDKBFQSVVEEMQSTVREHRRDGGHAGGIFNRYNLIKIQKVCNKKLW 1080
Qy 1081 ERYTHRRKEVSEENHNHANEMLFHGSPFVNAI IHKGDFERHAYIGGMFGAGIYFAENSS 1140
Db 1081 ERYTHRRKEVSEENHNHANEMLFHGSPFVNAI IHKGDFERHAYIGGMFGAGIYFAENSS 1140
Qy 1141 KSNQVYVIGGTCPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPPGHHSVT 1200
Db 1141 KSNQVYVIGGTCPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPPGHHSVT 1200
Qy 1201 GRPSVNGALAEYVYRGEQAYPEYLITYQIMRPEGVMDG 1240
Db 1201 GRPSVNGALAEYVYRGEQAYPEYLITYQIMRPEGVMDG 1240

RESULT 2

US-10-199-937-107

Sequence 107, Application US/10199937

Publication No. US20030190739A1

GENERAL INFORMATION:

APPLICANT: CHL-Anderson, Erik

APPLICANT: DeMaggio, Anthony J.
APPLICANT: Goldman, Phyllis S.
TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
FILE REFERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/606,035
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/141,582
NUMBER OF SEQ ID NOS: 178
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 107
LENGTH: 1262
TYPE: PRT
ORGANISM: Homo sapiens
US-10-199-937-107

Query Match 98.6%; Score 6375.5; DB 4; Length 1262;

Best Local Similarity 99.2%; Pred. No. 0;

Matches 1225; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

Qy 6 RGAAGGQAGQAGARVGAAGHTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLRLLAL 65
Db 29 RGRGAGSPARGAR-GRGHGTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLRLLAL 87
Qy 66 LLAVAAARIMSGRRRCAGGGAACASAAAAEVEPAARELFECACRNDGVERVKRLVTPKVS 125
Db 88 LLAVAAARIMSGRRRCAGGGAACASAAAAEVEPAARELFECACRNDGVERVKRLVTPKVS 147
Qy 126 RTAGRKSTPLHFAAGFGKDVVEYLLQNGANVQARDGGLIPLHNACSGHAEVNVNLL 185
Db 148 RDTAGRKSTPLHFAAGFGKDVVEYLLQNGANVQARDGGLIPLHNACSGHAEVNVNLL 207
Qy 186 RHGADPNARDNNYTPLEHAAIKGKIDVCILVLOHGAETPIRNTDGTALDADPSAKAV 245
Db 208 RHGADPNARDNNYTPLEHAAIKGKIDVCILVLOHGAETPIRNTDGTALDADPSAKAV 267
Qy 246 LTGEYKDKELLESARSNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLL 305
Db 268 LTGEYKDKELLESARSNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLL 327
Qy 306 QHGADVHAKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVE 365
Db 328 QHGADVHAKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVE 387
Qy 366 VCSLLLSYGADPTLLNCHNSAIDLAPTOLKERLAYEFKGHSLLOAAREADVTRIKKHL 425
Db 388 VCSLLLSYGADPTLLNCHNSAIDLAPTOLKERLAYEFKGHSLLOAAREADVTRIKKHL 447
Qy 426 SLEWVNFKHPQTHETALHCAASAPYPRKQICELLRKGANINEKTEFTPLHVAESEA 485
Db 448 SLEWVNFKHPQTHETALHCAASAPYPRKQICELLRKGANINEKTEFTPLHVAESEA 507
Qy 486 HNDVVEVVKHAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNISLQGTALQ 545
Db 508 HNDVVEVVKHAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNISLQGTALQ 567
Qy 546 MGNENVQOLLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLH 605
Db 568 MGNENVQOLLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLH 627
Qy 606 FAAGYNRVSVEVYLLQHGADVHAKGDLVPLHNACSYGHEVVAELLVKHGAVNVNADLW 665
Db 628 FAAGYNRVSVEVYLLQHGADVHAKGDLVPLHNACSYGHEVVAELLVKHGAVNVNADLW 687
Qy 666 KFTPLHEAAKGYEICKLLQHGADPTKKNRDGNTPLDLVKQDGTDIQDLRGDAALLD 725
Db 688 KFTPLHEAAKGYEICKLLQHGADPTKKNRDGNTPLDLVKQDGTDIQDLRGDAALLD 747
Qy 726 AAKKGCLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 785

Db 748 AAKGCLARVKLSSPDNNCRDTPQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 807
Qy 786 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWATPLHEAAQKGRTOCALLLAHAGADP 845
Db 808 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWATPLHEAAQKGRTOCALLLAHAGADP 867
Qy 846 TLKQEGQTPDLVSADDDVSALLTAAMPSPALPSYKQVNLGVRSFGATADALSSGSPSS 905
Db 868 TLKQEGQTPDLVSADDDVSALLTAAMPSPALPSYKQVNLGVRSFGATADALSSGSPSS 927
Qy 906 PSSLSAASLDNLSSPSSSVSSSGTEGASLEKKEVPGVDPSITQFVRNLGLEHLM 965
Db 928 PSSLSAASLDNLSSPSSSVSSSGTEGASLEKKEVPGVDPSITQFVRNLGLEHLM 987
Qy 966 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGS 1025
Db 988 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGS 1047
Qy 1026 GTILIDLPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERVTH 1085
Db 1048 GTILIDLPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERVTH 1107
Qy 1086 RRKEVSEENHNHANERMLFHGSPFFVNAIHHKGFDERHAYIGGMFGAGIYFAENSSKSNOY 1145
Db 1108 RRKEVSEENHNHANERMLFHGSPFFVNAIHHKGFDERHAYIGGMFGAGIYFAENSSKSNOY 1167
Qy 1146 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1205
Db 1168 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1227
Qy 1206 NGLALAEYVIYRGEQAYPEYLITYQIMRPEGVDG 1240
Db 1228 NGLALAEYVIYRGEQAYPEYLITYQIMRPEGVDG 1262

RESULT 3
US-10-199-937-133
; Sequence 133, Application US/10199937
; Publication No. US20030190749A1
GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: Damaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 133
; LENGTH: 1385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-133

Query Match 98.6%; Score 6375.5; DB 4; Length 1385;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1225; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

Qy 6 RGAAGGQAGRGARVGAHGTAPDPVTAGSQAARALSASSPGCLALLLAGPGLLRLLAL 65
Db 152 RGSRGAGSPARGAR-GRGHGTAPDPVTAGSQAARALSASSPGCLALLLAGPGLLRLLAL 210
Qy 66 LLAATAARIMSGRCGGGACASAAAEEAVEPAARELFEACNGDVERKRVTPTEKNS 125
Db 211 LLAATAARIMSGRCGGGACASAAAEEAVEPAARELFEACNGDVERKRVTPTEKNS 270
Qy 126 RDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHGAEEVNNLL 185

Db 271 RDTAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHGAEEVNNLL 330
Qy 186 RHGADPNARDNNWNTPLHEAAIKGKIDVICIVLLQHGABPTIRNTDGR TALDLADPSAKAV 245
Db 331 RHGADPNARDNNWNTPLHEAAIKGKIDVICIVLLQHGABPTIRNTDGR TALDLADPSAKAV 390
Qy 246 LTGEYKDELLESARSGNEEKOMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLL 305
Db 391 LTGEYKDELLESARSGNEEKOMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVQLLL 450
Qy 306 OHGADVHAKDGLVPLHNACSYGHEVTELLVKGHCANAMDLWQFPLHEAASKNVE 365
Db 451 OHGADVHAKDGLVPLHNACSYGHEVTELLVKGHCANAMDLWQFPLHEAASKNVE 510
Qy 366 VCSLLSYGADPTLLNCHNKSAIDLAPTPOLKERLAYEFKGHSLLOAAREADVTRIKKHL 425
Db 511 VCSLLSYGADPTLLNCHNKSAIDLAPTPOLKERLAYEFKGHSLLOAAREADVTRIKKHL 570
Qy 426 SLEWVNFKHPQTHETALHCAAAAPYKPKQICEILLRKGANINEKTEFLTPLHVASEKA 485
Db 571 SLEWVNFKHPQTHETALHCAAAAPYKPKQICEILLRKGANINEKTEFLTPLHVASEKA 630
Qy 486 HNDVVEVVKHAKVNALDNLGOTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGTALQ 545
Db 631 HNDVVEVVKHAKVNALDNLGOTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGTALQ 690
Qy 546 MGENVQOLLOEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDTEGROSTPLH 605
Db 691 MGENVQOLLOEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDTEGROSTPLH 750
Qy 606 FAAGYNRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGHEVTELLVKGHCANAMDLW 665
Db 751 FAAGYNRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGHEVTELLVKGHCANAMDLW 810
Qy 666 KFTPLHEAAAKGKYEICKLLQHGADPTKQORDGNTPDLVKDGTDOILLRGAALLD 725
Db 811 KFTPLHEAAAKGKYEICKLLQHGADPTKQORDGNTPDLVKDGTDOILLRGAALLD 870
Qy 726 AAKGCLARVKLSSPDNNCRDTPQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 785
Db 871 AAKGCLARVKLSSPDNNCRDTPQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKG 930
Qy 786 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWATPLHEAAQKGRTOCALLLAHAGADP 845
Db 931 GLIPLHNAASYGHVDVAALLIKYNACVNATDKWATPLHEAAQKGRTOCALLLAHAGADP 990
Qy 846 TLKQEGQTPDLVSADDDVSALLTAAMPSPALPSYKQVNLGVRSFGATADALSSGSPSS 905
Db 991 TLKQEGQTPDLVSADDDVSALLTAAMPSPALPSYKQVNLGVRSFGATADALSSGSPSS 1050
Qy 906 PSSLSAASLDNLSSPSSSVSSSGTEGASLEKKEVPGVDPSITQFVRNLGLEHLM 965
Db 1051 PSSLSAASLDNLSSPSSSVSSSGTEGASLEKKEVPGVDPSITQFVRNLGLEHLM 1110
Qy 966 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGS 1025
Db 1111 DIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGS 1170
Qy 1026 GTILIDLPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERVTH 1085
Db 1171 GTILIDLPDDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERVTH 1230
Qy 1086 RRKEVSEENHNHANERMLFHGSPFFVNAIHHKGFDERHAYIGGMFGAGIYFAENSSKSNOY 1145
Db 1231 RRKEVSEENHNHANERMLFHGSPFFVNAIHHKGFDERHAYIGGMFGAGIYFAENSSKSNOY 1290
Qy 1146 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1205
Db 1291 VYIGGGTGPCVHKDRSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSV 1350
Qy 1206 NGLALAEYVIYRGEQAYPEYLITYQIMRPEGVDG 1240

QY 132 KSTPLHFAAGFKDKVVEYLLQNGANVQARDGGIPLHNACSFGEAEVNVNLLLRHGADP 191
 Db 61 KSTPLHFAAGFKDKVVEYLLQNGANVQARDGGIPLHNACSFGEAEVNVNLLLRHGADP 120
 QY 192 NARDWNNTPLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYK 251
 Db 121 NARDWNNTPLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYK 180
 QY 252 KDELLESARSNGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVTIQLLQHGADV 311
 Db 181 KDELLESARSNGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVTIQLLQHGADV 240
 QY 312 HAKDGDVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVVCSSL 371
 Db 241 HAKDGDVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVVCSSL 300
 QY 372 SYGADPTLLCHNKSAIDLAFTPOLKERLAYEFKSHLLQAAREADVTRIKKHLSEWVN 431
 Db 301 SYGADPTLLCHNKSAIDLAFTPOLKERLAYEFKSHLLQAAREADVTRIKKHLSEWVN 360
 QY 432 FXHPQTHETALHCAASPYPKRKOICELLRLKGANINEKTEFLPLHVASEKAHNDVVE 491
 Db 361 FXHPQTHETALHCAASPYPKRKOICELLRLKGANINEKTEFLPLHVASEKAHNDVVE 420
 QY 492 VVVHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGTALQNGENV 551
 Db 421 VVVHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGTALQNGENV 480
 QY 552 QLLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYN 611
 Db 481 QLLQEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYN 540
 QY 612 RVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVEALLVKGAVNVNADLWKFPTLH 671
 Db 541 RVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVEALLVKGAVNVNADLWKFPTLH 600
 QY 672 EAAAKGKYEICKLLQHGADPTKQNRDGNTPDLVKDGDITDQLLARGDAALLDAKKG 731
 Db 601 EAAAKGKYEICKLLQHGADPTKQNRDGNTPDLVKDGDITDQLLARGDAALLDAKKG 660
 QY 732 LARVKLSPPDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLH 791
 Db 661 LARVKLSPPDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLH 720
 QY 792 NAASGHVDVVAALLIKYNACVNATDKWFTPLHEAAQKRTQICALLAHAGADPTLKQ 851
 Db 721 NAASGHVDVVAALLIKYNACVNATDKWFTPLHEAAQKRTQICALLAHAGADPTLKQ 780
 QY 852 GOTPLDVSADVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSLSA 911
 Db 781 GOTPLDVSADVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSLSA 840
 QY 912 ASSLNLGSGSFSELSSVSSSGTEGASSLEKKEVPGVDSITQFVRNLGLEHMDIFERE 971
 Db 841 ASSLNLGSGSFSELSSVSSSGTEGASSLEKKEVPGVDSITQFVRNLGLEHMDIFERE 900
 QY 972 QITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISQOQGLNPYTLNTSGSGTILID 1031
 Db 901 QITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISQOQGLNPYTLNTSGSGTILID 960
 QY 1032 LSPDDKEFOSVEEEMOSTVREHRDGHAGGIFNRVNLKIQKVCNKLWERVTHRRKEVS 1091
 Db 961 LSPDDKEFOSVEEEMOSTVREHRDGHAGGIFNRVNLKIQKVCNKLWERVTHRRKEVS 1020
 QY 1092 EENHNHANERMLFHGSPFVNALIHKGFDERHAYIGGMFGAGIYFAENSCKSNQYVYIGG 1151
 Db 1021 EENHNHANERMLFHGSPFVNALIHKGFDERHAYIGGMFGAGIYFAENSCKSNQYVYIGG 1080
 QY 1152 GTGCPVHKDRSCYICHRQLLFCRVTLGKSFLOPSAMKMAHSPGHHSVTGRPSVNGLALA 1211
 Db 1081 GTGCPVHKDRSCYICHRQLLFCRVTLGKSFLOPSAMKMAHSPGHHSVTGRPSVNGLALA 1140
 QY 1212 EYVIYRGEQAYPEYLITYQIMRPEGMDVG 1240

Db 1141 EYVIYRGEQAYPEYLITYQIMRPEGMDVG 1169
 RESULT 6
 US-09-972-115A-6
 ; Sequence 6, Application US/09972115A
 ; Publication No. US20030032769A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Geron Corporation
 ; APPLICANT: Gregg, Morin B.
 ; APPLICANT: Walcer, Funk D.
 ; APPLICANT: Miczyzlaw, Piatyszek A.
 ; TITLE OF INVENTION: A Second Mammalian Telomerase
 ; FILE REFERENCE: 080/003C
 ; CURRENT APPLICATION NUMBER: US/09/972,115A
 ; CURRENT FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: US 60/128,577
 ; PRIOR FILING DATE: 2000-04-10
 ; PRIOR APPLICATION NUMBER: US 60/129,123
 ; PRIOR FILING DATE: 1999-04-13
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 1166
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-972-115A-6
 Query Match 94.5%; Score 6108; DB 3; Length 1166;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 75 MSGRCAGGACGACASAAAEVPEARELFEACRNGDVERVKELVTPEKVNSTRDTAGRKST 134
 Db 1 MSGRCAGGACGACASAAAEVPEARELFEACRNGDVERVKELVTPEKVNSTRDTAGRKST 60
 QY 135 PLHFAAGFKDKVVEYLLQNGANVQARDGGIPLHNACSFGEAEVNVNLLLRHGADPNAR 194
 Db 61 PLHFAAGFKDKVVEYLLQNGANVQARDGGIPLHNACSFGEAEVNVNLLLRHGADPNAR 120
 QY 195 DNWNTYPLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYK 254
 Db 121 DNWNTYPLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYK 180
 QY 255 LLESARSNGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVTIQLLQHGADVNAK 314
 Db 181 LLESARSNGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVTIQLLQHGADVNAK 240
 QY 315 DKGDVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVVCSSL 374
 Db 241 DKGDVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVVCSSL 300
 QY 375 ADPTLLCHNKSAIDLAFTPOLKERLAYEFKSHLLQAAREADVTRIKKHLSEWVNFXH 434
 Db 301 ADPTLLCHNKSAIDLAFTPOLKERLAYEFKSHLLQAAREADVTRIKKHLSEWVNFXH 360
 QY 435 POTHTALHCAASPYPKRKOICELLRLKGANINEKTEFLPLHVASEKAHNDVVEV 494
 Db 361 POTHTALHCAASPYPKRKOICELLRLKGANINEKTEFLPLHVASEKAHNDVVEV 420
 QY 495 KHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGTALQNGENV 554
 Db 421 KHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIISLQGTALQNGENV 480
 QY 555 LOEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYN 614
 Db 481 LOEGISLGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYN 540
 QY 615 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVEALLVKGAVNVNADLWKFPTLHEA 674
 Db 541 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVEALLVKGAVNVNADLWKFPTLHEA 600

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QY 675 AKGYEICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDILLRGDAALLDAAKKGCLAR 734
DB 601 AKGYEICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDILLRGDAALLDAAKKGCLAR 660
QY 735 VKKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGILPLHNA 794
DB 661 VKKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGILPLHNA 720
QY 795 SYGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQT 854
DB 721 SYGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQT 780
QY 855 PLDLVSADVDVALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASS 914
DB 781 PLDLVSADVDVALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASS 840
QY 915 LDNLGSFSELSSVSSSGTEGASSLEKKEVPVDFPSITQFVRNLGLEHLMDFEREQIT 974
DB 841 LDNLGSFSELSSVSSSGTEGASSLEKKEVPVDFPSITQFVRNLGLEHLMDFEREQIT 900
QY 975 LDVLEVMGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPLYTLNTSGSGTILDLSP 1034
DB 901 LDVLEVMGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPLYTLNTSGSGTILDLSP 960
QY 1035 DDKEFQSVBEEMOSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEEN 1094
DB 961 DDKEFQSVBEEMOSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEEN 1020
QY 1095 HNHANERMLPHGSPFFVNAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGGGTG 1154
DB 1021 HNHANERMLPHGSPFFVNAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGGGTG 1080
QY 1155 CPVHKDRSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSVNGLALAEYV 1214
DB 1081 CPVHKDRSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSVNGLALAEYV 1140
QY 1215 IYRGEQAYPEYLITYQIMRPEGWVDG 1240
DB 1141 IYRGEQAYPEYLITYQIMRPEGWVDG 1166

RESULT 7
US-10-163-587A-15
; Sequence 15, Application US/10163587A
; Publication No. US2003009263A1
; GENERAL INFORMATION:
; APPLICANT: Oliveira, Marcos
; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING
; FILE REFERENCE: 50229-306
; CURRENT APPLICATION NUMBER: US/10/163,587A
; PRIOR FILING DATE: 2003-01-10
; PRIOR FILING DATE: 2003-01-10
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-587A-15

Query Match 94.5%; Score 6108; DB 4; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 MSGRRCAGGAAACASAAAEVPAARELFACRNGDVERVKRLVTPBKVNSRDTAGRKST 134
DB 1 MSGRRCAGGAAACASAAAEVPAARELFACRNGDVERVKRLVTPBKVNSRDTAGRKST 60
QY 135 PLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHGAEVVNLRLRHGADPNAR 194
DB 61 PLHFAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFHGAEVVNLRLRHGADPNAR 120
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QY 195 DNWNVYPLHEAAIKGKIDVICIVLLOHGAEPITRNTDGTALDLADPSAKAVLTGEYKKDE 254
DB 121 DNWNVYPLHEAAIKGKIDVICIVLLOHGAEPITRNTDGTALDLADPSAKAVLTGEYKKDE 180
QY 255 LLESARSNGEKKMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIIVOLLQHGADVHAK 314
DB 181 LLESARSNGEKKMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIIVOLLQHGADVHAK 240
QY 315 DKGDVPLHNACSYGHEVTELLVKGHGCANVMDLWQFTPLHEAASKNRVEVCSLLLSYG 374
DB 241 DKGDVPLHNACSYGHEVTELLVKGHGCANVMDLWQFTPLHEAASKNRVEVCSLLLSYG 300
QY 375 ADPTLNCNKSIAIDAPTQPKERLAYEFKSHLSLQAAREADVTRIKKHLSEMVNFKH 434
DB 301 ADPTLNCNKSIAIDAPTQPKERLAYEFKSHLSLQAAREADVTRIKKHLSEMVNFKH 360
QY 435 POTHETALHCAASAPYKPKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVV 494
DB 361 POTHETALHCAASAPYKPKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVV 420
QY 495 KHEAKVNALDNLGQTSIHRAAVCGHLOTCHLLLSYGCDPNIISLQGTALQMGHNQOL 554
DB 421 KHEAKVNALDNLGQTSIHRAAVCGHLOTCHLLLSYGCDPNIISLQGTALQMGHNQOL 480
QY 555 LOEGISLGNSEADROLLEAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVS 614
DB 481 LOEGISLGNSEADROLLEAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNNRVS 540
QY 615 VVEYLLQHGADVHAKDKGGVPLHNACSYGHEVVAEELLVKHGAVVNVADLWKFPTLHEAA 674
DB 541 VVEYLLQHGADVHAKDKGGVPLHNACSYGHEVVAEELLVKHGAVVNVADLWKFPTLHEAA 600
QY 675 AKGYEICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDILLRGDAALLDAAKKGCLAR 734
DB 601 AKGYEICKLLLOHGADPTKKNRDGNTPLDLVKDGTDIQDILLRGDAALLDAAKKGCLAR 660
QY 735 VKKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGILPLHNA 794
DB 661 VKKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGILPLHNA 720
QY 795 SYGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQT 854
DB 721 SYGHVDVAALLIKYNACVNATDKWFTPLHEAAQKGRTOQLCALLAHGADPTLKNQEGQT 780
QY 855 PLDLVSADVDVALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASS 914
DB 781 PLDLVSADVDVALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASS 840
QY 915 LDNLGSFSELSSVSSSGTEGASSLEKKEVPVDFPSITQFVRNLGLEHLMDFEREQIT 974
DB 841 LDNLGSFSELSSVSSSGTEGASSLEKKEVPVDFPSITQFVRNLGLEHLMDFEREQIT 900
QY 975 LDVLEVMGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPLYTLNTSGSGTILDLSP 1034
DB 901 LDVLEVMGHKELKEIGINAYGHRHKLKIGVERLISGOQGLNPLYTLNTSGSGTILDLSP 960
QY 1035 DDKEFQSVBEEMOSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEEN 1094
DB 961 DDKEFQSVBEEMOSTVREHRDGGHAGGIFNRYNLIKIQVCNKKLWERYTHRRKEVSEEN 1020
QY 1095 HNHANERMLPHGSPFFVNAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGGGTG 1154
DB 1021 HNHANERMLPHGSPFFVNAIITHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYGGGTG 1080
QY 1155 CPVHKDRSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSVNGLALAEYV 1214
DB 1081 CPVHKDRSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSVNGLALAEYV 1140
QY 1215 IYRGEQAYPEYLITYQIMRPEGWVDG 1240
DB 1141 IYRGEQAYPEYLITYQIMRPEGWVDG 1166
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RESULT 8
US-10-199-937-135
; Sequence 135, Application US/10199937
; Publication No. US20030190739A1
; GENERAL INFORMATION:
; APPLICANT: Christenson, Erik
; APPLICANT: DeMaggio, Anthony J.
; APPLICANT: Goldman, Phyllis S.
; APPLICANT: McElligott, David L.
; TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
; FILE REFERENCE: 27866/36559
; CURRENT APPLICATION NUMBER: US/10/199,937
; CURRENT FILING DATE: 2002-07-22
; PRIOR FILING DATE: US/09/606,035
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/141,582
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 135
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-937-135

Query Match      94.5%; Score 6108; DB 4; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 MSRRCCGGGACASAAAEVPEARELFACRNGDVERVKRLVTPKVNRSRD TAGRKST 134
Db 1 MSRRCCGGGACASAAAEVPEARELFACRNGDVERVKRLVTPKVNRSRD TAGRKST 60

Qy 135 PLHFAAGFRKDVVEYLLQNGANVOARDGGGLPLHNACSGHAEVNNLLRHGADPNAR 194
Db 61 PLHFAAGFRKDVVEYLLQNGANVOARDGGGLPLHNACSGHAEVNNLLRHGADPNAR 120

Qy 195 DNWNYTPLHEAAIKGIDVCIVLLQHGAEPTIRNTDGTALDADPSAKAVLTGEYKDE 254
Db 121 DNWNYTPLHEAAIKGIDVCIVLLQHGAEPTIRNTDGTALDADPSAKAVLTGEYKDE 180

Qy 255 LLESARSNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRKIVQLLQHGADVHAK 314
Db 181 LLESARSNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNNRKIVQLLQHGADVHAK 240

Qy 315 DKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKRVEVCSLLLSYG 374
Db 241 DKGDLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKRVEVCSLLLSYG 300

Qy 375 ADPTLLNCHNSAIDLAPTPQKRLAYEFKSHLSLQAAAREADVTRIKKHLSELMVNFKH 434
Db 301 ADPTLLNCHNSAIDLAPTPQKRLAYEFKSHLSLQAAAREADVTRIKKHLSELMVNFKH 360

Qy 435 PQTETHALHCAASPYPKRKQICEILLRKGANINEKTKFEFLTPLHVASEKAHNDVVEYV 494
Db 361 PQTETHALHCAASPYPKRKQICEILLRKGANINEKTKFEFLTPLHVASEKAHNDVVEYV 420

Qy 495 KHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGFALQNGENVOQL 554
Db 421 KHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGFALQNGENVOQL 480

Qy 555 LOEGISLGNSEADROLLEAAKAGDVETVKKLTQVQSVNCRDIEGROSTPLHFAAGYNRVS 614
Db 481 LOEGISLGNSEADROLLEAAKAGDVETVKKLTQVQSVNCRDIEGROSTPLHFAAGYNRVS 540

Qy 615 VVEYLLQHGADVHAKDGGVPLHNACSYGHEVTELLVKGACVNVNADLWKFTPLHEAA 674
Db 541 VVEYLLQHGADVHAKDGGVPLHNACSYGHEVTELLVKGACVNVNADLWKFTPLHEAA 600

Qy 675 AKGKYEICKLLQHGADPTKKNRDNPTPLDLVKQGDPTDQDLLRGDAALLDAAKKGCILAR 734
Db 601 AKGKYEICKLLQHGADPTKKNRDNPTPLDLVKQGDPTDQDLLRGDAALLDAAKKGCILAR 660

Qy 735 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAA 794
Db 661 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAA 720

Qy 795 SYGHVDVAALLIKYNACVNATDKWAFTPLHBAAGKRTQLCALLAHGADPTLKNQEGQT 854
Db 721 SYGHVDVAALLIKYNACVNATDKWAFTPLHBAAGKRTQLCALLAHGADPTLKNQEGQT 780

Qy 855 PLDLVSADDDVALLTAAMPSPALPCYKPOVLNGVRSPGATADALSSGSPSSLSAASS 914
Db 781 PLDLVSADDDVALLTAAMPSPALPCYKPOVLNGVRSPGATADALSSGSPSSLSAASS 840

Qy 915 LDNLSSGSFSELSSVSSSGTEGASLEKKEVPGVDFSIQTQVRNLGLEHLMDFEREQIT 974
Db 841 LDNLSSGSFSELSSVSSSGTEGASLEKKEVPGVDFSIQTQVRNLGLEHLMDFEREQIT 900

Qy 975 LDVLVENGHKLKEIGINAYCHRRHKLKGVRELISGQGLNPYLTANTSGSGTILIDLSP 1034
Db 901 LDVLVENGHKLKEIGINAYCHRRHKLKGVRELISGQGLNPYLTANTSGSGTILIDLSP 960

Qy 1035 DDKEFQSVBEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEEN 1094
Db 961 DDKEFQSVBEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEEN 1020

Qy 1095 HNHANERMLFHGSPFVNAILHKGFDERHAYTGGMFGAGIYFAENSSKSNQVYVIGGGTG 1154
Db 1021 HNHANERMLFHGSPFVNAILHKGFDERHAYTGGMFGAGIYFAENSSKSNQVYVIGGGTG 1080

Qy 1155 CPVHKDRSCYICHRQLLFCRVTLGKSFLOPSAMKMAHSPPGHHSVTGRPSVNGLALEYV 1214
Db 1081 CPVHKDRSCYICHRQLLFCRVTLGKSFLOPSAMKMAHSPPGHHSVTGRPSVNGLALEYV 1140

Qy 1215 IYRGEQAYPEYLIITYQIMRPEGMDG 1240
Db 1141 IYRGEQAYPEYLIITYQIMRPEGMDG 1166

RESULT 9
US-09-849-602-26
; Sequence 26, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 1227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-26

Query Match      90.9%; Score 5877; DB 3; Length 1227;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1148; Conservative 8; Mismatches 47; Indels 50; Gaps 5;

Qy 12 QGAQRGARVGNAA-----HGTAPDPTVAGSQAAARALSASSPGGLALLLAGPGLL 59
Db 1 QGAQRGARVGNAAAGLRRSGDREPSGPGPERVFGSGPRPPARGAGAPAPVAGAVAG---- 56

Qy 60 LRLALLLVAARAIMSGRRCAAG-----CGGQDQVHVSPLRRRSGGLRDAAAEVPEARELFACRN 108
Db 57 -----CGGQDQVHVSPLRRRSGGLRDAAAEVPEARELFACRN 96

Qy 109 GDVERVKRLVTPKVNRSRD TAGRKSTPLHFAAGFRKDVVEYLLQNGANVOARDGGGLIP 168
Db 97 GDVERVKRLVTPKVNRSRD TAGRKSTPLHFAAGFRKDVVEYLLQNGANVOARDGGGLIP 156

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Qy	169	LHNACSFHAEVNVNLLRHGADPNARDNWNYP	LHAAIKGKIDVICIVLLQHGABPTIRN	228
Db	157	LHNACSFHAEVNVNLLRHGADPNARDNWNYP	LHAAIKGKIDVICIVLLQHGABPTIRN	216
Qy	229	TGRTALDAPSAKAVLTGEYKDELLESARGNEEK	MALLTPLNVNCHASDGRKSTP	288
Db	217	TGRTALDAPSAKAVLTGEYKDELLESARGNEEK	MALLTPLNVNCHASDGRKSTP	276
Qy	289	LHLAAGYNRVKIVQLLQHGADVHAKDGLVPL	PHNACSYGHYEYVTELLVKGACVNAM	348
Db	277	LHLAAGYNRVKIVQLLQHGADVHAKDGLVPL	PHNACSYGHYEYVTELLVKGACVNAM	336
Qy	349	LWQFTPLHAAASKNRVEVCSLLSYGADPTL	LNCHNKSAIDLAPTQPKERLAYEFKGHS	408
Db	337	LWQFTPLHAAASKNRVEVCSLLSYGADPTL	LNCHNKSAIDLAPTQPKERLAYEFKGHS	396
Qy	409	LLOAREADVTRIKKHLSELNWFPHQPTHE	TALHCAAAAPYPRKQICELLRRKANIN	468
Db	397	LLOAREADVTRIKKHLSELNWFPHQPTHE	TALHCAAAAPYPRKQICELLRRKANIN	456
Qy	469	EKTKEFLPLHVASEKAHNDVVVVVHGA	KVNALDNLGQTSLHRAAYCGHLQTCRLJLS	528
Db	457	EKTKEFLPLHVASEKAHNDVVVVVHGA	KVNALDNLGQTSLHRAAYCGHLQTCRLJLS	516
Qy	529	YGCDDNIIISLQFTALQMGNEVQQLLEG	ISLGNSEADROLLEAAKAGDVTVKLCTV	588
Db	517	YGCDDNIIISLQFTALQMGNEVQQLLEG	ISLGNSEADROLLEAAKAGDVTVKLCTV	576
Qy	589	QSVNCRDIEGROSTPLHFAAGYNRVVVE	YLLQHGADVHAKDGGVPLPHNACSYGHYEV	648
Db	577	QSVNCRDIEGROSTPLHFAAGYNRVVVE	YLLQHGADVHAKDGGVPLPHNACSYGHYEV	636
Qy	649	AELLVKGAVNVNADLWFTPLHAAAKGK	YIECKLLQHGADPTKKNRDNNTPLDLVKD	708
Db	637	AELLVKGAVNVNADLWFTPLHAAAKGK	YIECKLLQHGADPTKKNRDNNTPLDLVKD	696
Qy	709	GBTDIQDLRLGDAALLDAKKGCLARVK	LSPPDNVNCRDTOGRHSTPLHLAGYNNLEV	768
Db	697	GBTDIQDLRLGDAALLDAKKGCLARVK	LSPPDNVNCRDTOGRHSTPLHLAGYNNLEV	756
Qy	769	AEYLLQHGADVNAOKGGIPLHNAASY	GHDVDAALLIKYNACVNATDKWATPLHRAAQ	828
Db	757	AEYLLQHGADVNAOKGGIPLHNAASY	GHDVDAALLIKYNACVNATDKWATPLHRAAQ	816
Qy	829	KGRTQCALLAHAGADPTLKNQEGQ	TPLDLVSADDSALLTAAMPSPALPSCKPQVLNG	888
Db	817	KGRTQCALLAHAGADPTLKNQEGQ	TPLDLVSADDSALLTAAMPSPALPSCKPQVLNG	876
Qy	889	VRSPGATADALSSGSPSSLSAASL	ONLSGFSLELSSVSSSGTEGASSLEKKEVPGV	948
Db	877	VRSPGATADALSSGSPSSLSAASL	ONLSGFSLELSSVSSSGTEGASSLEKKEVPGV	936
Qy	949	DFSITQFVRNLGLEHLMIDIFEREQ	ITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLI	1008
Db	937	DFSITQFVRNLGLEHLMIDIFEREQ	ITLDVLVEMGHKELKEIGINAYGHRHKLIKGVERLI	996
Qy	1009	SGQOGLNPLYTLNTSGSGTILDLSP	DDKEFOSVEEEMOSTVREHRDGHAGGIFNRYNI	1068
Db	997	SGQOGLNPLYTLNTSGSGTILDLSP	DDKEFOSVEEEMOSTVREHRDGHAGGIFNRYNI	1056
Qy	1069	LKIQKVCNKKLWERVTHRRKEVSE	BNHNANRMLFHGSPFFNAIHHKGFDRHAYIGGM	1128
Db	1057	LKIQKVCNKKLWERVTHRRKEVSE	BNHNANRMLFHGSPFFNAIHHKGFDRHAYIGGM	1116
Qy	1129	FGAGIYFAENSSKNQYVYIGGGT	GCPCVHK--DRSCYICHROLLFCRVTLGKSLQFSAM	1187
Db	1117	FGAGIYFAENSSKNQYVYIGGGT	GCPCVHK--DRSCYICHROLLFCRVTLGKSLQFSAM	1174
Qy	1188	KWAIHSPPGHHSVTGRPSVNG	LALAEYVYIRGQAYPEYLITYQIMRPEGWVDG	1240
Db	1175	ENGTSPPGHHSVTGRPSVNG	LALAEYVYIRGQAYPEYLITYQIMRPEGWVDG	1227

RESULT 10
US-10-616-101-8
; Sequence 8, Application US/10616101
; Publication NO. US20050074825A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossoskaya, Valeria
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods c
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-101-8

Query Match 89.2%; Score 5766; DB 5; Length 1100;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1099; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	141	GFGRKDVVEYLLQNGANVQARDGG	LPLHNACSFHAEVNVNLLRHGADPNARDNWN	200
Db	1	GFGRKDVVEYLLQNGASVQARDGG	LPLHNACSFHAEVNVNLLRHGADPNARDNWN	60
Qy	201	PLHEAAIKGKIDVICIVLLQHGABPT	IRNTDGRDTALDAPSAKAVLTGEYKDELLESAR	260
Db	61	PLHEAAIKGKIDVICIVLLQHGABPT	IRNTDGRDTALDAPSAKAVLTGEYKDELLESAR	120
Qy	261	SGNEEKMMALLTPLNVNCHASDGRK	STPLHLAGYNNRVKIVQLLQHGADVHAKDGLV	320
Db	121	SGNEEKMMALLTPLNVNCHASDGRK	STPLHLAGYNNRVKIVQLLQHGADVHAKDGLV	180
Qy	321	PLHNACSYGHYEYVTELLVKGACV	NAMDLMQFTPLHAAASKNRVEVCSLLSYGADPTLL	380
Db	181	PLHNACSYGHYEYVTELLVKGACV	NAMDLMQFTPLHAAASKNRVEVCSLLSYGADPTLL	240
Qy	381	NCHNKSAIDLAPTQPKERLAYEF	KGHSLLQAAREADVTRIKKHLSELMVNFKHQPTHET	440
Db	241	NCHNKSAIDLAPTQPKERLAYEF	KGHSLLQAAREADVTRIKKHLSELMVNFKHQPTHET	300
Qy	441	ALHCAAAAPYPRKQICELLRRKAN	INEKTEFLPLHVASEKAHNDVVVVVHKA	500
Db	301	ALHCAAAAPYPRKQICELLRRKAN	INEKTEFLPLHVASEKAHNDVVVVVHKA	360
Qy	501	NALDNLGQTSLHRAAYCGHLQ	TCRLJLSYGCDDNIIISLQFTALQMGNEVQQLQEGIS	560
Db	361	NALDNLGQTSLHRAAYCGHLQ	TCRLJLSYGCDDNIIISLQFTALQMGNEVQQLQEGIS	420
Qy	561	LGNSEADROLLEAAKAGDVT	VTKLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL	620
Db	421	LGNSEADROLLEAAKAGDVT	VTKLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLL	480
Qy	621	QHGADVHAKDGGVPLPHNAC	SYGHYEYVTELLVKGAVNVNADLWFTPLHAAAKGKYE	680
Db	481	QHGADVHAKDGGVPLPHNAC	SYGHYEYVTELLVKGAVNVNADLWFTPLHAAAKGKYE	540
Qy	681	ICKLLQHGADPTKKNRDN	NTPLDLVKDGDPTDQDLRLGDAALLDAKKGCLARVKKLSS	740
Db	541	ICKLLQHGADPTKKNRDN	NTPLDLVKDGDPTDQDLRLGDAALLDAKKGCLARVKKLSS	600

Qy	741	PDNVCRTDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD	800
Db	601	PDNVCRTDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD	660
Qy	801	VAALLIKYNACVNAATKWAFTPLHAAQKGRTOICALLAHGADPTLKNQEGQTPDLVLS	860
Db	661	VAALLIKYNACVNAATKWAFTPLHAAQKGRTOICALLAHGADPTLKNQEGQTPDLVLS	720
Qy	861	ADVSALLITAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG	920
Db	721	ADVSALLITAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG	780
Qy	921	SFSELSVVSSSGTGGASLEKKEVGVDFSTIQFVRLGLEHLMDFEREQITLDVLVE	980
Db	781	SFSELSVVSSSGTGGASLEKKEVGVDFSTIQFVRLGLEHLMDFEREQITLDVLVE	840
Qy	981	MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSGTILIDLSPDDKEFQ	1040
Db	841	MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSGTILIDLSPDDKEFQ	900
Qy	1041	SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE	1100
Db	901	SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE	960
Qy	1101	RMLFHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD	1160
Db	961	RMLFHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD	1020
Qy	1161	RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ	1220
Db	1021	RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ	1080
Qy	1221	APPEYLITYQIMRPEGWVDG 1240	
Db	1081	APPEYLITYQIMRPEGWVDG 1100	

RESULT 11

US-10-616-101-11

Sequence 11, Application US/10616101

Publication No. US20050074825A1

GENERAL INFORMATION:

APPLICANT: Luo, Ying

APPLICANT: Chan, Eva

APPLICANT: Xu, Xiang

APPLICANT: Huang, Betty

APPLICANT: Osbovska, Valeria

TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods

FILE REFERENCE: RIGL-010CIP3

CURRENT APPLICATION NUMBER: US/10/616,101

CURRENT FILING DATE: 2003-07-08

PRIOR APPLICATION NUMBER: US 09/843,159

PRIOR FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: US 09/696,668

PRIOR FILING DATE: 2000-10-25

PRIOR APPLICATION NUMBER: US 09/427,154

PRIOR FILING DATE: 1999-10-25

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin version 3.1

SEQ ID NO 11

LENGTH: 1100

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: synthetic mutant

US-10-616-101-11

Query Match 89.1%; Score 5760; DB 5; Length 1100;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1098; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 141 GFRKDVVEYLLQNGASVQARDGGLIPLHNAACSFHAEVNNLLRLRHGADPNARDNNYNT 200

Db	1	GFRKDVVEYLLQNGASVQARDGGLIPLHNAACSFHAEVNNLLRLRHGADPNARDNNYNT	60
Qy	201	PLHAAIKGKIDVCIVLLOHGAETPIRNTDGRALTADLADPSAKAVLTGEYKKDELLESAR	260
Db	61	PLHAAIKGKIDVCIVLLOHGAETPIRNTDGRALTADLADPSAKAVLTGEYKKDELLESAR	120
Qy	261	SGNEEKWALLTPLNVNCHASDGRKSTPLHAAAGYNNRKIVOLLQHGADVNAQDKGLI	320
Db	121	SGNEEKWALLTPLNVNCHASDGRKSTPLHAAAGYNNRKIVOLLQHGADVNAQDKGLI	180
Qy	321	PLHNAACSYGHEVTELLVKGACVNAADLWQFTPLHAAASKNRVEVCSLLISYGADPTLL	380
Db	181	PLHNAACSYGHEVTELLVKGACVNAADLWQFTPLHAAASKNRVEVCSLLISYGADPTLL	240
Qy	381	NCHNKSALDLAPTQKRLERLAYEFKGHSLLQAAAREADVTRIKGHSLEWVNFKHPQTHET	440
Db	241	NCHNKSALDLAPTQKRLERLAYEFKGHSLLQAAAREADVTRIKGHSLEWVNFKHPQTHET	300
Qy	441	ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPLVASEKAHNDVVEVVKHEAKV	500
Db	301	ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPLVASEKAHNDVVEVVKHEAKV	360
Qy	501	NALDNLGQTSLHRAAYCGHLQTCRLLLISYGCDPNIIISLOGFTALOMGNENVOQLLOEGIS	560
Db	361	NALDNLGQTSLHRAAYCGHLQTCRLLLISYGCDPNIIISLOGFTALOMGNENVOQLLOEGIS	420
Qy	561	LGNSEADQLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL	620
Db	421	LGNSEADQLLEAAKAGDVETVKKLCVQSVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLL	480
Qy	621	QHGADVHAKQKGLVPLHNAACSYGHEVVAELLVKHGAVVNVADLWKFPTLHAAAKGYE	680
Db	481	QHGADVHAKQKGLVPLHNAACSYGHEVVAELLVKHGAVVNVADLWKFPTLHAAAKGYE	540
Qy	681	ICKLLQHGADPTKKNRDGNTPLDKDGDYDIOQLLEGDAALLDAAKGGCLARVKLSS	740
Db	541	ICKLLQHGADPTKKNRDGNTPLDKDGDYDIOQLLEGDAALLDAAKGGCLARVKLSS	600
Qy	741	PDNVCRTDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD	800
Db	601	PDNVCRTDQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD	660
Qy	801	VAALLIKYNACVNAATKWAFTPLHAAQKGRTOICALLAHGADPTLKNQEGQTPDLVLS	860
Db	661	VAALLIKYNACVNAATKWAFTPLHAAQKGRTOICALLAHGADPTLKNQEGQTPDLVLS	720
Qy	861	ADVSALLITAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG	920
Db	721	ADVSALLITAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSLSAASSLDNLSSG	780
Qy	921	SFSELSVVSSSGTGGASLEKKEVGVDFPSITOPVRNLGLEHLMDFEREQITLDVLVE	980
Db	781	SFSELSVVSSSGTGGASLEKKEVGVDFPSITOPVRNLGLEHLMDFEREQITLDVLVE	840
Qy	981	MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSGTILIDLSPDDKEFQ	1040
Db	841	MGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSGTILIDLSPDDKEFQ	900
Qy	1041	SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE	1100
Db	901	SVEEMQSTVREHRDGGHAGGIFNRYNLIKQVCNKKLWERYTHRRKEVSEENHNHANE	960
Qy	1101	RMLFHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD	1160
Db	961	RMLFHGSPFVNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVYGGTGCPCVHKD	1020
Qy	1161	RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ	1220
Db	1021	RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ	1080
Qy	1221	APPEYLITYQIMRPEGWVDG 1240	
Db	1081	APPEYLITYQIMRPEGWVDG 1100	

RESULT 12	
US-10-616-101-12	
; Sequence 12, Application US/10616101	
; Publication No. US20050074825A1	
; GENERAL INFORMATION:	
; APPLICANT: Luo, Ying	
; APPLICANT: Chan, Eva	
; APPLICANT: Xu, Xiang	
; APPLICANT: Huang, Betty	
; APPLICANT: Osoevskaya, Valeria	
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods	
; FILE REFERENCE: RIGL-010CIP3	
; CURRENT APPLICATION NUMBER: US/10/616,101	
; CURRENT FILING DATE: 2003-07-08	
; PRIOR APPLICATION NUMBER: US 09/843,159	
; PRIOR FILING DATE: 2001-04-25	
; PRIOR APPLICATION NUMBER: US 09/696,668	
; PRIOR FILING DATE: 2000-10-25	
; PRIOR APPLICATION NUMBER: US 09/427,154	
; PRIOR FILING DATE: 1999-10-25	
; NUMBER OF SEQ ID NOS: 19	
; SOFTWARE: PatentIn version 3.1	
; SEQ ID NO 12	
; LENGTH: 1083	
; TYPE: PRT	
; ORGANISM: Artificial sequence	
; FEATURE:	
; OTHER INFORMATION: synthetic mutant	
US-10-616-101-12	
Query Match 87.5%; Score 5656; DB 5; Length 1083;	
Best Local Similarity 99.8%; Pred. No. 0;	
Matches 1079; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	141 GGRKDVVEYLLQNGANVOARDGGGLPLHNACSFQHAENVNLLRHGADPNARDNWT 200
DB	1 GGRKDVVEYLLQNGASVOARDGGGLPLHNACSFQHAENVNLLRHGADPNARDNWT 60
QY	201 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGTALDADPSAKAVLTGYKDELLESAR 260
DB	61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGTALDADPSAKAVLTGYKDELLESAR 120
QY	261 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 320
DB	121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLV 180
QY	321 PLHNACSYGHEVTELLVKGACVNMMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 380
DB	181 PLHNACSYGHEVTELLVKGACVNMMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
QY	381 NCHNKAIDLAPTPOLKERLAYEFKGHSLQAAREADVTRIKKHSLEWMVNFKHPOTHET 440
DB	241 NCHNKAIDLAPTPOLKERLAYEFKGHSLQAAREADVTRIKKHSLEWMVNFKHPOTHET 300
QY	441 ALHCAAAAPYKPKQICEILLRKGANINBKTEFTPLHVASEKAHNDVVEVVVHKAUV 500
DB	301 ALHCAAAAPYKPKQICEILLRKGANINBKTEFTPLHVASEKAHNDVVEVVVHKAUV 360
QY	501 NALDNLGQTSLHRAAYCGHLOTCRLLLSYGCDDPNIIISLOGFTALQNGNENVOQLLEGIS 560
DB	361 NALDNLGQTSLHRAAYCGHLOTCRLLLSYGCDDPNIIISLOGFTALQNGNENVOQLLEGIS 420
QY	561 LGNSEADROLLEAAKAGDVETVKKLTQVQSNCRDIEGRQSTPLHPAAGYNRVSVVEYLL 620
DB	421 LGNSEADROLLEAAKAGDVETVKKLTQVQSNCRDIEGRQSTPLHPAAGYNRVSVVEYLL 480
QY	621 QHGADVHAKDKGGLVPLHNACSYGHEVTELLVKGACVNMMDLWQFTPLHEAAAKGKYE 680
DB	481 QHGADVHAKDKGGLVPLHNACSYGHEVTELLVKGACVNMMDLWQFTPLHEAAAKGKYE 540
QY	681 ICKLLQHGADPTKKNRDGNTPDLVKGDDTDIQDLLRGDAALLDAAKGCCLARVKKLSS 740

Db	541 ICKLLQHGADPTKKNRDGNTPDLVKGDDTDIQDLLRGDAALLDAAKGCCLARVKKLSS	600
QY	741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD	800
DB	601 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD	660
QY	801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGQTPDLVS	860
DB	661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOCALLLAHGADPTLKNQEGQTPDLVS	720
QY	861 ADDVSALLTAAMPSPSALPCYKQVNLGVSPCATADALSSGSPSSLSAASLNDLSG	920
DB	721 ADDVSALLTAAMPSPSALPCYKQVNLGVSPCATADALSSGSPSSLSAASLNDLSG	780
QY	921 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDLVE	980
DB	781 SFSELSSVVSSSGTEGASSLEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDLVE	840
QY	981 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILDLSPDDKEFQ	1040
DB	841 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILDLSPDDKEFQ	900
QY	1041 SVEEEMQSTVREHRDGHAGGIENRYNLIKQVCKNKLWERYTHRRKEVSEENHNHANE	1100
DB	901 SVEEEMQSTVREHRDGHAGGIENRYNLIKQVCKNKLWERYTHRRKEVSEENHNHANE	960
QY	1101 RMLFHGSPFVNAIIHKGFDERHAYIGMGFAGIYFAENSCKSNQYVYGIGGTCGPVHKD	1160
DB	961 RMLFHGSPFVNAIIHKGFDERHAYIGMGFAGIYFAENSCKSNQYVYGIGGTCGPVHKD	1020
QY	1161 RSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPPGHSHSVTGRPSVNGLALAEYIYRGEQ	1220
DB	1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKWAHSPPGHSHSVTGRPSVNGLALAEYIYRGEQ	1080
QY	1221 A 1221	
DB	1081 A 1081	

RESULT 13

US-09-509-196A-2

; Sequence 2, Application US/09509196A

; Patent No. US20020037582A1

; GENERAL INFORMATION:

; APPLICANT: DALY, Roger J.

; APPLICANT: SUTHERLAND, Robert L.

; TITLE OF INVENTION: A Potential Effector for the Grb7 Family of Signalling

; TITLE OF INVENTION: Proteins

; FILE REFERENCE: 1871-129

; CURRENT APPLICATION NUMBER: US/09/509,196A

; CURRENT FILING DATE: 2000-03-23

; PRIOR APPLICATION NUMBER: P09388

; PRIOR FILING DATE: 1997-09-23

; PRIOR APPLICATION NUMBER: PCT AU98/00795

; PRIOR FILING DATE: 1998-09-23

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 1074

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-509-196A-2

Query Match 86.7%; Score 5602; DB 3; Length 1074;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1068; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY	167 IPLHNACSFQHAENVNLLRHGADPNARDNWTPLHEAAIKGKIDVCIVLLQHGAEPTI	226
DB	1 IPLHNACSFQHAENVNLLRHGADPNARDNWTPLHEAAIKGKIDVCIVLLQHGAEPTI	60
QY	227 RNTDGTALDADPSAKAVLTGYKDELLESARSGNEEKWALLTPLNVNCHASDGRKS	286

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Db      61  RNTDGRGTDALDPSAKAVLTGEYKDELLESARSNGNEEKMWALLTPLNVNCHASDGRKS 120
Qy      287  TPLHLAAGNVRVKIIVOLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGHCACNA 346
Db      121  TPLHLAAGNVRVKIIVOLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGHCACNA 180
Qy      347  MDLWQFTPLHEAASKNRVEVCSSLLSYGADPTLLNCHNKSALDAPTPOKLERLAYEFKG 406
Db      181  MDLWQFTPLHEAASKNRVEVCSSLLSYGADPTLLNCHNKSALDAPTPOKLERLAYEFKG 240
Qy      407  HSLLOAAREADVTRIKKHSLEWVNFKPQTHETALHCAAAAPYPRKQICELLRLKGAN 466
Db      241  HSLLOAAREADVTRIKKHSLEWVNFKPQTHETALHCAAAAPYPRKQICELLRLKGAN 300
Qy      467  INEKTKEFLTPLHVASEKAHNDVVEVVKHGAKNVADNLGOTSLHRAAYCGHLOTCLLL 526
Db      301  INEKTKEFLTPLHVASEKAHNDVVEVVKHGAKNVADNLGOTSLHRAAYCGHLOTCLLL 360
Qy      527  LSYGCDPNIISLGFTALQMGNEVQOLLQEGISLGNSEADQLLEAAKAGDVETVKKLC 586
Db      361  LSYGCDPNIISLGFTALQMGNEVQOLLQEGISLGNSEADQLLEAAKAGDVETVKKLC 420
Qy      587  TVQSVNCRDIEGRQSTPLHFAAGNVRVSVVYLLQHGADVHAKDGLVPLHNACSYGHI 646
Db      421  TVQSVNCRDIEGRQSTPLHFAAGNVRVSVVYLLQHGADVHAKDGLVPLHNACSYGHI 480
Qy      647  EVAELLVKGAVVNVADLWKFTPLHEAAKAGYEICKLLQHGADPTKQRDNTPLDLV 706
Db      481  EVAELLVKGAVVNVADLWKFTPLHEAAKAGYEICKLLQHGADPTKQRDNTPLDLV 540
Qy      707  KDGDITDIDLLRGDAALDAAKGGCLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNL 766
Db      541  KDGDITDIDLLRGDAALDAAKGGCLARVKLSSPDNVNCRDTQGRHSTPLHLAAGYNL 600
Qy      767  EVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVATDKWAFPLHEA 826
Db      601  EVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNASINATDKWAFPLHEA 660
Qy      827  AQKGTOLCALLAHGADPTLKNQEGOTPLDVSADDSALLTAAMPSPALSCYKQVPL 886
Db      661  AQKGTOLCALLAHGADPTLKNQEGOTPLDVSADDSALLTAAMPSPALSCYKQVPL 720
Qy      887  NGRVSPGATADALSQSPSPSSLSAASSLDNLSSGFSSELSSVSSGTEGASLEKEVP 946
Db      721  NGRVSPGATADALSQSPSPSSLSAASSLDNLSSGFSSELSSVSSGTEGASLEKEVP 780
Qy      947  GVDPSITQVNRNLGLEHMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVER 1006
Db      781  GVDPSITQVNRNLGLEHMDIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVER 840
Qy      1007  LISGOGLNPYLTNTSGSGTILDLSPDDKEFQSVVEEMQSTVREHRDGGHAGGIFNRY 1066
Db      841  LISGOGLNPYLTNTSGSGTILDLSPDDKEFQSVVEEMQSTVREHRDGGHAGGIFNRY 900
Qy      1067  NTLTKQVCKKWLERYTHRRKEVSEENHNANERMLFHGSPFVNAILHKGFDERHAYIG 1126
Db      901  NTLTKQVCKKWLERYTHRRKEVSEENHNANERMLFHGSPFVNAILHKGFDERHAYIG 960
Qy      1127  GMFGAGIYFAENSSKSNQVYVIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSLQFSA 1186
Db      961  GMFGAGIYFAENSSKSNQVYVIGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSLQFSA 1020
Qy      1187  MOWAHSPPGHHSVTRGPSVNGLALAEVYIYRGEQAYPEYLIITYQIMRPEGVDG 1240
Db      1021  MOWAHSPPGHHSVTRGPSVNGLALAEVYIYRGEQAYPEYLIITYQIMRPEGVDG 1074

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RESULT 14
 US-10-616-101-3
 ; Sequence 3, Application US/10616101
 ; Publication NO. US20050074825A1
 ; GENERAL INFORMATION:

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; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ossovskaya, Valeria
; FILE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods c
; FILE REFERENCE: RIGL-010CIP3
; CURRENT APPLICATION NUMBER: US/10/616,101
; CURRENT FILING DATE: 2003-07-08
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/843,159
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 1065
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-616-101-3

Query Match      86.4%; Score 5582; DB 5; Length 1065;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1064; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      141  GFGKDVVEYLLONGANYQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARNWNT 200
Db      1   GFGKDVVEYLLONGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARNWNT 60
Qy      201  PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 260
Db      61  PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 120
Qy      261  SGNEEKMWALLTPLNVNCHASDGRKSTPLHLAAGNVRVKIIVOLLQHGADVHAKDGLV 320
Db      121  SGNEEKMWALLTPLNVNCHASDGRKSTPLHLAAGNVRVKIIVOLLQHGADVHAKDGLV 180
Qy      321  PLHNACSYGHEVTELLVKGHCACNVAMDQFTPLHEAASKNRVEVCSSLLSYGADPTLL 380
Db      181  PLHNACSYGHEVTELLVKGHCACNVAMDQFTPLHEAASKNRVEVCSSLLSYGADPTLL 240
Qy      381  NCHNKSALDAPTPOKLERLAYEFKGHSLLQAAAREADVTRIKKHSLEWVNFKPQTHET 440
Db      241  NCHNKSALDAPTPOKLERLAYEFKGHSLLQAAAREADVTRIKKHSLEWVNFKPQTHET 300
Qy      441  ALHCAAAAPYPRKQICELLRLKGANINEKTKEFLTPLHVASEKAHNDVVEVVKHAEKV 500
Db      301  ALHCAAAAPYPRKQICELLRLKGANINEKTKEFLTPLHVASEKAHNDVVEVVKHAEKV 360
Qy      501  NALDNLGOTSLHRAAYCGHLOTCLLLSYGCDPNIISLGFTALQMGNEVQOLLQEGIS 560
Db      361  NALDNLGOTSLHRAAYCGHLOTCLLLSYGCDPNIISLGFTALQMGNEVQOLLQEGIS 420
Qy      561  LGNSADQLLEAAKAGDVETVKKICTVQSVNCRDIEGRQSTPLHFAAGNVRVSVVEYLL 620
Db      421  LGNSADQLLEAAKAGDVETVKKICTVQSVNCRDIEGRQSTPLHFAAGNVRVSVVEYLL 480
Qy      621  QHGADVHAKDGLVPLHNACSYGHEVVAELLVKGAVVNVADLWKFTPLHFAAAKGYE 680
Db      481  QHGADVHAKDGLVPLHNACSYGHEVVAELLVKGAVVNVADLWKFTPLHFAAAKGYE 540
Qy      681  ICKLLQHGADPTKQRDNTPLDLVKDGDITDIDLLRGDAALDAAKGGCLARVKKLS 740
Db      541  ICKLLQHGADPTKQRDNTPLDLVKDGDITDIDLLRGDAALDAAKGGCLARVKKLS 600
Qy      741  PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db      601  PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Qy      801  VAAALLIKYNACVATDKWAFPLHEAAKAGRTQCALLAHAGADPTLKNQEGOTPLDLVS 860

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Db 661 VAALLIKYNACVATDKWAFPLHEAAQKGRTOCALLLAHADPTLKNQEQTPDLVS 720
Qy 861 ADDVSALLTAAMPSPALPSCYKQVLNVRSPGATADALSGSPSPSSLSAASLDNLG 920
Db 721 ADDVSALLTAAMPSPALPSCYKQVLNVRSPGATADALSGSPSPSSLSAASLDNLG 780
Qy 921 SPSLSSVSSSGTEGASSLEKKVPVGDPSITQVRNGLGLEHLMDFEREQITLDVIVE 980
Db 781 SPSLSSVSSSGTEGASSLEKKVPVGDPSITQVRNGLGLEHLMDFEREQITLDVIVE 840
Qy 981 MGHKELKEIGNAYGHRHKLKIGVERLISGQGLNPVLTNTSGSGTILIDLSDDKEFQ 1040
Db 841 MGHKELKEIGNAYGHRHKLKIGVERLISGQGLNPVLTNTSGSGTILIDLSDDKEFQ 900
Qy 1041 SVEEMOSTVREHRDGGHAGGIFNRYNLIKQVCNKKLMERYTHRRKEVSEENHNHANE 1100
Db 901 SVEEMOSTVREHRDGGHAGGIFNRYNLIKQVCNKKLMERYTHRRKEVSEENHNHANE 960
Qy 1101 RMLFHGSPFVNAAITHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGCVPVHKD 1160
Db 961 RMLFHGSPFVNAAITHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGCVPVHKD 1020
Qy 1161 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTRGRPSV 1205
Db 1021 RSCYICHRQLLFCRVTLGKSLQFSAMKMAHSPPGHHSVTRGRPSV 1065

RESULT 15
US-09-972-115A-4
; Sequence 4, Application US/09972115A
; Publication No. US20030032769A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972.115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1267
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: The 'Xaa' at location 1 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc_feature
; LOCATION: (42)..(42)
; OTHER INFORMATION: The 'Xaa' at location 42 stands for Lys, Arg, Thr, or Met.
; NAME/KEY: misc feature
; LOCATION: (98)..(98)
; OTHER INFORMATION: The 'Xaa' at location 98 stands for Lys, Arg, Thr, or Met.
; NAME/KEY: misc_feature
; LOCATION: (110)..(110)
; OTHER INFORMATION: The 'Xaa' at location 110 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (114)..(114)
; OTHER INFORMATION: The 'Xaa' at location 114 stands for Asn, Ser, Thr, or Ile.
; NAME/KEY: misc feature
; LOCATION: (126)..(126)
; OTHER INFORMATION: The 'Xaa' at location 126 stands for Lys, or Asn.
; NAME/KEY: misc feature
; LOCATION: (139)..(139)
; OTHER INFORMATION: The 'Xaa' at location 139 stands for Ile, Val, Leu, or Phe.
; NAME/KEY: misc_feature
; LOCATION: (741)..(741)
; OTHER INFORMATION: The 'Xaa' at location 741 stands for Met, Val, or Leu.

; LOCATION: (144)..(144)
; OTHER INFORMATION: The 'Xaa' at location 144 stands for Thr.
; NAME/KEY: misc feature
; LOCATION: (153)..(153)
; OTHER INFORMATION: The 'Xaa' at location 153 stands for Thr.
; NAME/KEY: misc feature
; LOCATION: (166)..(166)
; OTHER INFORMATION: The 'Xaa' at location 166 stands for Ser, Gly, Arg, or Cys.
; NAME/KEY: misc feature
; LOCATION: (173)..(173)
; OTHER INFORMATION: The 'Xaa' at location 173 stands for Ile, Val, Leu, or Phe.
; NAME/KEY: misc feature
; LOCATION: (174)..(174)
; OTHER INFORMATION: The 'Xaa' at location 174 stands for Glu, or Lys.
; NAME/KEY: misc feature
; LOCATION: (183)..(183)
; OTHER INFORMATION: The 'Xaa' at location 183 stands for Val.
; NAME/KEY: misc feature
; LOCATION: (185)..(185)
; OTHER INFORMATION: The 'Xaa' at location 185 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (188)..(188)
; OTHER INFORMATION: The 'Xaa' at location 188 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (202)..(202)
; OTHER INFORMATION: The 'Xaa' at location 202 stands for His, or Pro.
; NAME/KEY: misc feature
; LOCATION: (204)..(204)
; OTHER INFORMATION: The 'Xaa' at location 204 stands for Glu, or Lys.
; NAME/KEY: misc feature
; LOCATION: (205)..(205)
; OTHER INFORMATION: The 'Xaa' at location 205 stands for Asn, Ser, Thr, or Ile.
; NAME/KEY: misc feature
; LOCATION: (207)..(207)
; OTHER INFORMATION: The 'Xaa' at location 207 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (211)..(211)
; OTHER INFORMATION: The 'Xaa' at location 211 stands for Gln, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (213)..(213)
; OTHER INFORMATION: The 'Xaa' at location 213 stands for Ser, Gly, Arg, or Cys.
; NAME/KEY: misc feature
; LOCATION: (215)..(215)
; OTHER INFORMATION: The 'Xaa' at location 215 stands for Lys, Asn, Glu, Asp, Gln, His,
; OTHER INFORMATION: , a stop codon, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: The 'Xaa' at location 227 stands for His, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (228)..(228)
; OTHER INFORMATION: The 'Xaa' at location 228 stands for Asn, Asp, His, or Tyr.
; NAME/KEY: misc feature
; LOCATION: (237)..(237)
; OTHER INFORMATION: The 'Xaa' at location 237 stands for Glu, or Asp.
; NAME/KEY: misc feature
; LOCATION: (238)..(238)
; OTHER INFORMATION: The 'Xaa' at location 238 stands for Asn, Ser, Thr, Ile, Asp, Gly
; OTHER INFORMATION: , Ala, Val, His, Arg, Pro, Leu, Tyr, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (667)..(667)
; OTHER INFORMATION: The 'Xaa' at location 667 stands for Tyr, Cys, Ser, or Phe.
; NAME/KEY: misc feature
; LOCATION: (725)..(725)
; OTHER INFORMATION: The 'Xaa' at location 725 stands for Lys, or Asn.
; NAME/KEY: misc feature
; LOCATION: (727)..(727)
; OTHER INFORMATION: The 'Xaa' at location 727 stands for His, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (735)..(735)
; OTHER INFORMATION: The 'Xaa' at location 735 stands for Glu, or Asp.
; NAME/KEY: misc feature
; LOCATION: (741)..(741)
; OTHER INFORMATION: The 'Xaa' at location 741 stands for Met, Val, or Leu.
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1

[illegible]

Search completed: December 18, 2006, 17:59:55
Job time : 158.857 secs

C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 31-Dec-2004
C:Accession: A55575
R:Kordeli, E.; Lambert, S.; Bennett, V.
J. Biol. Chem. 270, 2352-2359, 1995
A:Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the ax
A:Reference number: A55575; MUID:95138209; PMID:7836469
A:Accession: A55575
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-4377 <KOR>
A:Cross-references: UNIPROT:Q12955; UNIPARC:UPI000013C497; GB:U13616; NID:G608024; PIDN:
C:Genetics:
A:Gene: GDB:ANK3
A:Cross-references: GDB:424503; OMIM:600465
A:Map position: 10q21-10q21
C:Superfamily: EGF homology
C:Keywords: alternative splicing; peripheral membrane protein
F:73-105/Domain: ankyrin repeat homology <AN01>
F:106-138/Domain: ankyrin repeat homology <AN02>
F:139-171/Domain: ankyrin repeat homology <AN03>
F:172-200/Domain: ankyrin repeat homology <AN04>
F:201-233/Domain: ankyrin repeat homology <AN05>
F:234-266/Domain: ankyrin repeat homology <AN06>
F:267-299/Domain: ankyrin repeat homology <AN07>
F:300-332/Domain: ankyrin repeat homology <AN08>
F:333-365/Domain: ankyrin repeat homology <AN09>
F:366-398/Domain: ankyrin repeat homology <AN10>
F:399-431/Domain: ankyrin repeat homology <AN11>
F:432-464/Domain: ankyrin repeat homology <AN12>
F:465-497/Domain: ankyrin repeat homology <AN13>
F:498-530/Domain: ankyrin repeat homology <AN14>
F:531-563/Domain: ankyrin repeat homology <AN15>
F:564-596/Domain: ankyrin repeat homology <AN16>
F:597-629/Domain: ankyrin repeat homology <AN17>
F:630-662/Domain: ankyrin repeat homology <AN18>
F:663-695/Domain: ankyrin repeat homology <AN19>
F:696-728/Domain: ankyrin repeat homology <AN20>
F:729-761/Domain: ankyrin repeat homology <AN21>
F:762-794/Domain: ankyrin repeat homology <AN22>
F:795-827/Domain: ankyrin repeat homology <AN23>

Query Match 13.8%; Score 892.5; DB 2; Length 4377;
Best Local Similarity 30.7%; Pred. No. 1.6e-45;
Matches 277; Conservative 126; Mismatches 365; Indels 135; Gaps 21;

Qy 136 LHFAAGFRKDWVEYLLQNGANVQARDGGGLPLHNACSFHAEVWVLLRHGADPNARD 195
Db 78 LHLASKEGHVEVWSELLQREANVDAATKKGNTALHIALAGAEVVKVLTNGANVNAQS 137
Qy 196 NWNYTPLHEAAIKGIDYCVILLOHGAERTIRNTDGRDALDLA----DPSAKAVLTGEY 250
Db 138 QNGFTPLTMAAQENHLEVVKFLDNGASQSATEDGFTPLVALQOQHVDVSLLENDT 197
Qy 251 K---KDELLESARSNGEKKMALLTPLNVNCHASGRKSTPLHLAAGYNNRVKIVQLLQ 307
Db 198 KGVRLPALHIAARKDDTKAAALLQNDNADVESKSGFTPLHIAAHYGNINVTALLNR 257
Qy 308 GADVHAKDKGLVPLHNACSGHYEVTELLVKHGACVNAMDLWQFTPLHEAASKNRVEVC 367
Db 258 AAADVFTARNDTPLHVASKRGANVMVLLDRGAKIDAKTRDGLTPLHCGARSQEQV 317
Qy 368 SILLSYGADPTLLNCHNKSAIDLAFTPLQKRLAVFEFGHSLQAREADVTRIKKHL 427
Db 318 EMLDRAA-PILSKTKN-----GLSPLHMATOGD-----HLNC 349
Qy 428 EMVNFKH-----PQTHETALHCAASFPYKPKQICELLRLKGANINEKTFEPLTHV 480
Db 350 VQLLLQHNVPVDDVTNDYLTALHVAACHGCHKY---VAKVLLDKKANPNKALNGFTPLHI 406
Qy 481 ASEKANDVVEVVKHEAKVNALDNLGQTSLHRAAYCGHLCRLLLSYGCDPNIIISLG 540
Db 407 ACKKNRIKVMELLKHGASIQAVTESGLTPTHVAAFMGHVNIVSQLMHGHGASPNNTNVRG 466

Qy 541 FTALQMG-----NENVOQLLOEGISLGNSEADRO--LLEAAKAGADVETVKKLCCTV-QSVN 592
Db 467 ETALHMAARSGQAEVRYLVYDGAQVEAKXDQTPHLHSARLGKADIVVQLLQCGASPN 526
Qy 593 CRDTEGRSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSGHYEVAELL 652
Db 527 AATTSG--YTFPLHLSAREGHEDVAAFLDHDGASLSITTTKKGFTPLHVAARYKLEVANLL 584
Qy 653 VKHGAVNVNADLWKFTPLHEAAAKGKYEICKLLQHGADPTKKNRDGNTPLDL-VKGGDT 711
Db 595 LQKASPDPAAGSKGLTPLHVAAHYDNDQKVALLLDQASPHAAAKNGYTPHLHIAAKNQ 644
Qy 712 DIQDLL-----RGDAALLDAAKGCLARVKKLSSPD-NVNCRDQTQGRHSTPLH 758
Db 645 DIATTTLEYGADANAVTQGIASVHLAAQEGHVDVMSVLLLRNANVNLNKSQ--LTPH 702
Qy 759 LAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASVGHVDVAALLIKYNACVNAWK 818
Db 703 LAAQEDRVNVAEVLVNOGAHVDAQTQKGYTFLHVGCHYGNIKIVNFLQHSKAVNAKTN 762
Qy 819 AFTPLHEAAQKGRQTOLCALLLAHGADPTLKNQEGTPLDL-----VSADVSAALLT-AA 871
Db 763 GYTFELHQAQOQGHTHIINVLLQNNASPNELTVNGTALGIARRLGIYSVVDTLKIVTET 822
Qy 872 MPPSALPSCYK---PQVLNGVRSFCATADALSSGSPSSLSAASSLNDLSGSFSELSV 928
Db 823 MTTTTVTEKHKNVPEWTNEVLD-----MSDDEVKANAPEWLSQ----- 863
Qy 929 VSSSGTEGASLEKKEVPGVDFSIQFVRNLGLHLMDFIREQ-ITLDVLVEMGHKELK 987
Db 864 -----EYISDVEGEDAMTGTDTKYLGPQDLK 890
Qy 988 BIG 990
Db 891 ELG 893

RESULT 4
T42713
ankyrin 3, splice form 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42713
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, L.
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene f
the repeat domain.
A:Reference number: 222237; MUID:95340633; PMID:7615634
A:Accession: T42713
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1943 <PET>
A:Cross-references: UNIPROT:Q61307; UNIPARC:UPI0000028367; EMBL:L40632; NID:G710548; PID:
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Introns: 855/1
C:Function:
A:Description: supposed to play an important role in the polarized distribution of many i
A:Note: major kidney ankyrin
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match 13.8%; Score 891; DB 2; Length 1943;
Best Local Similarity 30.6%; Pred. No. 5.7e-46;
Matches 287; Conservative 127; Mismatches 380; Indels 144; Gaps 24;

Qy 105 ACRGNDVER-----VKRLVTEKYNRSDTAGKSTPLHFAAGFRKDWVEYLLQNGANVQA 160
Db 31 AARAGHLEKALDYTKNGV---DVNICNQNLNA--LHLASKEGHVEVWSELLQREANVDA 85
Qy 161 RDDGGLPLHNACSFHAEVWVLLRHGADPNARDNWNYPPLHEAAIKGIDVCIVLLOH 220

Db 86 ATKKGNATLHIAAGQAEVVKVLTNGANVNAQSQNGFTPLHMAAENHLEVVRFLLDN 145
Qy 221 GAETPIRTDGTALDLA-----DPSKAVLTGEYK---KDELESARSGNEEKMMALLT 272
Db 146 GASQSLATEDGFTPLAVALQGHQDVVSLLENDTKGKVRPALHIAARKDDTKAAALLL 205
Qy 273 PLNVNCHASGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLVPLHNAACSYGHE 332
Db 206 QNDTNADVESKSGFTPLHIAHYGNINIVATLLNRAAAVDFTARNDTPLHVASKRGAN 265
Qy 333 VTELLVHKGACVNAWDLWQFTPLHAAAKNRVEVCSLLSYGADPTLLNCHNKSALDAP 392
Db 266 MVKLLDRGAKIDAKTRDGLTPLHCGARGHEQVEMLLDRSA--PILSKYKN----- 316
Qy 393 TPOLKRLAVEFKHSLQAAREADVTRIKKHLSLEMVNFKH-----PQTHETALHCA 445
Db 317 -----GLSPHMAATQGD-----HLNCVQLLQHNVPVDDVTNDYLTALHVA 357
Qy 446 AASPYPRKQICELLLKRGANINEKTEFPLHVAASEKAHNDVVEVHGAENKVNALDN 505
Db 358 AHCGRHYK---VAKVLLDKKASPNKALNGETPLHIACKNRIRVMELLLKHGASIQAVTE 414
Qy 506 LGQTSLHRAAYCGHLCRLLSYGCDPNIIISLQGTALQMG-----NENVQQLLQEGIS 560
Db 415 SGLTPHVAAPFMGHVNIIVSQMHGASPTNTNVRGETALHMAARSGQAEVVRYLVQGAQ 474
Qy 561 LGNSEADQK---LLEBAKAGDVETVKKLCTV--QSVNCRDIEGRQSTPLHFAAGYNRVSV 617
Db 475 VEAKAKDDQTPHLSARLGKADIYQQLLQOGASPNAAATTSG--YTPLHLAAREGHEDVAA 532
Qy 618 YLLOHGADVHAKDKGLVPLHNAACSYGHEVVAELLVKHGAGVNVVADLWKFTPLHAAAKG 677
Db 533 FLDDHGASLSITTTKGGFTPLHVAAYKGLVSLQKASGLTPHVAAYHD 592
Qy 678 KYEICKLLOHGADPTKKNRDGNTPDLI--VKDGDTDIQLL-----RGDAALL 724
Db 593 NQKVALLLDQGASPHAAKNGYTPHIAKKNQMDIATSLLEYGADANAVTROGIIASVH 652
Qy 725 DAAKKGCLARVKLSSPD--NVNCRDIOQRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQD 783
Db 653 LAQEGHVDWVSYLLSRNANVNLKSG--LTPLHLAAGQEDRVNVAEVLVNGAHVDAQT 710
Qy 784 KGGILPLHNAASGHVDVAALLIKYNAQVNTDKWATPLHAAKQRTQCALLLAHGA 843
Db 711 KMGYTPLVHGYGNIKIIVNPLQHSKAVNAKTNGYTAHQAAQOQGHTHIINVLLQNA 770
Qy 844 DPTLKNQEGQTPDLVS-----ADVSALLTAAMPSPALPSCYK---PQVLNGVRS 893
Db 771 SPNELTVNGNTALAIARRLGVISVVDLTKVYTEIMTTTTITEKHKNVPEMTEVLD-- 828
Qy 894 ATADALSSGSPSSSLSAASSLDNLS--GSFSELSSVSSSGTEGASSLEKEVPGVDFSI 952
Db 829 -----MSDDEVKASAPEKLSDEY-----ISDSEEG----- 855
Qy 953 TQFVRNLGLEHLMDFIREQITLVLVEMGHKELKEIG 990
Db 856 -----EDAITGDTDKYLQDQLKELG 876

RESULT 5
T42715
ankyrin 3, splice form 3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42715
R:Peterson, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.
J. Cell Biol. 130, 313-330, 1995
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A:Reference number: 222237; PMID:95340633; PMID:7615634
A:Accession: T42715
A>Status: preliminary; translated from GB/EMBL/DBDJB

A:Molecule type: mRNA
A:Residues: 1-1940 <PET>
A:Cross-references: UNIPROT:Q61307; UNIPARC:UPI0000029ABD; EMBL:L40632; NID:g710548; PID:
A:Experimental source: strain C57BL/6J; kidney
C:Genetics:
A:Gene: Ank3
A:Map position: 10
A:Introns: 834/1
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing

Query Match 13.8%; Score 889; DB 2; Length 1940;

Best Local Similarity 27.9%; Pred. No. 7.5e-46;

Matches 337; Conservative 168; Mismatches 496; Indels 206; Gaps 38;

Qy 68 AVAAARIMSGRRCCAGGAAACASAAAEVPEARELFEACNGDVERVKRLVTPEKNSRD 127

Db 10 AKPAHRKRKKGKSDANASYLRAARAGHLEKA-----LDYIKNG-----VDVNICN 54

Qy 128 TAGRKSTPLHFAAGFRKDVVEYLLQNGANVQARDGGLIPLHNACSFCHAEVNNLLRH 187

Db 55 QNGLNA--LHLASKEGHVEVVSSELLQREANVDAATKKGNTALHIASLAGQAEVVKLVLTN 112

Qy 188 GADPNARDNNWYTPHHEAAIKGKIDVICVILLOHGAEPITIRNTDGTALDLA-----DPSA 242

Db 113 GANVNAQSQNGFTPLHMAAENHLEVVRFLLDNGASQSLATEDGFTPLAVALQGHQDV 172

Qy 243 KAVLTGEYK---KDELESARSGNEEKMMALLTPLNVNCHASGRKSTPLHLAAGYNRVK 299

Db 173 SLELENDTKGKVRPALHIAARKDDTKAAALLQNDTNADVESKSGFTPLHIAHYGNIN 232

Qy 300 IVOLLQHGADVHAKDKGLVPLHNAACSYGHEVTELLVKHGACVNAWDLWQFTPLHEAA 359

Db 233 VATLLNRAAAVDFTARNDTPLHVASKRGANVNVKLLDRGAKIDAKTRDGLTPLHCGA 292

Qy 360 SKNRVCSLLSYGADPTLLNCHNKSALDIAPTPOLKRLAVEFKHSLQAAREADV 419

Db 293 RSHEQVEMVLLDRSA--PILSKYKN-----GLSPHMAATQGD-- 328

Qy 420 RIKKHLSLEMVNFKH-----PQTHETALHCAASPYPRKQICELLLKRGANINEKTK 472

Db 329 ----HLNCVQLLQHNVPVDDVTNDYLTALHVAACHGHYK---VAKVLLDKKASPNKAL 381

Qy 473 EFTPLHVAASEKAHNDVVEVHGAENKVNALDNLGQTSLHRAAYCGHLCRLLSYGCD 532

Db 382 NGFTPLHIACKNRIRVMELLLKHGASIQAVTESGLTPHVAAPFMGHVNIIVSQMHGAS 441

Qy 533 PNIISLQGTALQMG-----NENVQQLLQEGISLGNSEADQK---LLEBAKAGDVETVKKL 585

Db 442 PNTNVRGETALHMAARSGQAEVVRYLVQDGAQVEAKAKDDQTPHLSARLGKADIYQQL 501

Qy 586 CTV--QSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGLVPLHNAACSYG 644

Db 502 LQOGASPNAAATTSG--YTPLHLAAREGHEDVAAFLDDHGASLSITTTKGGFTPLHVAAYK 559

Qy 645 HYEVAELLVKHGAVNVVADLWKFTPLHAAAKGYEICKLLOHGADPTKKNRDGNTPDL 704

Db 560 KLEVASLLQKASPDAAKSGSLTPHVAAYHQNQKVALLLDQGASPHAAKNGYTPHLH 619

Qy 705 L-VKDGDTDIQLL-----RGDAALLDAAKKGCLARVKKLSSPD--NVNCRDQ 750

Db 620 IAAKKNQMDIATSLLEYGADANAVTROGIIASVHLAAGEHVDVMSLLSRNANVNLNKS 679

Qy 751 GRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASGHVDVAALLIKYNA 810

Db 680 G--LTPLHLAAQEDRVNVAEVLVNGAHVDAQTKMGYTPHVGCHYGNIKIIVNPLQHSA 737

Qy 811 CVNATDKWATPLHAAKQRTQCALHAGADPTLKNQEGQTPDLVS-----ADD 863

Db 738 KVNAKTNGYTAHQAAQOQGHTHIINVLLQNNASPNELTVNGNTALAIARRLGVISVVD 797

Qy 864 VSALLTAAMPSPALPSCYK---PQVLNGVRS 900

Db 798 LKVVTEIMTTTTITEKHGMVNPETMNEVLDMDDGDKCTWFKIPKQVQLVKSEDAIT 857
 Qy 901 S-----CP-----SSPSSLSAASSLNLGSGFSELSVVS-----SSGTEGASSL 940
 Db 858 GDTDKYLGPDQLKELGDDSLPAEGVYGSIGARSLSRFSDSRSTYTLNRSYARDSMMI 917
 Qy 941 EKKEVPGVDFISITOPVNLGLEHLMIDIFERQITLDVL-----VEMGHKELKEIGINAY 994
 Db 918 BELLVPSKEQHLT-PTREFDSDSLRH-YSWAADTLDNVNLVSSPVHSGF--LVSFMDAR 973
 Qy 995 G-----HRKLI-----KGVRLISGCGGLNPNLYTLNTSSGTHLIDLSDD 1036
 Db 974 GSGMRGSRHGMRIIPRCKTAPTRICRLVGRKHLANPPMVEGEGLASRLVEMGPAG 1033
 Qy 1037 KEFQS-VEEEMQSTVREHDDGHAGGIFNRVNLKIQKCNKCLWE--RYTHRKEVSE- 1092
 Db 1034 AQLGPGVIVEIP-----HFGSMRGKRELIIVLRSNGETWKEHQPSKNEDLAEL 1083
 Qy 1093 ----ENHNHANERMLFHGSPFVNIIHKGFDERHAYIGMGFAGIYFAENS---SKSNQY 1145
 Db 1084 LMGDEELDSPEEL--GTGKICRIITKDFPQ-----YFAVVSRIKQESNQ- 1126
 Qy 1146 VYIGGG 1152
 Db 1127 -IGPEGG 1132

RESULT 6

B35049
 N;Ankyrin 1, erythrocyte splice form 3 - human
 N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
 C;Species: Homo sapiens (man)
 C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
 C;Accession: B35049
 R;Lambert, S.; Yu, H.; U.S.A. 87, 1730-1734, 1990
 Proc. Natl. Acad. Sci.
 A;Title: cDNA sequence for human erythrocyte ankyrin.
 A;Reference number: A35049; MUID:90175370; PMID:1689849
 A;Accession: B35049
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1856 <LAM>
 A;Cross-references: UNIPARC:UPI0000177546
 C;Genetics:
 A;Gene: GDB:ANK1; ANK
 A;Cross-references: GDB:118737; OMIM:182900
 A;Map position: 8p11.2-8p11.2
 C;Superfamily: ankyrin; ankyrin repeat homology
 C;Keywords: alternative splicing
 F;2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>
 F;2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
 F;44-76/Domain: ankyrin repeat homology <AN01>
 F;77-109/Domain: ankyrin repeat homology <AN02>
 F;110-142/Domain: ankyrin repeat homology <AN03>
 F;143-171/Domain: ankyrin repeat homology <AN04>
 F;172-204/Domain: ankyrin repeat homology <AN05>
 F;205-237/Domain: ankyrin repeat homology <AN06>
 F;238-270/Domain: ankyrin repeat homology <AN07>
 F;271-303/Domain: ankyrin repeat homology <AN08>
 F;304-336/Domain: ankyrin repeat homology <AN09>
 F;337-369/Domain: ankyrin repeat homology <AN10>
 F;370-402/Domain: ankyrin repeat homology <AN11>
 F;403-435/Domain: ankyrin repeat homology <AN12>
 F;436-468/Domain: ankyrin repeat homology <AN13>
 F;469-501/Domain: ankyrin repeat homology <AN14>
 F;502-534/Domain: ankyrin repeat homology <AN15>
 F;535-567/Domain: ankyrin repeat homology <AN16>
 F;568-600/Domain: ankyrin repeat homology <AN17>
 F;601-633/Domain: ankyrin repeat homology <AN18>
 F;634-666/Domain: ankyrin repeat homology <AN19>
 F;667-699/Domain: ankyrin repeat homology <AN20>
 F;700-732/Domain: ankyrin repeat homology <AN21>

F;733-765/Domain: ankyrin repeat homology <AN22>
 F;766-798/Domain: ankyrin repeat homology <AN23>

Query Match 13.6%; Score 880.5; DB 2; Length 1856;
 Best Local Similarity 26.0%; Pred. No. 2.3e-45;
 Matches 294; Conservative 156; Mismatches 374; Indels 307; Gaps 29;
 Qy 105 ACRGNDVERKRLVTPEKVNRSRDTAGRKSTPLHFAAGFGRKDVVVEYLQNGANVOARDG 164
 Db 52 ASKEGHVKNVVELLHKE-IILETTTKGNTALHIALAGQDEVVRELNVYGANVNAQSQK 110
 Qy 165 GLIPLHNACSGHAHVNNLLRHGADPNARDNNMYTPLHAAIKGKIDVICVILLOHGABP 224
 Db 111 GFTPLYMAAGBNHLEVVKFLLENGANQVATEDFTPLAVALQOCHENVAHLINYGTKG 170
 Qy 225 TI-----RNTDGTALDLADPSAKAVLTGKYKDELLESARSNGEKKMALLTPLN 275
 Db 171 KVRPLALHIAARNDDTETA-----AVLLQNDPNPDLV--SKTG-----FTPLH 211
 Qy 276 VNCHASD-----GRKS-----TPHLAAGYNRVKIVQLLLOHGADVHAKDKG 317
 Db 212 IAAHYENLVNAQALLNRGSSVNFPPQGITPLHIASRGNVIMVRLLLDRGAQIETKTKD 271
 Qy 318 DLVPLHNACSYGHYEVTELLAVKHGACVNMADLMQFTPLHAAASKNRVEVCVSLLSYGADP 377
 Db 272 ELTELHCAARNGHVRISEILLDHGAPIQAKTKNGLSPIHMAAQGDHLDCLVLLQYDAE- 330
 Qy 378 TLLNCHNKSALDAPTQLKERLAYEFKSHSLLOQAAREADVTRIKKLSLEWVNFKHPQT 437
 Db 331 -----ID-----DIT-----LD 337
 Qy 438 HETALHCAAAAPYPRKQICELLRLKGNANTKEFTPLHVASBKAHNDVVEVVKHE 497
 Db 338 HLTPLVHAA---HCGHHRVAKVLLDKGAKPNSRALNGFTPLHIAACKNHNVRMELLTKG 394
 Qy 498 AKVNALDNLGQTSLSHRAAYCGHLQTCRLLSYCGDPNIIISLQGTALQMG-----NENVQ 552
 Db 395 ASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVSVKVVETPLHMAARAGHTEVAK 454
 Qy 553 QLLQE-----GISLGNSEADROLLE-----AAKAG 577
 Db 455 YLLQNKAKVNAKAKDDQTPLFCAARIIGHTNNVKLLLENNANPNLATTAGTPLHIAAREG 514
 Qy 578 DVETVKKLCTVO--SVNCRDIEGRQSTPLHFAAGYNRVVVEYLLOHGADVHAKDKGLVP 636
 Db 515 HVEIVLALLSEKASQACMTKKG--FTPLHVAATKGVKRVAEELLERDAHPNAAKNGLTP 572
 Qy 637 LHNACSYGHYEVAELLVKHGAVNVNADLWK-FTPLHEAAAARKYEICKLILQHGADPTKK 695
 Db 573 LHVAVHNNLDIVKLLLPGRGSPH-SPAWNIGYTPPLHIAAKQNVQVEVARSLLQYGSANAE 631
 Qy 696 NRQDNTPLDL-VKDGDTDIQDLRLGDAALLDAKKGCLARVKKLSPPDNVNCRDTOGRHS 754
 Db 632 SVQGVTPHLAAQEGHAEVALL-----LSKQANGNLKSG--L 669
 Qy 755 TPLHLAAGYNVLEVAEYLLOHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNACVNA 814
 Db 670 TPLHLVAQEGHVPADVLIKHGMVMDATTRMGYTPPLHVASHYGNIKLVKFLLOHQADVNA 729
 Qy 815 TDKWAFTPLHEAAQKGTOLCALLLAHGADPTLKNQSGQTPDL-----VS 860
 Db 730 KTKLGYSPHLQAQQOQHTDIVTLLLNKGNASPNVSSDGTTPLAIAKRLGYISVTDVLKV 789
 Qy 861 ADDVSALLTAAMPSPALPSC-----YKQP 884
 Db 790 TDETSFVLVSDKHRMSPFETVDEILDVSEGEBELISFKAERDRSRDVEDEKELLDVFPK 849
 Qy 885 VLNGVRSPPGATADALSGPSSPSLS-----AASLDNLGSGFSELSVVSSSGTEGASS 939
 Db 850 LDQWVESPAI-----PRIPCAMPETVTVIRSEEQQASKEYDEDESLIPSSPATETSDN 901
 Qy 940 LEKKEVPGVDFSIQTQFVRNLGLEHLMIDIFEREQITLDVLVEMGHKELKEIGINAYGHRHK 999

Db 902 ISPVASPVHTGFLVSFM-----VDARGSGMRGSRHN 932

Qy 1000 LIKGVE-----RLISQQGLNPYLTLNTSGSTILIDLSP----- 1034

Db 933 GLRVVIPPRTCAAPTRITCLRVKPKQLSTPPPLAEEGLASRIIALGPTGAQFLSPVIVE 992

Qy 1035 -----DDKEFQSVSEEMOSTVREHGRDGHAGGIFNRYNLIKIOKVCN 1076

Db 993 IPHFASHGRGDRELVLVRSNGSVWKEHR-----SRYGESYLDQILN 1034

RESULT 7

A35049

ankyrin 1, erythrocyte splice form 2 - human

N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

C;Species: Homo sapiens (man)

C;Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004

R;Accession: A35049

R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A;Title: cDNA sequence for human erythrocyte ankyrin.

A;Reference number: A35049; MUID:90175370; PMID:1689849

A;Accession: A35049

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1880 <LAM>

A;Cross-references: UNIPROT:P16157; UNIPARC:UPI0000177545; GB:M28880

C;Genetics:

A;Gene: GDB:ANK1; ANK

A;Cross-references: GDB:118737; OMIM:182900

C;Map position: 9p11.2-9p11.2

C;Superfamily: ankyrin; ankyrin repeat homology

C;Keywords: alternative splicing; cytoskeleton

P;2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>

P;2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>

P;44-76/Domain: ankyrin repeat homology <AN01>

F;77-109/Domain: ankyrin repeat homology <AN02>

F;110-142/Domain: ankyrin repeat homology <AN03>

F;143-171/Domain: ankyrin repeat homology <AN04>

F;172-204/Domain: ankyrin repeat homology <AN05>

F;205-237/Domain: ankyrin repeat homology <AN06>

F;238-270/Domain: ankyrin repeat homology <AN07>

F;271-303/Domain: ankyrin repeat homology <AN08>

F;304-336/Domain: ankyrin repeat homology <AN09>

F;337-369/Domain: ankyrin repeat homology <AN10>

F;370-402/Domain: ankyrin repeat homology <AN11>

F;403-435/Domain: ankyrin repeat homology <AN12>

F;436-468/Domain: ankyrin repeat homology <AN13>

F;469-501/Domain: ankyrin repeat homology <AN14>

F;502-534/Domain: ankyrin repeat homology <AN15>

F;535-567/Domain: ankyrin repeat homology <AN16>

F;568-600/Domain: ankyrin repeat homology <AN17>

F;601-633/Domain: ankyrin repeat homology <AN18>

F;634-666/Domain: ankyrin repeat homology <AN19>

F;667-699/Domain: ankyrin repeat homology <AN20>

F;700-732/Domain: ankyrin repeat homology <AN21>

F;733-765/Domain: ankyrin repeat homology <AN22>

F;766-798/Domain: ankyrin repeat homology <AN23>

Query Match 13.6%; Score 880.5; DB 2; Length 1880;

Best Local Similarity 26.0%; Pred. No. 2.4e-45;

Matches 294; Conservative 156; Mismatches 374; Indels 307; Gaps 29;

Qy 105 ACRNGDVERVKRLVTPPEKNSRDYAGKSTPLPHFAAGFGKDVVBYLLQNGANVOARDG 164

Db 52 ASKEGHVWVVELLHKE-IILLETTKGNTALHIALAGQDEVVRELNYNGANVNAQSQK 110

Qy 165 GLIPLHNACSGFHAEVNNLLRHGHADPNARDNNVTPPLHEAAIKGIDVCIVLLQHGAP 224

Db 111 GFTPLYMAAQENHLEVVVKFLLNGANQNVATEDGFTPLAVALQQGHENVAHLINYGTKG 170

Qy 225 TI-----RNTDGRDALDADPSAKAVLTGEYKDKDELLESARSGNEEKWALLTPLN 275

Db 171 KVLPLALHIAARNDDTRTA-----AVLLQNDPNPDVL--SKTG-----FTPLH 211

Qy 276 VNCASD-----GRKS-----TPLHLAAGYNRVKIVQLLQHGADVHAKDKG 317

Db 212 IAAHYENLNVAQLLNRGSSVNFPTQNGITPLHIAASRGNVIMVRLLLDRGAQIETKTKD 271

Qy 318 DLVPLHNACSYGHVEVTELLVKHGACVAMDLWQFTPLHEAASKNRVEVCSLLLSYGADP 377

Db 272 ELTPLHCAARNGHVRISEILLDHGAPIQAKTKNGLSPIHMAAQGDHDCVRLLLQYDAE- 330

Qy 378 TLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAREADVTRIKKHSLESMVNFKHPQT 437

Db 331 -----ID-----DIT-----LD 337

Qy 438 HETALHCAASAPYKPKQICELLRLKGANINEKTEFLTPHLVASEKAHNDVVVVVKE 497

Db 338 HLTPLHVA--HCGHHRVAKVLLDKGAKPNRSLNGFTPLHIACKKNHVRVMEILLKTG 394

Qy 498 AKVNALDNLGOTSLHRAAYCGHLQTCRLLSYGCDPNIIISLOQFTALOMG-----NENVQ 552

Db 395 ASIDAVTESGTLPLHVASFMGHLPIVKNLLQRCASPNVSNVKVETPLHMAARAGHTEVAK 454

Qy 553 QLLQE-----GISLGNSEADROLLE-----AAKAG 577

Db 455 YLLQNKAKVNAKAKDDQTPLHCAARIGHTNMVYKLLLENNANPNLATTAGHTPLHIAAREG 514

Qy 578 DVETVKLCITVQ--SVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGLVP 636

Db 515 HVETVLALLEKEASQACMTKKG--FTPLHVAAYKGVRAELLERDAHPNAGKNGLTP 572

Qy 637 LHNACSYGHYEVAELLVKHGAVVNVADLWK--FTPLHEAAAKGYEICKLLLOHGADPTKK 695

Db 573 LHVAVHHNLDIVKULLPRGSGPH--SPAWNGYTPHLHIAKQKQNEVARSLQYGGANAE 631

Qy 696 NRDGNTPDL--VKQGDGTDIQDLRLGDAALLDAAKGCGLARVKLSPDNVNCRDTOGRHS 754

Db 632 SVQGVTPHLAAQEGHAEMVALL-----LSQANGNLGNKSG--L 669

Qy 755 TPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNACVNA 814

Db 670 TPLHLVAQEGHVPVADVLIKHGVWVDATTRMGYTPHLHVASHYGNIKLVKFLQHQADVNA 729

Qy 815 TDKWAFTPLHEAAQKRTQLCALLAHGADPTLKNQEGOTPLDL-----VS 860

Db 730 KTKLGYSLPHQAQGGHTDITVLLKNGASPNVSDGTTPLAIKRLGYISVTDVLKVV 789

Qy 861 ADDVSALLTAAMPSPALPSC-----YKPK 884

Db 790 TDETSFVLVSDKHRMSFPETVDEILDVSEDEBELISPKAERRDSRDVEKELLDVFPK 849

Qy 885 VLVNGVRSPGATADALSSGSPSSSL--AASSLDNLSGSFSESSVSVSSSGTEGASS 939

Db 850 LDQVVESPA-----PRIPCAMPETVIVRSEEQEASKEYDEDSLIPSSPATETSDN 901

Qy 940 LEKKEVPGVDFSIOTFVRNLGLEHLDIFEREQITLDVLVEMGHKELKEIGINAYGHRHK 999

Db 902 ISPVASPVHTGFLVSFM-----VDARGSGMRGSRHN 932

Qy 1000 LIKGVE-----RLISQQGLNPYLTLNTSGSTILIDLSP----- 1034

Db 933 GLRVVIPPRTCAAPTRITCLRVKPKQLSTPPPLAEEGLASRIIALGPTGAQFLSPVIVE 992

Qy 1035 -----DDKEFQSVSEEMOSTVREHGRDGHAGGIFNRYNLIKIOKVCN 1076

Db 993 IPHFASHGRGDRELVLVRSNGSVWKEHR-----SRYGESYLDQILN 1034

RESULT 8

SUHK

ankyrin 1, erythrocyte splice form 1 - human

N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N;Contains: ankyrin 2.2

Query Match 13.6%; Score 878.5; DB 1; Length 1881;
Best Local Similarity 25.8%; Pred. No. 3.2e-45;

Matches	292;	Conservative	157;	Mismatches	375;	Indels	307;	Gaps	28
Qy	105	ACRNGDYVERKRLVLTPEKNSRDTAGRKSTPLHFAAGFGRKDYVEYLLQNGANVQARDG	164						
Db	52	ASKEGHVGMVVELLHKE-IIETTTKKGNTALHIAALAGQDEVVRELVNYGANVNAQSOK	110						
Qy	165	GLPLHNACSFGEAEVNVLLRRGADPNARDNNYTPLEHAAAIKGIKDVCIVLLOHGAE	224						
Db	111	GFTPLPMAAQENHLEVVKFLLENGANQNATEDGFTPLAVALOQGHENVVAHLINTGTG	170						
Qy	225	TI-----RNTDGRALTDLADPSAKAVLTGEYKDKDELLESARSNEBEKMAWLLTPLN	275						
Db	171	KVRLPALHIAARNDTRTA-----AVLLQNDPNPDVL-----SKTG-----FTPLH	211						
Qy	276	VNCHASDGRKS-----TPLHAAAGYNRVKIVQLLOLHGHADVHARDKG	317						
Db	212	IAAHYENLNVALLNRGASVNFPPQNGITPLHIASRRGNVIMVRLLDORGAIKTKTD	271						
Qy	318	DIAPLHNACSYGHYEVTELLVKGICACVNAMDLWQFTPLHBAASKNRYEVCSSLLLSYGADP	377						
Db	272	ELTPLHCAARNGHVRISIELLDHGAPIQAKTKNGLSPIHMAAQGDHLDCLRLLLOYDAE-	330						
Qy	378	TLLNCHNSKAIDLAPTTPOLKERLAYEFKGHSLLQAAAREADVTRI KKHLSLEWMVNFKHQPT	437						
Db	331	-----ID-----GISIGNSEADQILLE-----DIT-----LD	337						
Qy	438	HETALHCAAASPYPKRKQICELLRLRGANINEKTEBFLTPLHVASAKAHNDVVEVVVKGHE	497						
Db	338	HLTPLHVA--HCGHHRVAKVLLDKGAKPNSRALNGFTPLHITACKKNHVRVWELLKTKG	394						
Qy	498	AKYNALDNIGQTSLHRAAYCGHLQTCRLLLSYGCDDNIIISLQGF TALQWG-----NENVO	552						
Db	395	ASIDAVTESGLTPLHVASFMEGHLPIVKNLLQORGASPNVSNVKVETPLHMAARAGHTEVAK	454						
Qy	553	QLLQOE-----GISIGNSEADQILLE-----RAKG	577						
Db	455	YLLQNKAKNVAKAKAQDQTPHCAARTIGHTNMVKLLLENNANPNLATAGHTPLHIAAREG	514						
Qy	578	DVETVKKLCTVQ-SVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDKGLVP	636						
Db	515	HVETVLLALLEKESAOACMTKKG--FTPLHVAKYGKVRVAELLERDAHPNAGKNGLTP	572						
Qy	637	LHNACSYGHYEVAELLVKGGA VVNVADLWK-FTPLHAAAKGKYETCKILLQHGADPTKK	695						
Db	573	LHVAVHNNLDIVKLLPRGGSPH-SPAWNVTPLHIAAKQNEVARSLQYGGSANAE	631						
Qy	696	NRDQNTPLDI-VKQDGTDIQDILRGDAALLDAAKCKCLARVKLSLSPDNVNCEDTQGRHS	754						
Db	632	SVQGVTPPLHAAQGEAEVWALL-----LSKQANGNLGNKSG--L	669						
Qy	755	TPHLAAGYNNLEVAEYLLQHGADVNAODKGLIPLHNAASYGHVDVAALLIKYNACVNA	814						
Db	670	TPHLVVAQSGHPVADVLIKHWVDWATTRMGYTPLVAVASHVGNIKLVKFLQHQADVNA	729						
Qy	815	TDKMAFTPLHEAAQKGRQTOLCALLLAHAGADPTLKNQEGQTPLDL-----VS	860						
Db	730	KTKLGYSPHLQAAQOQGTDIVTLLKNGASPNESVSDGTTPLAIAKRLGYISVTDVLKV	789						
Qy	861	ADDVSALLTAAMPSPALPSC-----YKQ	884						
Db	790	TDSTSFVLVSDKHRMSFPETVDEILDVSEDEGEELISFKAARRDRSDVDDEKELDLFVK	849						
Qy	885	VLNGVESPATADALSSGSPSSILS-----AASLDNLSGSFSELSVSVSSSGTEGASS	939						
Db	850	LDQVESPAL-----PRICAMPETVVISBEQEQASKEYDEDSLIPSSPATETSDN	901						
Qy	940	LEKKEYPGVDFSIQTVRNVLGLEHMLDIFEREQITLDVLVEMGHKELKEIGINAYGHRHK	999						
Db	902	ISPVASPVHTGFLVSPM-----VDARGSGMRGSRHN	932						
Qy	1000	LKIGVE-----RLISGOQGLNPYTLNTSGGTTLLIDLSP-----	1034						
Db	933	GRVVTIPRPTCAAPTRITCRLVKPKSLPFPPLABEEGLASRIIALGPTGAQFLSPVIVE	992						

Db 821 TTTTITTEK-----HKLNPVTMTVEVL-----DVSDEGDDTWTGDBGYLRPEDLK 868
Qy 926 ----SSVSSSTEGGASSLEKEVCPVDSITQFV--RNGLGLEHLMDFPERQIITLDVLY 979
Db 869 ELGDDSLPSSQFLDGMNLYRLSLEGRSDRSFSDRSHTLASHAS--YLRDSAVMDDSV 926
Qy 980 EMGHKELKEIGINAYGHRHKLKIGVERL 1007
Db 927 VIPSHOVSTLAKEAERNRYLSWGTENL 954

RESULT 10
S37771
Ankyrin, erythrocyte - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S37771
R:Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.
J. Biol. Chem. 268, 9533-9540, 1993
A:Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found an
A:Reference number: S37771; MUID:93252825; PMID:8486643
A:Accession: S37771
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1848 <BIR>
A:Cross-references: UNIPROT:Q61302; UNIPARC:UPI0000028360; EMBL:X69063; NID:G311816; PID
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:48-80/Domain: ankyrin repeat homology <AN01>
F:81-113/Domain: ankyrin repeat homology <AN02>
F:114-146/Domain: ankyrin repeat homology <AN03>
F:147-175/Domain: ankyrin repeat homology <AN04>
F:176-208/Domain: ankyrin repeat homology <AN05>
F:209-241/Domain: ankyrin repeat homology <AN06>
F:242-274/Domain: ankyrin repeat homology <AN07>
F:275-307/Domain: ankyrin repeat homology <AN08>
F:308-340/Domain: ankyrin repeat homology <AN09>
F:341-373/Domain: ankyrin repeat homology <AN10>
F:374-406/Domain: ankyrin repeat homology <AN11>
F:407-439/Domain: ankyrin repeat homology <AN12>
F:440-472/Domain: ankyrin repeat homology <AN13>
F:473-505/Domain: ankyrin repeat homology <AN14>
F:506-538/Domain: ankyrin repeat homology <AN15>
F:539-571/Domain: ankyrin repeat homology <AN16>
F:572-604/Domain: ankyrin repeat homology <AN17>
F:605-637/Domain: ankyrin repeat homology <AN18>
F:638-670/Domain: ankyrin repeat homology <AN19>
F:671-703/Domain: ankyrin repeat homology <AN20>
F:704-736/Domain: ankyrin repeat homology <AN21>
F:737-769/Domain: ankyrin repeat homology <AN22>
F:770-802/Domain: ankyrin repeat homology <AN23>

Query Match 13.6%; Score 876; DB 2; Length 1848;
Best Local Similarity 29.7%; Pred. No. 4.4e-45;
Matches 250; Conservative 132; Mismatches 281; Indels 178; Gaps 21;

Qy 105 ACRNGDVERKRLVTPKEKNSRDTAGRKSTPLHFAAGFGKDVVEYLLQNGVANQARDGG 164
Db 56 ASKEGHVKMVVELLHKE-IILETTTKGNTALHIAALAGQDEVRELVNNGANVAQSQK 114
Qy 165 GLIPLHNACSFGEAVNVLRLHGDADPNARDNNVYTPLHEAAIKGKIDYCVILLQGAEP 224
Db 115 GTPLYMAAQENHLEVVKVFLLENGANQNVATDGTFTPLAVLQQGHENVAHLINYGTK 174
Qy 225 TT-----RNTDQRTALDLPKSAKAVLGEYKKBELLESARSGBEKKWALLTPLN 275
Db 175 KVRLLPALHTAARNDDTRTA-----AVLLQNDPNPVL--SKTG-----FTPLH 215
Qy 276 VNCHASDGRKS-----TPLHLAGYNNRVKIVQLLQHGADVHAKDKG 317
Db 216 IAAHYENLVNVAQLLNRRGASVNFPTQGITPLHIASRRGNVIMVRLLDGRGAIETRTKD 275

Qy 318 DLVPLHNACSYGHEVTELLVKHGACVNMADLWOTPLHEAASKNRVVEVCSLLSYGADP 377
Db 276 ELTPLHCAARNGHVRISILLDHGAPIQAKTKNGLSPIHMAAQGDHDLQVLLQYNAB- 334
Qy 378 TLLNCHNKASIDLAPTTPOLKERLAYEFKHSLLQAAREADVTRIKKHLSLEWVNFKHPOT 437
Db 335 -----ID-----DIT-----LD 341
Qy 438 HETALHCAASPYPKRKQICELLRLKGANINEKTEFLTPHLHVAASEKAHNDVVEVVKHE 497
Db 342 HLTPLVHAA---HCGHHRVAKVLLDKGAKPNRSLNGFTPLHIACKKHIRWELLKTKG 398
Qy 498 AKVNALDNLGOTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLQGFALQW---GNENVQQ 553
Db 399 ASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVSNKVVETPLHMAARAGTEVAK 458
Qy 554 LLOEGISLGNSEAD-----RQLE-----AAKAG 577
Db 459 YLLQWAKANAKAKDDQDTPHCAARIGHTGMVKLLLENGASPNLATTAGHTPLHTAAREG 518
Qy 578 DVETVKLCTVQ--SVNCRDIEGRQSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDKGLVP 636
Db 519 HVDTALALLEKEASQACMTKG--FTPLHVAAYKGVRLAELELLEHDAHNAAGNGLTP 576
Qy 637 LHNACSYGHEVVASILLVKHGAVNVNADLWK--FTPLHEAAAKGKYBICKLLLOHGADPTKK 695
Db 577 LHVAVHNHNLDIVKLLPRGSGSPH--SPAANGVTPLHIAAKNQIEVARSLQLYGGSANAE 635
Qy 696 NRDGNTPDL--VKGDGTDIQLLRGDAALLDAAKKGCLARVKKLSPPNVNCRDTQGRHS 754
Db 636 SVQGVTPHLAAQEGHTEWALL-----LSQANGNLGNKSG--L 673
Qy 755 TPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASVGHVDVAALLIKYNACVNA 814
Db 674 TPLHLVSEQEHPVADVLIKHGTVDTATRCGYTPLHVAASHYGNIKLVKFLQHQADVNA 733
Qy 815 TDKNWAFPLHEAAQKGRGTQCALIILAHGADPTLKNQEGQTPLDL-----VSADVDVALL 868
Db 734 KTKLGYSPHQAAQGGHTDIVTLLLLKNGASPNVSSNGTTPLAIAKRLGYISVTDVLKV 793
Qy 869 T 869
Db 794 T 794

RESULT 11
I49502
Ankyrin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49502
R:White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
Mamm. Genome 3, 281-285, 1992
A:Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory dome
A:Reference number: I49502; MUID:92345717; PMID:1386265
A:Accession: I49502
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1862 <RES>
A:Cross-references: UNIPROT:Q02357; UNIPARC:UPI000002921E; GB:M84756; NID:G191939; PID:1
C:Genetics:
A:Gene: Ank-1
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:40-72/Domain: ankyrin repeat homology <AN01>
F:73-105/Domain: ankyrin repeat homology <AN02>
F:106-138/Domain: ankyrin repeat homology <AN03>
F:139-167/Domain: ankyrin repeat homology <AN04>
F:168-200/Domain: ankyrin repeat homology <AN05>
F:201-233/Domain: ankyrin repeat homology <AN06>
F:234-266/Domain: ankyrin repeat homology <AN07>
F:267-299/Domain: ankyrin repeat homology <AN08>
F:300-332/Domain: ankyrin repeat homology <AN09>


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Db 579 RGPV-----DIEGKQVTPHVAHAHNNKVMALLLENG 613
Qy 777 ADVNAQDKGLIPLHNAASYGHVDAALLIKYNACVNATDKMAFTPLHEAAQKGRITOLCA 836
Db 614 ASAKAAAKNGYTPHLIAAKKQMEIATLLQPKADPNKSRAGTPLHLQAQEGHKEISG 673
Qy 837 LLLAHGADPTLKNQEGQTPLDLSADD-----VSALLTAAMPSPSALPCYK 882
Db 674 LLIENGSDVGAKANGLTAMHLCAQEDHPVPAQILYNGAEINSKTWAGYTPHLHV-ACHF 732
Qy 883 PQVLNGYR---SPGATADALSSGSPSSLSAASSLONLSGSPSELSSVSSSGTEGASS 939
Db 733 GQ-LNMWKFVLENGADVGEKTRASYTPPLHQAQQOQHNNVCYLLLE-----NGASP 781
Qy 940 LEKEVPGVDFSTQFVRNLG----LEHLMDFPREQITLDVLVEMGHKELKEIGIN--- 992
Db 782 NEQATGQTPLSIAQ---RLGVSVWETRTVTITTTTVDERYKQPQNPAMNETM 838
Qy 993 -----AYGHRKLI-----KGVRLISGOOGLNPVTLTNSG--- 1024
Db 839 FSESEDEQAABEAVAHAHEKDFSDNLTQGLQDSTGVHMIHTGSQLQSQELENGGAIP 898
Qy 1025 --SGTILIDLPDKFQSFQVEEMQS---TVREHRDG--GHAGGIFNRYNLIKIQVC 1075
Db 899 KINSQ-----GMSPT-EKEFAKTAIPVATSPATSNQSQFGLAPRAGSISGFGQQOPLHGAG 953
Qy 1076 NKKLWERYTHRRKE--VSEENHNHANERMLPHGS-----PFVNAIHKGF-----DERHA 1123
Db 954 PEDNLEELVRAQNHPIAGNYDNGGVAMLENGHADNVPIGHVHTQPSFLISPLVDARGG 1013
Qy 1124 YIGMFAGIYFAENSCKSNQYVIGGGTCCPVHKDRSCVICHRLQLFCRVTLGKSKFLQ 1183
Db 1014 AMRCRHSVGRVILVPPRKASQ-----PIR-----VTCRY-LRKD--- 1046
Qy 1184 PSAMKNAHSPP 1194
Db 1047 ----KLAHPPP 1053

RESULT 14
T42691
hypothetical protein DKFZp434D2328.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42691
R;Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, November 1999
A:Reference number: 222230
A:Accession: T42691
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-791 <AAA>
A:Cross-references: UNIPROT:Q9UPA4; UNIPARC:UPI000006DC92; EMBL:AL133087
A:Experimental source: adult testis; clone DKFZp434D2328
C:Genetics:
A>Note: DKFZp434D2328.1

Query Match
Beat Local Similarity 10.2%; Score 657; DB 2; Length 791;
Matches 243; Conservative 115; Mismatches 331; Indels 172; Gaps 29;

Qy 102 LFEACRNGDVERVKRLVT-PEKVNRSRTAGRKSTPLHFAAGFGKRVVYLLQNGANVQA 160
Db 7 LHAASAGQINQVVKHLLMLGVEIDEINVG--NTALHIACYNGQDQAVVNELIDYGANVQ 64
Qy 161 RDCGGLTPLHNACSGFH-ABVVNLLRHGADPNARDNNVYTPLEAAKIDVICVILQ 219
Db 65 PNNNGFTPLHFAAASHTGALCIELLVNNGADVNTQSKDGKSPLHMTAVHGFRTRSQTLLQ 124
Qy 220 HGABFTTRNTDGTALDIALDPSAKAVLTGYEYKQDELLESARSNGNEKMMALLT----- 272
Db 125 NGGEIDCVDKDGNTPHVA-----ARYGHELLINTLITSGADTAK 164
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Qy 273 -----PLN---VNCHA-----SDGRK-----STP-----L 289
Db 165 CGHSMFPPLHLAALNAHSDCCRKLLSGGQKYSVLSFNSNEHVLVSAGFEITDPKFGRTCL 224
Qy 290 HLAAGYNRVKIVOLLQHQHADVHAKDKGLVPLHNACSYGHYEVTELLVHKHACVNAMD 349
Db 225 HAAAAGNVCEIKLQSSGADPHKDKCGRTPLHYAANACHFHCIETLVTTGANNVETDD 284
Qy 350 WQTPPLHAAAKNRNEVCSSLLLSYGDPTLL-NCHNKAIDLAPTPOPKER---LAYEFK 405
Db 285 WGRTHLYAAASD-----MDRNKTILGNADHNS-ELERARELKEKEATLCLEF- 332
Qy 406 GHSLLQAAREADVTRIKKLSLEWVAFKHPQTHE---TALHCAAAASPYPKPKOICELL 461
Db 333 ---LLQ-----NDANPSIRDKEGYSIHIAAAYGH---ROCLELL 367
Qy 462 RKGANINEKTEFLT--PLHVASEKAHNDVVVVVHKAQVNAKDNLGQTSLHRAAYCGH 519
Db 368 ERTNSGFEESSDGNATKPLHAAVNGHQALEVLQSLVDLDIRDEKGRALTDLAAFKGH 427
Qy 520 LQTCRLLSYGCDPNTISLQGFALTQNGNENVOQLQEGISLGNSEADROLLEAAKAGDV 579
Db 428 TECVEALIN-----QGASIFVKDNTKRTPLHASVINGHTLCRLLEIAD--- 473
Qy 580 ETVKKLTQSVNCRDIEGRSQSTPLHFAAGYNRVSVVYLLQHGADVHAKDKGLVPLHN 639
Db 474 -----NPEADVQKAKQ--TPLMLVAAYGHIDAVSLLEKEANVDTVDILGCTALHR 524
Qy 640 ACSYGHYEAVALLVKGGVAVNVADLWKFTPLHEAAAAGKYEICKLLQHG---ADPTKGN 696
Db 525 GIMTGHEECVOMLEGEVSLCKDSRGRTPLHYAAGHATLSELLOMALSEEDCCCFKD 584
Qy 697 RDGNTPLD--LVKGDGTDIDLLR-----GD-----AALLDAAKGCLARVKLS 739
Db 585 NQGYTPLHWACYNGNENCIEVLEQKCFKFIQNPFTPLHCAIINDHG--NCASILLGAI 642
Qy 740 SPDVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADYNAODKGLIPLHNAASYGHV 799
Db 643 DSSIVSCRDDKGR--TPLHAAAFADHVECIQLLRHSAPVNAVNSGKTALMAAENGQA 700
Qy 800 DVAALLI-KYNACVNATDKWAFPLHEAAQKGRITQLCALLAHGADPTL---KNOEGQTP 855
Db 701 GAVDILVNSAQADLTVKDKDLNTPHLACSKGHEKCALLILDKIQDESLINEKNALQTP 760
Qy 856 LDIVSADDVSALLTAAMPSPA 876
Db 761 LHVAARNGLVVVEELIAKGA 781

RESULT 15
H71274
probable ankyrin - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: H71274
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
r, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: H71274
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-934 <COL>
A:Cross-references: UNIPROT:O83807; UNIPARC:UPI000000D32A9; GB:AE001254; GB:AE000520; NID:
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0835
C:Superfamily: syphilis spirochete probable ankyrin; ankyrin repeat homology
F;281-313/domain: ankyrin repeat homology <AN2>

Query Match
8.7%; Score 563.5; DB 1; Length 934;
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Best Local Similarity 23.8%; Pred. No. 2.2e-26; Matches 254; Conservative 159; Mismatches 373; Indels 281; Gaps 36;

86 ACASAAAEAVEPAARELFEACRNGDVERVKRLVTEKNSRDTAGRKSTPLHFAAGFRK 145
24 SCTTSSSPQ-ASVDLFEWARGDLDLTUFRGKDSVNVDRANG--DTLLH--VGVLRN 78
146 D--VVEYLLQNGANYQARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNNYTPH 203
79 DAHVDFLLSMGADTEAQDASGTPLMVAVENTCFESVRMLIARDASLFSRDAQDTPLT 138
204 EAAIKGKIDVICV-----LLQH-----GAEPTINTDGRTA 234
139 RAIRKGTAEHLVTRKTLLOKDSGKTPWHWVRALDRDLIKHLVTLGPTQERDADGHTP 198
235 LQADPSAKAVLTGEYKDELLESAR--SGNEEKWALLTPLNVNCHASDGRKSTPLHLA 292
199 LSLAYSSSSDARAAEVAADLLGGALMHGSPSEFIAVLKKNYDLHFTDG--STPLHVM 256
293 AGYNRVKIVQLLQHGADVHAKDKGDLVPLHNACSYGHEVTELLVKGACVNMADLMQF 352
257 AKGYTGFGVQFLVDRKVNNAK-----NLSSA 283
353 TPLHEAASKNRVEVCSLLSYGADPTLNNCHNKSAILD--APTPQKRLAYEFKGHSLLQ 411
284 TPLHEAVRAGQVDAAVLLIRSGADPNVRDASGNTCLHLVAPAP-FRVRIV-----GALLD 337
412 AAREADVTRIKKHLISLEWNPKHQTHETALCAAASPYKPKQICEILLRKGANINEKT 471
338 AGASVAI-----KDYGETPLHVAAR--LGMDFRFRVRLVVGAGADISERN 380
472 KEFLTPLHVASEKAHNDVVVVVKEAKVNALDNLGQTSIHRAAYCGHLQTCRLLLS--- 528
381 KGETPLVLTIDRDHRLDTAYFVSLGADIHAEDMERGETPLTKALARG-LETVKIVVTDN 439
529 -----YGDPNIIISLQGTALQMGNNVQQLQEGISLGNSEADROLLEAAKAGDVETV 582
440 LYKQDVWGRDPLHVAVSRAHLDI-----VKFLFRE-----PKQMI----- 475
583 KCLTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLLQHGAD----- 625
476 -----ARDTWG--NTLLHYAVANDDRADVGFLEMRGADIFSTNVHGVSPKLTALT 523
626 -----VHAKDKGGLVPLHNACSYGHEVAELLVKHGAVVNVADLWKFTPLH 671
524 TSGREDWILTAANVHAQDTGGNTPLHLACEWKLTAINGILRKAEIERNLNQETPLF 583
672 EAAAKGKYEICKLLQHGADPTKKNRDGNTPLDLVKOGDTDIQLLRGDAALLDAKKGC 731
584 SAVKSDAAEIVISILLHPQA-----GNPALVDA----- 610
732 LARVKLSSPDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLL-----QHGADVNAQDKG 786
611 -----RDVAG--NTVLHACVRWSARSADVLIREADARHVSLLNARNLSG 653
787 LIPLHNAASYGHVDVAALLIKYNACNATDKWAFPLHEAAQKRTQCALLLAHGADPT 846
654 KEPLHLARAGNVDPTRILLSHRVALHMGDETKSALTDAVLADQEEVHMLLSAGANPV 713
847 LKNQEGQTPDLVSDADDVSAITAAAMPSPALPSCYKQVNLNGVSPGATADALSSGSPSP 906
714 QQDMYGRTPH-----EAVL-----CNSQSVIAALRAAGGNPFARDSYGTTT 755
907 SLSAASSLDNLGSEFSELSVVSSSGTEGASSLE---KKEVPGVDFTSQFVNLGLEH 963
756 LSLALLKG-DTFVGAVWGKPLANS--DGQTPHLAVMENVPQTF-----RLLLAK 805
964 LMDIFEREQITLDLVEMGHKELKEIGINAYGHRKLIK-GVERLISGOQGLNP---YLT 1019
806 GYPIDKRDHMGSSALVLAIKKORSDL-----CHELLAIGADLFIANNVGESPALLVLS 858
1020 LNTSGSGTIL-IDLSPDDKQFQSV-----EEMOSTVREHRDG 1056

Db 859 KNTSILKTLVGFVAVNKTDGAGESILHYAAKVADEKTLQGLLAMNRF 905

Search completed: December 18, 2006, 17:35:54
Job time : 46.1952 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:21:50 ; Search time 248 Seconds
(without alignments)
4625.078 Million cell updates/sec

Title: US-10-616-101-4
Perfect score: 6464
Sequence: 1 RCSARRGAAGGQAGRGARV.....AYPELYTYIMRPEGMVDG 1240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6108	94.5	1166	1	TNKS2 HUMAN
2	5760.5	89.1	1167	2	Q800E0 CHICK
3	5103.5	79.0	1327	1	TNKS1 HUMAN
4	5098	78.9	1320	2	Q6PFX9 MOUSE
5	5095.5	78.8	1327	2	Q4G0F2 HUMAN
6	5074	78.5	1266	2	Q800D9 CHICK
7	5010.5	77.5	1303	2	Q5XGK5 XENLA
8	4875.5	75.4	1212	2	Q4RG97 TETNG
9	4681.5	72.4	1055	2	Q59FX0 HUMAN
10	4285.5	66.3	976	2	Q8BX62 MOUSE
11	4156.5	64.3	1168	2	Q7PYH8 ANOGA
12	4005	62.0	1181	2	Q9VBF3 DROME
13	3997	61.8	1181	2	Q9XZ37 DROME
14	3324	51.4	1047	2	Q4S372 TETNG
15	3066	47.4	601	2	Q8BXH7 MOUSE
16	3013	46.6	589	2	Q3UES3 MOUSE
17	2063	31.9	408	2	Q6P537 MOUSE
18	1944.5	30.1	471	2	Q4FZM0 XENLA
19	906	14.0	1806	2	Q574D8 RAT
20	906	14.0	1984	2	Q574D7 RAT
21	904	14.0	1136	2	Q3N180 BOVIN
22	897	13.9	1861	2	Q7Z3G4 HUMAN
23	895	13.8	1765	2	Q4U258 MOUSE
24	895	13.8	1961	2	Q4U256 MOUSE
25	894	13.8	1861	2	Q5CZ99 HUMAN
26	893	13.8	1726	2	Q4VC68 MOUSE
27	892.5	13.8	4377	1	ANK3 HUMAN
28	891	13.8	1943	2	Q4U259 MOUSE
29	889	13.8	1940	2	Q4U257 MOUSE
30	888.5	13.7	1762	2	Q88521 RAT
31	885.5	13.7	2622	2	Q70511_RAT

32	882	13.6	4372	2	Q5VXD5 HUMAN	Q5vxd5 homo sapien
33	880.5	13.6	1863	2	Q723L5 HUMAN	Q723l5 homo sapien
34	880	13.6	1856	2	Q99407 HUMAN	Q99407 homo sapien
35	878.5	13.6	1719	2	Q13768 HUMAN	Q13768 homo sapien
36	878.5	13.6	1880	1	ANK1 HUMAN	P16157 homo sapien
37	877	13.6	1899	2	Q59FF2 HUMAN	Q59fp2 homo sapien
38	877	13.6	3924	1	ANK2 HUMAN	Q01484 homo sapien
39	876	13.6	1848	2	Q61302 MOUSE	Q61302 mus musculus
40	876	13.6	1878	2	Q3UHP2 MOUSE	Q3uhp2 mus musculus
41	876	13.6	1907	2	Q3UHP2 MOUSE	Q3uhp2 mus musculus
42	876	13.6	1950	2	Q4RT14 TETNG	Q4rt14 tetraodon n
43	875.5	13.5	4408	2	Q4RNF0 TETNG	Q4rnf0 tetraodon n
44	874	13.5	1862	1	ANK1 MOUSE	Q02357 mus musculus
45	872	13.5	1219	2	Q8C9R3_MOUSE	Q8c9r3 mus musculus

ALIGNMENTS

RESULT 1
TNKS2 HUMAN
ID TNKS2 HUMAN STANDARD; PRT; 1166 AA.
AC Q9H2K2; Q9H8F2; Q9HAS4;
DT 27-MAR-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2001, sequence version 1.
DT 07-MAR-2006, entry version 41.
DE Tankyrase 2 (EC 2.4.2.30) (TANK2) (Tankyrase II) (TNKS-2) (TRF1-
interacting ankyrin-related ADP-ribose polymerase 2) (Tankyrase-like
protein) (Tankyrase-related protein).
DE protein) (Tankyrase-related protein).
GN Names=TNKS2; Synonyms=PARP5B, TANK2, TNKL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal brain;
RX MEDLINE=21072550; PubMed=11205898;
RA Monz D., Munnia A., Comtesse N., Fischer U., Steudel W.-I., Feiden W.,
Glass B., Meese E.U.;
RT "Novel tankyrase-related gene detected with meningioma-specific
sera.";
RL Clin. Cancer Res. 7:113-119(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary carcinoma;
RX MEDLINE=21190090; PubMed=11294570; DOI=10.1038/sj.gene.6363722;
RA Kuimov A.N., Kuprash D.V., Petrov V.N., Vdovichenko K.K.,
Scanlan M.J., Jongeneel C.V., Lagarkova M.A., Nedospasov S.A.;
RT "Cloning and characterization of TNKL, a member of tankyrase gene
family.";
RL Genes Immun. 2:52-55(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE, AND SUBCELLULAR LOCATION.
RC TISSUE=Liver;
RX MEDLINE=21264473; PubMed=11278563; DOI=10.1074/jbc.M009756200;
RA Lyons R.J., Deane R., Lynch D.K., Ye Z.-S.J., Sanderson G.M.,
Eyre H.J., Sutherland G.R., Daly R.J.;
RT "Identification of a novel human tankyrase through its interaction
with the adaptor protein Grb14.";
RL J. Biol. Chem. 276:17172-17180(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE, AND SUBCELLULAR LOCATION.
RC TISSUE=Placenta;
RX MEDLINE=21443728; PubMed=11454873; DOI=10.1074/jbc.M105968200;
RA Kaminker P.G., Kim S.-H., Taylor R.D., Zebrafidian Y., Funk W.D.,
Morin G.B., Yaswen P., Campisi J.;
RT "TANK2, a new TRF1-associated poly(ADP-ribose) polymerase, causes
rapid induction of cell death upon overexpression.";
RL J. Biol. Chem. 276:35891-35899(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE, FUNCTION, AND INTERACTIONS WITH TRF1 AND

RP LNPEP/OTASE.
RC TISSUE=Skeletal muscle;
RX MEDLINE=21661461; PubMed=11802774; DOI=10.1042/0264-6021.3610451;
RA Sbioio J.I., Lodish H.F., Chi N.-W.;
RT "Tankyrase-2 oligomerizes with tankyrase-1 and binds to both TRF1
RT (telomere-repeat-binding factor 1) and IRAP (insulin-responsive
RT aminopeptidase).";
RL Biochem. J. 361:451-459(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RA Yin Y., Gelmann E.P.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15164054; DOI=10.1038/nature02462;
RA Deloukas P., Earthworm M.E., Graham D.V., Rubinfeld M., French L.,
RA Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K.,
RA Hunt S.E., Andrews T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,
RA Taylor A., Batties J., Bird C.P., Ainscough R., Almeida J.P., Bailey J.,
RA Ashwell R.I.S., Ambrose K.D., Babbage A.K., Baggeley C.B., Bailey J.,
RA Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,
RA Brown J.Y., Burford D.C., Burrill W., Burton J., Cahill P., Camire D.,
RA Carter N.P., Chapman J.C., Clark S.V., Clarke G., Clee C.M., Clegg S.,
RA Corby N., Coulson A., Dhani P., Dutta I., Dunn M., Faulkner L.,
RA Frankish A., Frankland J.A., Garner P., Garnett J., Gribble S.,
RA Griffiths C., Grocock R., Gustafson E., Hammond S., Harley J.L.,
RA Hart E., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,
RA Huckle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,
RA Kimberley A.M., Kershaw J.K., Kokkinaki M., Laird G.K., Lawlor S.,
RA Lee H.M., Leongamornlert D.A., Laird G., Lloyd C., Lloyd D.M.,
RA Loveland J., Lovell J., McLaren S., McIay K.E., McMurray L.,
RA Madhaghi-Mohammadi M., Matthews L., Milne S., Nickerson T.,
RA Nguyen M., Overton-Larty E., Palmer S.A., Pearce A.V., Peck A.I.,
RA Pelan S., Phillimore B., Porter K., Rice C.M., Rogosin A., Ross M.T.,
RA Sarafidou T., Sehra H.K., Showkhen R., Skuce C.D., Smith M.,
RA Standing L., Sycamore N., Teater J., Thorpe A., Torcaso W.,
RA Tracey A., Tromans A., Isolas J., Wall M., Walsh J., Wang H.,
RA Weinstock K., West A.P., Willey D.L., Whitehead S.L., Wilming L.,
RA Wray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,
RA Siebert R., Fichtel K., Bentley D., Durbin R., Hubbard T.,
RA Doucette-Stamm L., Beck S., Smith D.R., Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 10.";
RL Nature 429:375-381(2004).
RN [8]
RP TISSUE=Placenta;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Negahari K.,
RA Murakami K., Yaeuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosioki T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hirakawa K., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hottu T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Toshiya S., Komai F., Hara R., Takeuchi K., Arita M., Inose N.,
RA Mueshino K., Yuuki H., Ohshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yanazaki M., Watanabe K., Kunagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiya M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [9]
RP FUNCTION, AND ADP-RIBOSYLATION.
RX MEDLINE=21602874; PubMed=11739745; DOI=10.1128/MCB.22.1.332-342.2002;
RA Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
RT "Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and 2
RT at human telomeres.";
RL Mol. Cell. Biol. 22:332-342(2002).
RN [10]
CC -!- FUNCTION: May regulate vesicle trafficking and modulate the
CC subcellular distribution of SLC2A4/GLUT4-vesicles. Has PARP
CC activity and can modify TRF1, and thereby contribute to the
CC regulation of telomere length.
CC -!- CATALYTIC ACTIVITY: NAD(+) + (ADP-D-ribose)1(n)-acceptor =
CC nicotinamide + (ADP-D-ribose)1(n+1)-acceptor.
CC -!- SUBUNIT: Oligomerizes and associates with TNKS. Interacts with the
CC cytoplasmic domain of LNPEP/OCase in SLC2A4/GLUT4-vesicles. Binds
CC to the N-terminus of Grb14 and TRF1 with its ankyrin repeat
CC region.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and
CC with juxtanuclear SLC2A4/GLUT4-vesicles. Also found around the
CC pericentriolar matrix of mitotic centrosomes. During interphase, a
CC small fraction of TNKS2 is found in the nucleus, associated with
CC TRF1.
CC -!- TISSUE SPECIFICITY: Highly expressed in placenta, skeletal muscle,
CC liver, brain, kidney, heart, thymus, spinal cord, lung, peripheral
CC blood leukocytes, pancreas, lymph nodes, spleen, prostate, testis,
CC ovary, small intestine, colon, mammary gland, breast and breast
CC carcinoma, and in common-type meningioma. Highly expressed in
CC fetal liver, heart and brain.
CC -!- SIMILARITY: Contains 15 ANK repeats.
CC -!- SIMILARITY: Contains 1 PARP catalytic domain.
CC -!- SIMILARITY: Contains 1 SAM (sterile alpha motif) domain.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: AF305081; AAG25674.1; ALT INIT; mRNA.
CC EMBL: AF264912; AAG44694.1; -; mRNA.
CC EMBL: AF329696; AAK13463.1; -; mRNA.
CC EMBL: AF342982; AAK25811.1; -; mRNA.
CC EMBL: AF309033; AAK82330.1; -; mRNA.
CC EMBL: AF438201; AAL40795.1; -; mRNA.
CC EMBL: AL359707; CAC78760.1; -; Genomic DNA.
CC EMBL: AK023746; BAB14665.1; ALT_INIT; mRNA.
CC HSSP: P16157; IN11.
CC Ensembl: ENSG00000107854; Homo sapiens.
CC HGNC: HGNC:15677; TNKS2.
CC MIM: 607128; Gene.
CC InterPro: IPR001290; PARP.
CC InterPro: IPR012317; PARP_catalytic.
CC InterPro: IPR001660; SAM.
CC InterPro: IPR011510; SAM_2.
CC Pfam: PF00023; Ank; 17.
CC Pfam: PF06644; PARP; 1.
CC Pfam: PF07647; SAM_2; 1.
CC SMART: SM00248; ANK; 15.
CC SMART: SM00454; SAM; 1.
CC PROSITE: PS00297; ANK_REPEAT; 1.
CC PROSITE: PS00088; ANK_REPEAT; 15.
CC PROSITE: PS01059; PARP_CATALYTIC; 1.
CC PROSITE: PS0105; SAM_DOMAIN; 1.
KW ADP-ribosylation; ANK repeat; Chromosomal protein;
KW Glycosyltransferase; Golgi stack; NAD; Nuclear protein; Repeat;
KW Telomere; Transferase.
FT CHAIN 1 1166 Tankyrase 2.
FT REPEAT 57 89 ANK 1.
FT REPEAT 90 122 ANK 2.

Db 961 DDKEFQSQVEEMOSTVREHDDGGHAGGI FNRYNILKIQKCNKKLWERYTHRRKVEEEN 102

Qy 1095 HNHANERMLFHGSPFNVAIIHKGFDERHAYIGMGFAGIYFAENSSKSNOYVYIGGGTG 1154

Db 1021 HNHANERMLFHGSPFNVAIIHKGFDERHAYIGMGFAGIYFAENSSKSNOYVYIGGGTG 1080

Qy 1155 CPVHKORSCHVICHROLLFCRVTLGKSPLORSAMMAHSPGCHHSVTCGRPSVNGLALEYV 1214

Db 1081 CPVHKORSCHVICHROLLFCRVTLGKSPLORSAMMAHSPGCHHSVTCGRPSVNGLALEYV 1140

Qy 1215 IYRGEQAYPEYLITYQIMRPEGMVDG 1240

Db 1141 IYRGEQAYPEYLITYQIMRPEGMVDG 1166

RESULT 2

Q800EO.CHICK

ID Q800EO.CHICK PRELIMINARY; PRT; 1167 AA.

AC Q800EO;

DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.

DT 01-JUN-2003, sequence version 1.

DT 07-FEB-2006, entry version 14.

DE Tankyrase 2.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22615216; PubMed=12589701; DOI=10.1042/BU20021450;

RA De Rycker M., Venkatesan R.N., Wei C., Price C.M.;

RT "Vertebrate tankyrase domain structure and sterile alpha motif (SAM) -

RL mediated multimerization.";

RL Biochem. J. 372:87-96(2003).

CC

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CC

CC EMBL: AY142107; IAN41650.1; -; mRNA.

DR HSPP; Q00420; IAWC.

DR Ensemble; ENSGALG0000011438; Gallus gallus.

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.

DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR001290; PARP.

DR InterPro; IPR012317; PARP catalytic.

DR InterPro; IPR001660; SAM.

DR InterPro; IPR011510; SAM_2.

DR Pfam; PF00023; Ank; 19.

DR Pfam; PF00644; PARP; 1.

DR Pfam; PF07647; SAM_2; 1.

DR PRINTS; PR01415; ANKYRIN.

DR SMART; SM00248; ANK; 15.

DR SMART; SM00454; SAM; 1.

DR PROSITE; PS00297; ANK REP REGION; 1.

DR PROSITE; PS00088; ANK_REPEAT; 15.

DR PROSITE; PSS1059; PARP_CATALYTIC; 1.

DR PROSITE; PS0105; SAM_DOMAIN; 1.

DR ANK repeat; Repeat.

KW ANK repeat; Repeat.

SQ SEQUENCE 1167 AA; 126932 MW; 7842BF482B229E9 CRC64;

Query Match 89.1%; Score 5760.5; DB 2; Length 1167;

Best Local Similarity 93.8%; Pred. No. 0;

Matches 1095; Conservative 33; Mismatches 36; Indels 3; Gaps 3;

Qy 75 MSRRRCAGGGAACASA--AAEAPEAPARELFEACRNGDVERVKRLVTPPEKNSRDTAGRK 132

Db 1 MAARRCAGGAALAEAPGGSAREP-ARELFEACRNGDVERVKRLVTPPENNSRDTAGRK 59

Qy 133 STLPHFAAGFRKDVVEYLLQNGANYOARDGGLIPLHNACSFGEAEVNLRLRHGADPN 192

Db 60 SSPLHFAAGFRKDVVEYLLQSGANVHARDGGGLIPLHNACSPGHAENVNLLLRHGANPN 119
Qy 193 ARDNWNTPLHEAAIKGKIDVCIIVLLQHGAEPTIRNTDGRALTDLADSPSAKAVLTGYKK 252
Db 120 ARDNWNTPLHEAAIKGKIDVCIIVLLQHGAEPTIRNTDGRALTDLADSPSAKAVLTGYKK 179
Qy 253 DELLESARGNEEKWALLPLPNVNCASDGRKSTPLHLAAGYNRVKIVQLLQHGADVH 312
Db 180 DELLESARGNEEKWALLPLPNVNCASDGRKSTPLHLAAGYNRVKIVQLLQHGADVH 239
Qy 313 AKDGDVPLHNACSYGHEVTELLVKGACVAMNDLWQFTPLHEAASKRVEVCSLLS 372
Db 240 AKDGDVPLHNACSYGHEVTELLVKGACVAMNDLWQFTPLHEAASKRVEVCSLLS 299
Qy 373 YGADPTLLNCHNKSAIDLAPTPQLKERLAYEFKGHSLLQAAAREADVTRIKGHSLEWVNF 432
Db 300 YGADPTLLNCHNKSTIDLAPTPQLKERLAYEFKGHSLLQAAAREADVARIKKHLSLETVNF 359
Qy 433 KHPQTHETALHCAASPYPKRKOICELLRLKGANINEKTEFLTPLVASEKAHNDVVEV 492
Db 360 KHPQTHETALHCAASPYPKRKOICELLRLKGANINEKTDPLPLVASEKAHNDVVEV 419
Qy 493 VVKEAKVNALDNLGQTSLHRAACGHLQTCRLLLSYGCDPNIIISLQGFALQNGENVQ 552
Db 420 VVKEAKVNALDNLGQTSLHRAACGHLQTCRLLLSSGCDPSIVSLQGFALQNGESVQ 479
Qy 553 QLLQEGISLGNSEADROLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHPAAGYNR 612
Db 480 QLLQEGISLGNSEADROLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHPAAGYNR 539
Qy 613 VSVVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVAMNDLWQFTPLHE 672
Db 540 VSVVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVAMNDLWQFTPLHE 599
Qy 673 AAAGKYEICKLLQHGADPTKKNRDNPTDLVDKGDGTIDQLLRGDAALLDAKKGCL 732
Db 600 AAAGKYEICKLLQHGADPTKKNRDNPTDLVDKGDGTIDQLLRGDAALLDAKKGCL 659
Qy 733 ARVKLSGSPDNVNCRDQTGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHN 792
Db 660 ARVKLSGSPDNVNCRDQTGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHN 719
Qy 793 AASGHVDVAALLIKYNACVNAQDKWFTPLHEAAGKRTQLCALLAHGADPTLKNQEG 852
Db 720 AASGHVDVAALLIKYNACVNAQDKWFTPLHEAAGKRTQLCALLAHGADPTLKNQEG 779
Qy 853 QTPDLVLSADVDVALLTAAMPSPALPCYKQVNLGVRSFGATADALSSGSPSSLSAA 912
Db 780 QTPDLVLSADVDVALLTAAMPSPALPCYKQVNLGVRSFGATADALSSGSPSSLSAA 839
Qy 913 SSLDNLGSGFSELSSVSSSGTEGASLEKKEVPGVDFSIQFVRNIGLEHLMDFEREQ 972
Db 840 SSLDNLGSGFSELSSVSSSGTEGASLEKKEVPGVDFSIQFVRNIGLEHLMDFEREQ 899
Qy 973 ITLDVLMVGHKELKEIGINAYGRHKLIKVERLISQOGLNPLYLNTSSGFTLIDL 1032
Db 900 ITLDVLMVGHKELKEIGINAYGRHKLIKVERLISQOGLNPLYLNTSSGFTLIDL 959
Qy 1033 SPDDKEFQSVSEEMQSTVREHDDGAGGIFNRRYNIILKIQKCNKLUWERYTHRRKEVSE 1092
Db 960 SPDDKEFQSVSEEMQSTVREHDDGAGGIFNRRYNIILKIQKCNKLUWERYTHRRKEVSE 1019
Qy 1093 ENHNHNERMLFHGSPFVNAIIHKGFDERHAYIGMFGAGIYFAENSCKNQYVYGIGG 1152
Db 1020 ENHNHNERMLFHGSPFVNAIIHKGFDERHAYIGMFGAGIYFAENSCKNQYVYGIGG 1079
Qy 1153 TGCPIHDKRSCYICHRQLIFCRVTLGKSFLOFSAMKWAHSPGHSHVTRGPRSVNGLALAE 1212
Db 1080 TGCPIHDKRSCYICHRQLIFCRVTLGKSFLOFSAMKWAHSPGHSHVTRGPRSVNGLALAE 1139
Qy 1213 YVIVRGEQAYPEYLITVQIMPEGVND 1239
Db 1140 YVIVRGEQAYPEYLITVQIVKPEATTE 1166

RESULT 3

TKNS1 HUMAN
ID TKNS1_HUMAN STANDARD; PRT; 1327 AA.
AC O95271; O95272;
DT 27-MAR-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-1999, sequence version 1.
DT 07-MAR-2006, entry version 45.
DE Tankyrase 1 (EC 2.4.2.30) (TANK1) (Tankyrase I) (TNKS-1) (TRF1-
DE interacting ankyrin-related ADP-ribose polymerase).
GN Name=TNKS; Synonyms=PARPSA, PARPL, TINI, TINP1, TNKSI;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2).
RC TISSUE=Testis;
RX MEDLINE=99040105; PubMed=9822378; DOI=10.1126/science.282.5393.1484;
RA Smith S., Giriat I., Schmitt A., de Lange T.;
RT "Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";
RL Science 282:1484-1487(1998).
RN [2]
RP SUBCELLULAR LOCATION.
RX MEDLINE=99454782; PubMed=10523501;
RA Smith S., de Lange T.;
RT "Cell cycle dependent localization of the telomeric PARP, tankyrase,
RT to nuclear pore complexes and centrosomes.";
RL J. Cell Sci. 112:3649-3656(1999).
RN [3]
RP FUNCTION, AND PHOSPHORYLATION.
RX MEDLINE=20556282; PubMed=10988299; DOI=10.1074/jbc.M007635200;
RA Chi N.-W., Lodish H.F.;
RT "Tankyrase is a Golgi-associated mitogen-activated protein kinase
RT substrate that interacts with IRAP in GLUT4 vesicles.";
RL J. Biol. Chem. 275:38437-38444(2000).
RN [4]
RP FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
RX MEDLINE=21602874; PubMed=11739745; DOI=10.1128/MCB.22.1.332-342.2002;
RA Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
RT "Role for the related poly(ADP-ribose) polymerases tankyrase 1 and 2
RT at human telomeres.";
RL Mol. Cell. Biol. 22:332-342(2002).
RN [5]
RP IDENTIFICATION IN A COMPLEX WITH POT1; TERF1 AND TINP2.
RX MEDLINE=22711258; PubMed=12768206; DOI=10.1038/nature01688;
RA Leayza D., De Lange T.;
RT "POT1 as a terminal transducer of TRF1 telomere length control.";
RL Nature 424:1013-1018(2003).
CC -1- FUNCTION: May regulate vesicle trafficking and modulate the
CC subcellular distribution of SLC2A4/GLUT4-vesicles. Has PARP
CC activity and can modify TERF1, and thereby contribute to the
CC regulation of telomere length.
CC -1- CATALYTIC ACTIVITY: NAD(+) + (ADP-D-riboseyl)(n)-acceptor =
CC nicotinamide + (ADP-D-riboseyl)(n+1)-acceptor.
CC -1- SUBUNIT: Oligomerizes and associates with TNKS2. Interacts with
CC the cytoplasmic domain of LMNPEP/Otase in SLC2A4/GLUT4-vesicles.
CC Binds to the N-terminus of telomeric TERF1 via the ANK repeats.
CC Found in a complex with POT1, TERF1 and TINP2.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and
CC with juxtanuclear SLC2A4/GLUT4-vesicles. A minor proportion is
CC also found at nuclear pore complexes and around the pericentriolar
CC matrix of mitotic centrosomes. During interphase, a small fraction
CC of TNKS is found in the nucleus, associated with TERF1.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O95271-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O95271-2; Sequence=VSP_004538, VSP_004539;
CC Note=No experimental confirmation available;

-!- TISSUE SPECIFICITY: Ubiquitous; highest levels in testis.
-!- PTM: Phosphorylated on serine residues by MAPK kinases upon insulin stimulation.

-!- PTM: ADP-ribosylated (-auto).

-!- SIMILARITY: Contains 15 ANK repeats.

-!- SIMILARITY: Contains 1 PARP catalytic domain.

-!- SIMILARITY: Contains 1 SAM (sterile alpha motif) domain.

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EMBL; AF082556; AAC79841.1; -; mRNA.

EMBL; AF082557; AAC79842.1; -; mRNA.

EMBL; AF082558; AAC79843.1; -; mRNA.

EMBL; AF082559; AAC79844.1; -; mRNA.

HSSP; P16157; 1N11

Ensembl; ENSG00000173273; Homo sapiens.

HGNC; HGNC:11941; TNKS.

MIM; 603303; gene.

GO; GO:0000781; C:chromosome, telomeric region; IDA.

GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IDA.

GO; GO:0005515; F:protein binding; IPI.

GO; GO:0007004; P:telomerase-dependent telomere maintenance; NAS.

InterPro; IPR0012317; PARP.

InterPro; IPR001660; SAM.

InterPro; IPR011510; SAM_2.

Pfam; PF00023; Ank; 19.

Pfam; PF00644; PARP; 1.

Pfam; PF07647; SAM; 2; 1.

SMART; SM00248; ANK; 15.

SMART; SM00454; SAM; 1.

PROSITE; PS02097; ANK_REPEAT; 1.

PROSITE; PS00088; ANK_REPEAT; 15.

PROSITE; PS51059; PARP_CATALYTIC; 1.

PROSITE; PS50105; SAM_DOMAIN; 1.

ADP-ribosylation; Alternative splicing; ANK repeat;

Chromosomal protein; Glycosyltransferase; Golgi stack; NAD;

Nuclear protein; Phosphorylation; Repeat; Telomere; Transferase.

CHAIN 1 1327

/FTID=PRO_0000211333.

REPEAT 215 247

REPEAT 248 280

REPEAT 281 313

REPEAT 368 400

REPEAT 401 433

REPEAT 434 466

REPEAT 521 556

REPEAT 557 589

REPEAT 590 622

REPEAT 683 715

REPEAT 716 748

REPEAT 749 781

REPEAT 836 868

REPEAT 869 901

REPEAT 902 934

DOMAIN 1030 1089

DOMAIN 1112 1317

COMPBIAS 9 14

COMPBIAS 27 34

COMPBIAS 128 134

COMPBIAS 137 145

VARSPPLIC 641 643

FTID=VSP_004538.

Missing (in isoform 2).

FTID=VSP_004539.

H->A: Loss of activity; when associated with A-1291.

E->A: Loss of activity; when associated with A-1184.

SEQUENCE 1327 AA; 142011 MW; E14DE985C710B957 CRC64;

Query Match 79.0%; Score 5103.5; DB 1; Length 1327;

Best Local Similarity 79.2%; Pred. No. 1.7e-291;
Matches 963; Conservative 110; Mismatches 128; Indels 15; Gaps 3;

QY 22 AAHGTADPDVYTAGSOARALSSSPGGALLALLAGPGLLRLLALLAVAAARIMSGRCA 81
DB 112 SAAGVAPNPAGSGNNPSSSSSTSSSSPSPPG-----SSLAESPEAGVSSSTAPL 165
QY 82 GGGACASAAAEVPAARELFEACRNGDVRVRLVTPPEKVNRSRDTAGRKSTPLHFAAG 141
DB 166 GPGAAGPCTGVPVSGALRELLEACRNGDVRVRLVDAANVNAKMAGRKSSPLHFAAG 225
QY 142 FGRKDVVEYLQNGANVOARDDGLIPLHNACSFGEAEVNMLLRHGADPNARDNWTTP 201
DB 226 FGRDVVVEHLIQMGANVHARDGGLIPLHNACSFGEAEVNMLLRCQAGADPNARDNWTTP 285
QY 202 LHEAAIKGKIDVCIVLQHGAEPTIRNTDGRALDADPSAKAVLTGTYKDELESARS 261
DB 286 LHEAAIKGKIDVCIVLQHGADPNIRNTDGSALDADPSAKAVLTGTYKDELESARS 345
QY 262 GNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLQHGADVHAKOKGDLVP 321
DB 346 GNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLQHGADVHAKOKGDLVP 405
QY 322 LHNACSYGHEVETELLVKHGACVNMADLWQPTPLHEAASKNRVEVCSLLLSYGADPTLLN 381
DB 406 LHNACSYGHEVETELLVKHGACVNMADLWQPTPLHEAASKNRVEVCSLLLSYGADPTLLN 465
QY 382 CHNKSADLAPTPOKRLAYEFKGHSLLQARADVTRIKKHSLEVMVFKHPOTHETA 441
DB 466 CHGKSAVDMAPTPELRRLTYEFKGHSLLQARADLAKVKTLLALEIINPKQPOSHETA 525
QY 442 LHCAASGPYKPKKOICELLRKGANINEKTEFTPLHVASSEKANDVVEVVVHKAQVN 501
DB 526 LHCAVASLHPKPKQVTELLLRKANVNEKNKDFWTPPLHVAERAHNDVMEVLHKGAKQN 585
QY 502 ALDNLGQTSLHRAAYCGHLOTCTRLLSYCGDPNIIISLQFTALQNGNENVOQLQEGISL 561
DB 586 ALDTLQGTALHRAALAGHLQTCRLLSYCGSPSIISLQFTAAQMGNEAVQOILSESTPI 645
QY 562 GNSADQLLEAAKAGDVETVKKLCVQSVNCRDIEGQSTPLHFNAGYNNRVSVVEYLQ 621
DB 646 RTSDVDYRLLEASKAGDLETVKQLCSSQNVNCRDLGHRHSTPLHFAAGYNNRVSVVEYLH 705
QY 622 HGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVNADLWKFTPLHAAAAGKYEI 681
DB 706 HGADVHAKDKGGLVPLHNACSYGHEVAELLVRHGASVNVADLWKFTPLHAAAAGKYEI 765
QY 682 CKLLQHGADPTKKNRDGNTPLDLVKQDGTDIQDLRGDAALLDAKKGCLARVKKLSPP 741
DB 766 CKLLQHGADPTKKNRDGNTPLDLVKQDGTDIQDLRGDAALLDAKKGCLARVKKLSPP 825
QY 742 DNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASVGHVDV 801
DB 826 ENINCRDTQGRNSTPLHLAGYNNLEVAEYLLHLEGADVNAQDKGLIPLHNAASVGHVDI 885
QY 802 AALLIKYNACVNAQDKWAFPLHEAAOKRGTOLCALLLHAGADPTLKNQEGTPTLDLYSA 861
DB 886 AALLIKYNACVNAQDKWAFPLHEAAOKRGTOLCALLLHAGADPTLKNQEGTPTLDLYSA 945
QY 862 DDVSAALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSPSLSAASSLDNLSSG 921
DB 946 DDVSAALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSPSLSAASSLDNLSSG 998
QY 922 PSELSSVSSSGTSGASSLEK--EVPQVDPSITQFVNLGLEHMDIFEREQITLDVIV 979
DB 999 LAELAVGASNAGDGAAGTERKEGEVAGLDNMIISQFLKSLGLEHLRDLFEFEQITLDVLA 1058
QY 980 EMGHEKEKEIGINAYGHRHKLKIGVERLSQOQGLNPLYTLNTSGSTILLDLSPDDKEF 1039
DB 1059 DMGHEEKEKEIGINAYGHRHKLKIGVERLGGQGGQGTNPVLTFCVNGQGTILLDLAPDEKEY 1118
QY 1040 QSVSEEMQSTVREHRDGGHAGGIENRNILKIQKCNKKLWERYTHRRKKEYSEENHNHAN 1099

Db 1119 QSVSEEMQSTIREHRDGNAGGIENRNVIRIQVNVNKLBERFCHRQKEVSEBNHHN 1178
 Qy 1100 ERMFLPHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSCKSNQYVYGGGTGCPVHK 1159
 Db 1179 ERMFLPHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSCKSNQYVYGGGTGCPVHK 1238
 Qy 1160 DRSCYICHRQLFCRVTLGKSFLOFSAMKNHSPGHHSVTGRPSVNGLALAEVYVIRGE 1219
 Db 1239 DRSCYICHRQLFCRVTLGKSFLOFSAMKNHSPGHHSVTGRPSVNGLALAEVYVIRGE 1298
 Qy 1220 QAYPEYLITQIMRPE 1235
 Db 1299 QAYPEYLITQIMRPE 1314
 RESULT 4
 ID Q6PFX9 MOUSE PRELIMINARY; PRT; 1320 AA.
 AC Q6PFX3;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE Tnks protein.
 GN Name=Tnks;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Beak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonCommercial License
 CC -----
 CC EMBL; BC057370; AAH57370.1; -, mRNA.
 DR HSPP; Q00420; IAWC.
 DR Ensembl; ENSMUSG00000031529; Mus musculus.
 DR MGI; MGI:1341087; Tnks.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
 DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR001290; PARP.
 DR InterPro; IPR012317; PARP_catalytic.
 DR InterPro; IPR001660; SAM.

DR InterPro; IPR011510; SAM_2.
 DR Pfam; PF00023; Ank; 19.
 DR Pfam; PF00644; PARP; 1.
 DR Pfam; PF07647; SAM_2; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 15.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PSS0297; ANK_REPEAT; 1.
 DR PROSITE; PSS0088; ANK_REPEAT; 15.
 DR PROSITE; PSS1059; PARP_CATALYTIC; 1.
 DR PROSITE; PSS0105; PARM_DOMAIN; 1.
 KW ANK repeat; Repeat.
 SQ SEQUENCE 1320 AA; 140944 MW; A90360DC665FFCC0 CRC64;
 Query Match 78.9%; Score 5098; DB 2; Length 1320;
 Best Local Similarity 79.2%; Pred. No. 3.6e-291;
 Matches 966; Conservative 105; Mismatches 130; Indels 18; Gaps 5;
 Qy 22 AANGTAPDPVTAGSQAAR--ALSASSP--GGALLAGPGLLLRLLALLLAVAAARIMSGR 78
 Db 102 AAVGVAPTPAGGGGGGNNSSASSPTSSSSSPSPG-----SSLASPEAAGVST 155
 Qy 79 RCAGGGAACASAAAEAVEPAARELFEACRNGDVERVKRLVTPKVNRSRDTAGRKSTPLHF 138
 Db 156 ATLGAGAGLPGVPVAVSGALRELLEACRNGDVSRLVDAANVNADKAGRKSSPLHF 215
 Qy 139 AAGFGRKDVVYELLQNGANYQARDGGGLIPLHNACSFGEAEVNVNLLRHGADPNARDNN 198
 Db 216 AAGFGRKDVVYELLQNGANYQARDGGGLIPLHNACSFGEAEVNVNLLRHGADPNARDNN 275
 Qy 199 YTPLHEAAIKGKIDVCIVLQHGAEPIRTDGTALDLPSPKAVITGEYKDELLES 258
 Db 276 YTPLHEAAIKGKIDVCIVLQHGAEPIRTDGTALDLPSPKAVITGEYKDELLES 335
 Qy 259 ARSNEEKMALITPLNVNCHASDGRKSTPLHLAAGVNVYKIVQLLQHGADVHAKDKGD 318
 Db 336 ARSNEEKMALITPLNVNCHASDGRKSTPLHLAAGVNVYKIVQLLQHGADVHAKDKGG 395
 Qy 319 LVPLHNACSYGHYEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVCVSLLSYGADPT 378
 Db 396 LVPLHNACSYGHYEVTELLVKHGACVNMADLWQFTPLHEAASKNRVVCVSLLSYGADPT 455
 Qy 379 LLNCHNSATDLAPTOLKERLAYEPKHSILQNAAREADVTRICKHLSLEVMVFKHQTH 438
 Db 456 LVNCHGKSVDMAPTPELRERLTVEFKHSLQQAAREADLAKVKKTLALEILINFKQPOSH 515
 Qy 439 ETALHCAASPYKPKQICELLRKGANINEKTEFLTLPHVASEKAHNDVVEVVVKEHA 498
 Db 516 ETALHCAVASLHPKPKQVAVELLRKGANVNEKNKDFMTPLHVAERAHNDVMEVLHKGA 575
 Qy 499 KVALDNLGQTSLHRAAYCGHLOTCRLLLSYGCDDPNTIISLQGFALQNGENVQQLQEG 558
 Db 576 KVALDSLGQTLHRAALAGHLQTCRLLLSYGSDDPSIISLQGFATAQMGNEAVQQLISES 635
 Qy 559 ISLGNSEADQLLEAAKAGADVETVKKLTCTVQSVNCRDIEGRQSTPLHFAAGYNSVVVEY 618
 Db 636 TPMRTSDVYRLLEAKAGDLETVKQLCSPQNVNCRDLEGRHSTPLHFAAGYNSVVVEY 695
 Qy 619 LLOHGADVHAKDKGGLVPLHNACSYGHYEAELLVKHGAVNVVADLWKFTPLHEAAAKGK 678
 Db 696 LLHGADVHAKDKGGLVPLHNACSYGHYEAELLVRHGASVNVADLWKFTPLHEAAAKGK 755
 Qy 679 YEICKLLQHGADPTKKNRDGNTPLDLVKDGDGTDIQLLRGDAALLDAAKGKGLARVKKL 738
 Db 756 YEICKLLQHGADPTKKNRDGNTPLDLVKEGDGTDIQLLRGDAALLDAAKGKGLARVKKL 815
 Qy 739 SSPDNVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASVGH 798
 Db 816 CTPENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASVGH 875
 Qy 799 VDVAAALLIKYNACVNAATDKWAFPLHEAAQKGRITQLCALLLAHAGADPTLNKQEGQTPDL 858
 Db 876 VDTAALLIKYNTCVNATDKWAFPLHEAAQKGRITQLCALLLAHAGADPTLNKQEGQTPDL 935

QY	859	VSADDVSALLTAMPPPSALSCYKQVINGVRSPGATADALSSGSPSPSSLSAASSIDLNL	918
Db	936	ATADDIRALLIDAMPPEALPTCFKQAT-----VVSASLISPASTPSCLSAASSIDLNL	988
QY	919	SGSFSELSVVSSSGTGASLSLEKK--EVPQDFSIQFVRLNGLGLEHLMDIFEREQITLD	976
Db	989	TGPITDVLAVGASNAGDGAAGAERKEVAGLDMNISOFLKGLGLEHLRDIFFETEQTLD	1048
QY	977	VLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILILDSPDD	1036
Db	1049	VLDAMGHEELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILILDSPDD	1108
QY	1037	KEFQSVSEEMQSTVREHRDGHAGGIFNRYNLIKQKCNKKLWERYTHRRKEVSEENHN	1096
Db	1109	KEYQSVSEEMQSTIREHRDGNAGGIFNRYNIRIQKVNKKLRERFCHQKEVSEENHN	1168
QY	1097	HANERMLFHGSPFVNALIHKGFDERHAYIGMFGAGIYFAENSKSNQYVYIGGGTGCP	1156
Db	1169	HNHERMLFHGSPFVNALIHKGFDERHAYIGMFGAGIYFAENSKSNQYVYIGGGTGCP	1228
QY	1157	VHKDRSCYIHROLLFCRVTLGKSLFQFSAMKMAHSPGHHSVTGRPSVNGLALAEVYI	1216
Db	1229	THKDRSCYIHRQMLFCRVTLGKSLFQFSAMKMAHSPGHHSVTGRPSVNGLALAEVYI	1288
QY	1217	RGEQAYPEYLITYQIMRPE	1235
Db	1289	RGEQAYPEYLITYQIMRPE	1307

RESULT 5

Q4G0F2 HUMAN

ID Q4G0F2 HUMAN PRELIMINARY; PRT; 1327 AA.

AC Q4G0F2;

DT 30-AUG-2005, integrated into UniProtKB/TrEMBL.

DT 30-AUG-2005, sequence version 1.

DT 07-FEB-2006, entry version 4.

DE Tissue, TRF1-interacting ankyrin-related ADP-ribose polymerase.

GN Names=TNKS;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

[1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Testis;

RX MSDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.2426030899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Mada N.A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Testis;

RX NIH MGC Project;

RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.

[illegible]

Db 766 CKLLKHGADFTKNDGNTPLDIVKEGDTDIQLLRGDAALLDAKKGCLARVQKLCPT 825
Qy 742 DNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLORHGADVNAQDKGLIPLHNAASYGHVDV 801
Db 826 ENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLLEHGADVNAQDKGLIPLHNAASYGHVDI 885
Qy 802 AALLIKYNACVNAKTKWAFTHLHAAQKGRTOQLCALLLAHGAADPTLNKQEGQTPDLVSA 861
Db 886 AALLIKYNTCVNATDKWAFTHLHAAQKGRTOQLCALLLAHGAADPTLNKQEGQTPDLVSA 945
Qy 862 DDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSSI-SAASSLDNLSGS 921
Db 946 DDIRALLIDAMPSPALPFCFPQAT-----VVSAISIPASTPSCLSAASSIDNLTGP 998
Qy 922 FSELSSVVSSGTGASSLEKK--EVPQVDPSITQFVRNLGLEHLMDFIFEREQITLDVLV 979
Db 999 LAGLAVGASNAGDGAAGTERKEGEVAGLDWNIQSFLKSLGLEHLRDFEFETEITLDVLA 1058
Qy 980 EMGHKELKEIGINAYGHRHKLKIGVERLIISQOQGLNPVLTJNTSGSGTILIDLSPDKF 1039
Db 1059 DMGHEELKEIGINAYGHRHKLKIGVERLLGQOQGTNPVLTJNTHCVNQGTILIDLAPEDKEY 1118
Qy 1040 QSVREEMQSTVREHRDGHAGGIENRNYILKIQVCNKKLWERVTHRKEVSEENHNHAN 1099
Db 1119 QSVREEMQSTIREHRDGNAGGIENRNYIRIKQVNVKKLERFCHQKEVSEENHNHN 1178
Qy 1100 ERMFLHSGSPFVNAIHHKGFDRHAYIGMFGAGIYFAENSSKSNQYVVGIGGTCFVHK 1159
Db 1179 ERMFLHSGSPFINAIIHKGFDRHAYIGMFGAGIYFAENSSKSNQYVVGIGGTCFTHK 1238
Qy 1160 DRSCYICHRQLLFCRVTLGKSFLOPSAKMAHSPGHHSVTGRPSVNGLAELAEVVIYRGE 1219
Db 1239 DRSCYICHRQMLFCRVTLGKSFLOPSIKMAHAPPGHHSVTGRPSVNGLAELAEVVIYRGE 1298
Qy 1220 QAYPEYLITYQIMRPE 1235
Db 1299 QAYPEYLITYQIMRPE 1314
RESULT 6
ID Q800D9_CHICK PRELIMINARY; PRT; 1266 AA.
AC Q800D9;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Tankyrase 1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22615216; PubMed=12589701; DOI=10.1042/BJ20021450;
RA De Rycker M., Venkatesan R.N., Wei C., Price C.M.;
RT "Vertebrate tankyrase domain structure and sterile alpha motif (SAM) -
mediated multimerization.";
RL Biochem. J. 372:87-96(2003).
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CC -----
DR EMBL; AY142108; AAN41651.1; -; mRNA.
DR HSSP; P16157; IN11.
DR Ensembl; ENSGALG00000011438; Gallus gallus.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001290; PARP.
DR InterPro; IPR012317; PARP_catalytic.

DR InterPro; IPR001660; SAM.
DR InterPro; IPR011510; SAM_2.
DR Pfam; PF00023; Ank; 19.
DR Pfam; PF00644; PARP; 1.
DR Pfam; PF07647; SAM_2; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 15.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS00297; ANK_REPEAT; 1.
DR PROSITE; PS00088; ANK_REPEAT; 15.
DR PROSITE; PS1059; PARP_CATALYTIC; 1.
DR PROSITE; PS01005; SAM_DOMAIN; 1.
DR ANK repeat; Repeat.
KW SEQUENCE 1266 AA; 136212 MW; 14B8617EF930B6E0 CRC64;
Query Match 78.5%; Score 5074; DB 2; Length 1266;
Best Local Similarity 77.6%; Pred. No. 8.7e-290;
Matches 964; Conservative 109; Mismatches 120; Indels 50; Gaps 6;
Qy 5 RRGAGGQG-----AQRGARVGAAGHTAPDPVTAGSQAARALSSSPGGLALLAGPGLL 59
Db 49 RHSLAGPEGEAPPDAERPPAPCESEGAAPGP-PFGSGSSGSSASS----- 93
Qy 60 LRLALLLAVAAARINSGRCAGGACASAAABAEVPA-----RELFEACRNGDVERV 114
Db 94 -----SSSSSTSSSVASSPAESPAAGPSGAFRELLACRNGDTRV 137
Qy 115 KRLVTPKVNRSRTAGKSTPLHFAAGFGRKDVVYLLQNGANYQARDDGLIPLHNACS 174
Db 138 KRLVDAGNVNAKDWAGKSTPLHFAAGFGRKDVVEHLLQTGANVHARDGGLIPLHNACS 197
Qy 175 FGAHVNVLLRHGADNARDNNYTPHLEAAIKGKIDVICVILLOHGAETIRNTDGRTA 234
Db 198 FGAHVYVSLLCQADFNARDNNYTPHLEAAIKGKIDVICVILLOHGAENIRNTDOKSA 257
Qy 235 LDLDAPSAKAVLTGEYKKBELLESARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAG 294
Db 258 LDLDAPSAEAVLTGEYKKBELLESARSGNEEKWALLTPLNVNCHASDGRKSTPLHLAAG 317
Qy 295 YNRVKIVQLLQHGADVHAKDGLVPLHNACSYGHYEVTETLLVKHGACVNAMDLDWQFTP 354
Db 318 YNRVRIVQLLQHGADVHAKDGLVPLHNACSYGHYEVTETLLVKHGACVNAMDLDWQFTP 377
Qy 355 LHEAASKNRVEVCSLLSYGADPTLLNCHNKSALDAPTOLKRLAYEPKSHSLLOAAR 414
Db 378 LHEAASKNRVEVCSLLSHGADPTLVNCHGKSAVDMAPTPELRERLTYEPKSHSLLOAAR 437
Qy 415 EADVTRIKHLSLEWNVFHPQTHETALHCAASAPYPRKQICELLRKGANINEKTKEF 474
Db 438 EADLAKYKKTALAEIINFQPSHETALHCAVAAPHKPKQVTELLLRKGANVNEKNKDF 497
Qy 475 LTPLHVASEKAHNDVVEVYVVKHAKVNALNLOGTSLHRAAYCGHLOTCLRLLSYGCDPN 534
Db 498 MTLHVAAAEKAHNDVMEVLHKHGAKNALDTLQGTALHRAALAGHLQTCRLLLNYGSDPS 557
Qy 535 IISLQGTALOMNENVOQLLOEGISLGNSEADRLLEAAKAGDVEVTKLCTVQSVNCR 594
Db 558 IISLQGTAAQIGNEAVQQLSESTPVRTSDVYRLLLEASKAGDLETVTKQLCSQPNVNCR 617
Qy 595 DIEGROSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDGGVPLHNACSYGHYEVAELLVK 654
Db 618 DLGRHSTPLHFAAGYNNRVSVVEYLLHGGADVHAKDGGVPLHNACSYGHYEVAELLVR 677
Qy 655 HGAVVNVADLWKFTPLHHEAAAKGKYEICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQ 714
Db 678 HGASVNVADLWKFTPLHHEAAAKGKYEICKLLKHGADPTKKNRDGNTPLDLVKEGDTDIQ 737
Qy 715 DLIRGDAALIDAAKKGCLARVKLSPDNVCNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQ 774
Db 738 DLLRGDAALIDAAKKGCLARVKQLCTPENINCRTDQGRNSTPLHLAAGYNNLEVAEYLL 797
Qy 775 HGADVNAQDKGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAFTHLHAAQKGRTOQL 834

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Qy 835 CALLIAHAGADPTLKNOEGOTPLDVSADDSVALLTAAMPSSALPSCYKPOVLNGVRSFGA 894
Db 858 CALLIAHAGADPTMKNOEGOTPLDADATADDIALLIDAMPPEALPTCFKLOAT-----V 910
Qy 895 TADALSSGPPSSLSAASSIDNLGSPSESSVSSVSSGTEGASSLEKK--EVPQVDFSI 952
Db 911 VSASLISPASPTSCLSAASSIDNLGTPLAELAVGASNTGDAAGTERKEGVSGLDNI 970
Qy 953 TOFVNRLGLEHMDIFERQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISQQ 1012
Db 971 TOFLKSLGLEHLRDFETEQTITLDVLADMGHEELKEIGINAYGHRHKLKIGVERLISQQ 1030
Qy 1013 GINPVLTLNTSSGTTLDLSDPDDKFEFOSVEEMOSTVREHDDGHGAGIFNRYNLIKQ 1072
Db 1031 GTNPVLTFTCVSQGLTLDLADPDDKEYOSVEEMOSTVREHDDGNGAGIFNRYNIRIQ 1090
Qy 1073 KYCNKKLWERYTHRRKEVSEENHNHANERMLPHGSPFFVNAIHKGFDRHAYIGGMFGAG 1132
Db 1091 KVNKKLBERPCHRQKEVSEENHNHNERMLPHGSPFFVNAIHKGFDRHAYIGGMFGAG 1150
Qy 1133 IYFAENSKSNQYVYIGGGTGCPCVHDKRSCYCHIRQLLFCRVTLGKSFLOFSAMKMAHS 1192
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Qy 1193 PGHHSVTCRPSVNGALAEVYIYGEQAYPEYLITYQIMRPE 1235
Db 1211 PGHHSVTCRPSVNGALAEVYIYGEQAYPEYLITYQIVKPE 1253

RESULT 7
Q5XGK5 XENLA
ID Q5XGK5 XENLA PRELIMINARY; PRT; 1303 AA.
AC Q5XGK5;
DT 23-NOV-2004, integrated into UniProtKB/TrEMBL.
DT 23-NOV-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE LOC495279 protein.
GN Name=LOC495279;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL: BC084432; AAH84432.1; -: mRNA.
DR GO: 0005634; C:nucleus; IEA.
DR GO: 0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR GO: 0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR012317; PARP_catalytic.
DR InterPro: IPR001660; SAM.
DR InterPro: IPR011510; SAM_2.
DR Pfam: PF00023; ANK; 18.
DR Pfam: PF0644; PARP; 1.
DR Pfam: PF07647; SAM_2; 1.
DR PRINTS: PR01415; ANKYRIN.
DR SMART: SM00248; ANK; 15.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS50297; ANK REP REGION; 1.
DR PROSITE: PS50088; ANK REPEAT; 15.
DR PROSITE: PS51059; PARP CATALYTIC; 1.
DR PROSITE: PS50105; SAM_DOMAIN; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 1303 AA; 5F4C3F89329D5F8B CRC64;
Query Match 77.5%; Score 5010.5; DB 2; Length 1303;
Best Local Similarity 77.0%; Pred. No. 5e-286;
Matches 947; Conservative 110; Mismatches 108; Indels 65; Gaps 5;
Qy 28 PDPTVAGSQARALSASSP-----GGALLLAGPGLLLRLLALL 67
Db 104 PPAPSSGSSS-----SSSPSSNSLSSGSPSPSPESGVIGVSSIGIGPG----- 149
Qy 68 AVAAARIMSGRRRCAGGGAACAASAAEAVEPAARELFEACRNGDVERVRLVPEKVNRSR 127
Db 150 -----GPLSAVSGAFRELFEACRNGDVSRRVRLLEPGVNAKD 187
Qy 128 TAGRKSTPLHFAAGFGKRDVVEYLLQNGANYOARDGGLIPLHNAACSFHAEVVMLLRH 187
Db 188 MAGRKSTPLHFAAGFGKRDVVEYLLQNGANYOARDGGLIPLHNAACSFHAEVVMLLCQ 247
Qy 188 GADPNARDNWNYYTPLHAAIKGKIDVCIVLQHGAEPTIRNTDGTALDLPSPKAVLT 247
Db 248 GADPNARDNWNYYTPLHAAIKGKIDVCIVLQHGADPSIRNTDGSALDLPSPKAVLT 307
Qy 248 GEYKDELLSARGSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVLLOLQ 307
Db 308 GEYKDELLSARGSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVLLOLQ 367
Qy 308 GADVHAKDKGDLVPLHNAACSYGHVEVTELLVKHGACVNMADLWQFTPLHAAASKNRVEVC 367
Db 368 GADVHAKDKGDLVPLHNAACSYGHVEVTELLVKHGACVNMADLWQFTPLHAAASKNRVEVC 427
Qy 368 SLLISYGADPTLLNCHNKSAIDLAPTPOKRLAYEFKHSLLQAAERADVTRIKHLSL 427
Db 428 SLLISYGADPTLLNCHNKSAIDLAPTPOKRLAYEFKHSLLQAAERADVTRIKHLSL 487
Qy 428 EWNVFKHPQTHETALHCAASPYKPKKQICELLARKGANINEKTEFELTPLHVAASEKHN 487
Db 488 EILNFPQSHETALHCAVASLPPKPKQITELLARKGASVNEKNKDFMTPLHVASERAHN 547
Qy 488 DVVEVVKHEAKVNALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDDPNIIISLQGFALQMG 547

442 L-----HCAASPPKPKQICELLRLKGANINEKTEPLTLHVASEKAHNDVVEV 492
QY
Db LMLKVAAYFQHCASVAPKPKQVTELLRLKGANINDKNDKQFMTPLHVAEERAHNDILEV 408
493 VVKHAKVNALDNLGOTSILHRAAYCHLQTCRLLLSYGCDDPHIISLOQFTALQMGNNVQ 552
QY
Db LQKHGAKVNAADTLGQTLALHRAALAGHTQCTKLLLSYGADPAIVSLOQFTAAQMGNEAVQ 468
553 QLLQGISLGNSEADRLLEAKAGDVETV-----KKLCTV 588
QY
Db QILNENVPTRNSDVYRFLKAAKAGDQTVQVWSLALRLVSEGMRLOKVLVSQOLCSP 528
589 QSVNCRDIEGROSTPLHFAAGYNNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHYEV 648
QY
Db QNVNCRDIEGHRSTPLHFAAGYNNRVVVEYLLHFGADVHAKDGLVPLHNACSYGHYEV 588
649 AELLVKGAVNVADLWKTPLHFAAAGKYBI CKLLLOHGADPTKQNRDGNTPLDLVKD 708
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Db AELLVHKGASVNVADLWKTPLHFAAAGKYBI CKLLLOHGADPTKQNRDGNTPLDLVKD 648
709 GDTDIQDILLRGAALLDAAKGLCLARVVKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEV 768
QY
Db GDTDIQDILLRGAALLDAAKGLCLARVVKLSPPDNVNCRDTOGRHSTPLHLAAGYNNLEV 708
769 AEYLLQHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAPTPLHEAAQ 828
QY
Db AEYLLQHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNACVNATDKWAPTPLHEAAQ 768
829 KGRTOCALLAHAGADPTLKNQGGTPLD-----LVSADD 863
QY
Db KGRTOCALLAHAGADPTLKNQGGTPLD-----LVSADD 863
864 VSALLTAAMPSPALSCYKPO---VLNGVRSPCATADALSGSPSSISAASSIDNLSSG 920
QY
Db IRALLIDAMPDPALPCFKPQATVVSASVISPAST-----PCLSAASSIDNLSSG 878
921 SPSELSSVVSSSGT-----EGASSLEKK--EVPVDFSFITQFVRNLGLHLMDFEREQIT 974
QY
Db PLTELAAAVSTGSSGVADGATGSRKEGEMTMDNLSQFLKSLGLDHLRDIFFEREQIT 938
975 LDVLVEMGHKELKEIGINAYGHRHLKIGVERLISGOQGLNPLYTLNTSGSTILIDLSP 1034
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Db LDVLADMGEELKEIGINAYGHRHLKIGVERLISGOQGLNPLYTLNTSGSTILIDLSP 998
1035 DDKEQSVSEEMOSTVREHGDGHAGGIPNRNLIKIKVCKKLEWYTHRKEVSEEN 1094
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Db DDKEYQSVSEEMOSTVREHGDGHAGGIPNRNLIKIKVCKKLEWYTHRKEVSEEN 1058
1095 HNHNEMRLFHGSPFNALIHKGPDHAYIGCMFGAGIYFAENSSKSNQYVYGGGTG 1154
QY
Db HNHNEMRLFHGSPFNALIHKGPDHAYIGCMFGAGIYFAENSSKSNQYVYGGGTG 1118
1155 CPVHKDRSICYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSTVGRPSVNGLAAYV 1214
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Db CPVHKDRSICYICHRQLLFCRVTLGKSFLOFSAMKWAHSPGHHSTVGRPSVNGLAAYV 1178
1215 IYRGEQAYPEYLITYQIMRPE 1235
QY
Db IYRGEQAYPEYLITYQILKPE 1199

RESULT 9
Q59FX0 HUMAN PRELIMINARY; PRT; 1055 AA.
AC Q59FX0;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Tankyrase, TRF1-interacting ankryrin-related ADP-ribose polymerase
DE variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

Homo.
NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE.
TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RC Chara O., Nagase T., Kikuno F.R.;
RT "None Title";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; AB293339; BAD92576.1; -; mRNA.
DR Ensembl; ENSG00000173273; Homo sapiens.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001290; PARP.
DR InterPro; IPR012317; PARP_catalytic.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR011510; SAM_2.
DR Pfam; PF00023; Ank; 17.
DR Pfam; PF00644; PARP; 1.
DR Pfam; PF07647; SAM_2; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 13.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PS02097; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00088; ANK_REPEAT; 13.
DR PROSITE; PS1059; PARP_CATALYTIC; 1.
DR PROSITE; PS0105; SAM_DOMAIN; 1.
KW ANK repeat.
KW NON_TER
FT NON_TER 1 1
SQ SEQUENCE 1055 AA; 115234 MW; 9210519D299EB805 CRC64;

Query Match 72.4%; Score 4681.5; DB 2; Length 1055;
Best Local Similarity 82.9%; Pred. No. 9e-267;
Matches 870; Conservative 94; Mismatches 76; Indels 9; Gaps 2;

QY 189 ADPNARDNNWYTPPLHEAAIKGKIDVICIVLLQHGAPPTIRNTDGTALDAPSAKAVLTG 248
Db 1 ADPNARDNNWYTPPLHEAAIKGKIDVICIVLLQHGADPNIRNTDGTALDAPSAKAVLTG 60
QY 249 EYKDELLESARSNGEKKMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIVQLLQHG 308
Db 61 EYKDELLEAARSNGEKKMALLTPLNVNCHASDGRKSTPLHLAAGYNNRVIVQLLQHG 120
QY 309 ADVHAKDKGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCS 368
Db 121 ADVHAKDKGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAASKNRVEVCS 180
QY 369 LLLSYGADPTLLNCHNKSADLAPTPQKRLAYEFKGHSLLOAAREADVTRIKKHSLE 428
Db 181 LLLSHGADPTLVNCHGKSAVDMAPTPELRERLTYEFKGHSLLOAAREADLAKVKKTLAE 240
QY 429 MWNFKHPOTHETALHCAASPYPKRKQICEILLRKGANINEKTEPLTLHVASEKAHND 488
Db 241 IINFKQPSQTHETALHCAASPYPKRKQVTELLRKGANINEKTEPLTLHVASEKAHND 300
QY 489 VVEVVKHKAQVNALDNLGOTSILHRAAYCHLQTCRLLLSYGCDDPHIISLOQFTALQMG 548
Db 301 VVEVVKHKAQVNALDNLGOTSILHRAALAGHTQCTKLLLSYGCDDPHIISLOQFTALQMG 360
QY 549 ENVQQLQEGISLGNSEADRLLEAKAGDVETVVKLCTQVSNCRDIEGROSTPLHFAA 608
Db 361 EAVQQLSESTPIRTSDVDVYLLLEASKAGDLETVKQLCSSQNVNCRDIEGHRSTPLHFAA 420
QY 609 GYNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLH 668
Db 421 GYNRVSVVEYLLHGHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLH 480

Qy 669 PLHEAAKGYEICKLLOHAGDPTKKNRGNTPLDLVKDQDTDIQLLRGDAALLDAK 728
 Db 481 PLHEAAKGYEICKLLOHAGDPTKKNRGNTPLDLVKDQDTDIQLLRGDAALLDAK 540
 Qy 729 KGCLARVKLLSSPNVNCRDTOGRHSTPLHLAAGNNLEVAEYLLQHGADVNAQDKGLI 788
 Db 541 KGCLARVKLLSSPNVNCRDTOGRHSTPLHLAAGNNLEVAEYLLQHGADVNAQDKGLI 600
 Qy 789 PLHNAASVGHVDVAALIKYNACVNATDKWAFTPLHEAAQKGRTOQLCALLAHGADPTLK 848
 Db 601 PLHNAASVGHVDIAALIKYNTCVNATDKWAFTPLHEAAQKGRTOQLCALLAHGADPTMK 660
 Qy 849 NQEGOTPLDVSADVSALLTAAMPPLALSCYKPOVLNGVRSPCATADALSSSPSPSS 908
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 Qy 909 LSAASSIDNLGSGSELSVSSVSSGSGASLEKK--EVPQVDFSTQFVRLNGLHLM 966
 Db 714 LSAASSIDNLGSGSELSVSSVSSGSGASLEKK--EVPQVDFSTQFVRLNGLHLM 966
 Qy 967 IFEREQITDLVEMGHKELKEIGINAYGHRHKLKIGVERLISQOQGLNPLYTLNTSGS 1026
 Db 774 IFEREQITDLVEMGHKELKEIGINAYGHRHKLKIGVERLISQOQGLNPLYTLNTSGS 1026
 Qy 1027 TILDLSPDDKDFQSVSEEMQSTVREHRDGHAGGIFNRYNLIKQVCKKLWERTHR 1086
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 Qy 1087 RKEYSEENHNHNERMLPHGSPFFVNAIHKGFDRHAYIGMFGAGIYFAENSCKSNQYV 1146
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RESULT 10
 Q8BX62_MOUSE PRELIMINARY; PRT; 976 AA.
 AC Q8BX62; 976 AA.
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 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 20.
 DE 0 day neonate cerebellum cDNA, RIKEN full-length enriched library,
 DE clone: C230076f23 product: tankyrase, TRF1-interacting ankyrin-related
 DE ADP-ribose polymerase, full insert sequence.
 GN Name=TNks;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
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 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 (2)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC PubMed=141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi A., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,

BA Baxsal M., Baxter L., Beisel K.W., Bergano T., Bono H., Chalk A.M.,
 BA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.D., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
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 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
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 RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
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 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
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 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
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 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
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 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group
 RA (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs. ";
 RL Nature 420:563-573(2002).
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 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
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 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
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 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
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 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076961; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Hatanai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Kizuna M., Nishine T., Harada A.,
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 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
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 RL Genome Res. 10:1757-1771(2000).
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 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
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 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NonCommercial License
 CC -----
 CC EMBL; AK048860; BAC33475.1; -; mRNA.
 DR HSP; F6157; IN11.
 DR Ensembl; ENSMUSG00000031529; Mus.musculus.
 DR MGI; MGI:1341087; Tnks.
 DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
 DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR001290; PARP.
 DR InterPro; IPR012317; PARP_catalytic.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR011510; SAM_2.
 DR Pfam; PF00023; ANK; 15.
 DR Pfam; PF00644; PARP; 1.
 DR Pfam; PF07647; SAM_2; 1.
 DR PRINTS; PR01415; ANKYRN.
 DR SMART; SM00248; ANK; 12.
 DR SMART; SM00454; SAM; 1.
 DR PROSITE; PS50297; ANK_REPEAT; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 12.
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 KW ANK repeat; Repeat.
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Db	771	EEBMQSTIREHRDGGNAGGIFNRYNIRIQKVNKKLRERFCHRKVEVSEENHNHNERM	830
Qy	1103	LFGSPSPVNAIIHKGFDERHAYIGMFGAGIYFAENSCKSNQTVYVYGGGTGCPVHKDRS	1162
Db	831	LFGSPFPFNAIIHKGFDERHAYIGMFGAGIYFAENSCKSNQTVYVYGGGTGCPVHKDRS	890
Qy	1163	CYTCRQLLFCRVTLGKSFLOFSAMKMAHSPGHHSVTGRPSVNGIALABYVYRGEQAY	1222
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DT	15-DEC-2003,	integrated into UniProtKB/TrEMBL.	
DT	06-DEC-2005,	sequence version 2.	
DT	07-FEB-2006,	entry version 21..	
DE	ENSANGP0000019360.		
GN	ORFNames=ENSANG000000015871;		
OS	Anopheles gambiae str. PEST.		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;		
OC	Anophelinae; Anopheles..		
OX	NCBI_TaxID=180454;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN-PEST;		
RG	The Anopheles gambiae Sequence Committee;		
RT	"Anopheles gambiae re-annotation."		
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN-PEST;		
RG	The Anopheles gambiae Sequence Committee;		
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.		
CC	-1- CAUTION: The sequence shown here is derived from an		
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is		
CC	preliminary data.		
CC	-----		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		
CC	Distributed under the Creative Commons Attribution-NoDerivs License		
CC	-----		
DR	EMBL; AAB01008987; EAA01120.2; -; Genomic_DNA.		
DR	GO; GO:0005634; C:nucleus; IEA.		
DR	GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.		
DR	GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.		
KW	ANK repeat; Repeat.		
QY	SEQUENCE 1168 AA; 12698 MW; 0386A4161210012B CRC64;		
Query Match			
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Matches 791; Conservative 160; Mismatches 178; Indels 71; Gaps 10;			
Qy	75	MSGRRCAGGAAACASAAAEVAPAAELFACRNGDVERKRLVTPKEKNSRDTAGRKST	134
Db	1	MSANRGRSMISVNLEAAAMANDP-LRELFEACKTGDLAKVKKLIITPOTVNARDTAGRKST	59
Qy	135	PLHFAAGFGKRDVVVEYLONGANVQARDGGLIPLHNACSFGEAEVNNLLRHGADPNAR	194
Db	60	PLHFAAGYGRDVEFLANGASIQARDGGLPLHNACSFGEADVVRLLEAGANPNTR	119
Qy	195	DNNYTPPLHFAA1KGKIDVICIVLQHGAEPTIRNTDGRALTALDADPSAKAVLTGEYKDE	254

Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).

[4]

RP NUCLEOTIDE SEQUENCE.

RP MEDLINE=22426069; PubMed=12537572;

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RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,

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RT systematic review.";

RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

[5]

RP NUCLEOTIDE SEQUENCE.

RP Berkeley Drosophila Genome Project;

RA Celisner S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,

RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,

RA Yu C., Rubin G.;

RT "Drosophila melanogaster release 4 sequence.";

RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[6]

RP NUCLEOTIDE SEQUENCE.

RP FlyBase;

RG Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.

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CC

CC EMBL; A5003752; AAF56487.1; -; Genomic_DNA.

DR HSP; P20749; 1K1B.

DR FlyBase; FBgn0027508; tankyrase.

DR GO; GO:0003634; C:nucleus; IEA.

DR GO; GO:0003950; F:NAD+ ADP-riboseyltransferase activity; IEA.

DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR001290; PARP.

DR InterPro; IPR012317; PARP catalytic.

DR InterPro; IPR001660; SAM_

DR InterPro; IPR011510; SAM_2.

DR Pfam; PF00023; Ank; 17.

DR Pfam; PF00644; PARM; 1.

DR Pfam; PF07647; SAM 2; 1.

DR PRINTS; PR01415; ANKYRIN.

DR SMART; SM00248; ANK; 15.

DR SMART; SM00454; SAM; 1.

DR PROSITE; PS0297; ANK REP REGION; 1.

DR PROSITE; PS0088; ANK REPEAT; 14.

DR PROSITE; PS01059; PARP CATALYTIC; 1.

DR PROSITE; PS01005; SAM_DOMAIN; 1.

KW ANK repeat; Repeat.

SW SEQUENCE 1181 AA; 127945 MW; EB6F0F94E6A3D504 CRC64;

Query Match 62.0%; Score 4005; DB 2; Length 1181;

Best Local Similarity 65.3%; Pred. No. 7.9e-227;

Matches 772; Conservative 166; Mismatches 189; Indels 56; Gaps 13;

QY 91 AA AEVPEPAARELFEACRNGDVERVKELVTPPEKNSRDTAGRKSTPLHFAAGFGKDVVEY 150

DB 17 AVMANDP-LRELFEEACKTEGIAKVKLLTPQTWARDTGRKSTPLHFAAGYGRREVVEV 75

QY 151 LQIONAVOARDGGILPLHNACSFGHAEVNNLLLRHGADPNARDNNWYTPLEAAIKGK 210

DB 76 LINSGHASIQADGGGLHPLHNCCSFGHAEVNNLLLRKAGASPNWYTPLEAAIKGK 135

QY 211 IDVCIVLLQGAPEPTIRNTDGRFTALDAPSAKAVLTGYEKDDELLESARGNEEKMMAL 270

DB 136 VDVCIALIQGHANHTIRNSEQKTPLEADATRPVLTGEYKDELLEAAARGAEDRLAL 195

QY 271 LTPLVNCHASDGRKSTPLHLAGYNRKIVQLLOHGDADVHAKDGLVPLHNACSYGH 330

DB 196 LTPLVNCHASDGRSTPLHLAGYNRIGIVETLLANGADVHAKDGLVPLHNACSYGH 255


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Db 256 FDVTKLLIQAGANVNDLWAFTHLHFAASKRVEVCSLLSRGADPTLLNCHSKSAIDA 315
Qy 391 APTPOLKRLAYEPKGHSLHQAAREADVTRIKHLSLEMVNFKHPQTHETALHCAASPY 450
Db 316 APTRELRLERAFYKGHCLLDACKRCDVSRKULVCAEIVNFVHPYTGDTPLHLAVNSPD 375
Qy 451 PRRQICELLRRKGANINEKTEKFTPLHFAASKRVEVCSLLSYGADPTLLNCHNKSIDL 510
Db 376 GKRQKLMELLTRKGSLLNKNKAFPLTHLHFAASKRVEVCSLLSRGADPTLLNCHSKSAIDA 435
Qy 511 LHRAAYCHLOTCLLLSYGCDPHNISLQGTALQMGNVNVQQLLQSGISLGNSEADROL 570
Db 436 LHRCA--RDEQVRLLSYAADTNIVSLEGLTAAQLASDSDS-----NPPDSETHL 488
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Qy 629 KDKGGLVPLHNACSYGHEVAELLVHGA VVNVADLWKFTPLHFAAAKGYEICKLLQH 688
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Qy 689 GADPTKQRDGTPLDLVKGDDTDIDLLRGDALLDAKKGCLARVKLSSPDNVCNRD 748
Db 609 GADPMKQRDGTADPLVKESDHDVALLRGPSSALLDAKKGCLARVQLVTPESINCRD 668
Qy 749 TQGRHSTPLHAGVNVLEVAEYLQHGADVNAQDKGLIPLHNAASVGHVDVAALLIKY 808
Db 669 AQGRNSTPLHAGVNVFECAYELLENADVNAQDKGLIPLHNAASVGHLDIAALLIKH 728
Qy 809 NACVNATDKWAFTPLHFAAAKQRTQLCALLAHGADPTLKNQEGQTPDLVSDADVSA 868
Db 729 KTVVNATDKWFTPLHFAAAKQRTQLSLLAHGADAVYMKNGEQGTPIELATADVVKLL 788
Qy 869 TAAMPSS-----ALPSCYKQVNLVGRSPGATADALSSGPPSS--LSAASSLDNLSSGF 922
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Qy 923 SELSSV-----VSSS-----GTGASLEKKEVPGVD--PSITQFVNKLGLEH 963
Db 848 SMILSVPLPLSSSTRISPAQGAANGAEGSSDDL--LPDATTNVSGFLSSQQLHH 905
Qy 964 LMDIFEREQITDLVLEMGHKLKEIGINAYGHRHKLKIGVERLISGQQLNPLYTLNTS 1023
Db 906 LIELFEREQITDLILAEMGHDDLQGVSAVGFPRKILKGIAQLRS-----TT 953
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AC Q9XZ37;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 26.
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DE Hypothetical protein.
GN Name=tankyrase; ORFNames=CG4719;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Ephydroidea; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
RA Agbavani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C.,
RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Friese E.,
RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
RA Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
RA Ceiniker S.E.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AF132196; AAD34784.1; -; mRNA.
DR HSBP; P20749; IK1B.
DR FlyBase; FBgn0027508; tankyrase.
DR GO; GO:0005834; C:nucleus; IEA.
DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001290; PARP.
DR InterPro; IPR012317; PARP_catalytic.
DR InterPro; IPR001660; SAM_2.
DR InterPro; IPR011510; SAM_2.
DR Pfam; PF00023; Ank; 17.
DR Pfam; PF00644; PARP; 1.
DR Pfam; PF07647; SAM 2; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 15.
DR SMART; SM00454; SAM; 1.
DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PSS0088; ANK_REPEAT; 14.
DR PROSITE; PSS1059; PARP_CATALYTIC; 1.
DR PROSITE; PSS0105; SAM_DOMAIN; 1.
KW ANK repeat; Hypothetical protein; Repeat.
SQ SEQUENCE 1181 AA; 127885 MW; 4E2BF31549BBA2D9 CRC64;
Query Match 61.8%; Score 3997; DB 2; Length 1181;
Best Local Similarity 65.2%; Pred. No. 2.4e-226;
Matches 771; Conservative 166; Mismatches 190; Indels 56; Gaps 13;
Qy 91 AAEAVEPAARELFEACRNGDVERVKRLVTEKYNRSRTAGRKSTPLHFAAGFGRKDVVEY 150
Db 17 AVWANDP-LRELSEACKTGIAKVKLLITPQTVNARDTAGRKSTPLHFAAGYGRREVVEF 75
Qy 151 LLONGANVQARDGGLIPLHNACSFHAEVNVLLLRHGDNPARNNNYTPLEHAAIKGK 210
Db 76 LLMSGASIQACDEGLHPLNCCSFHAEVVRLLLKAGASPTTDDNNYTPLEHAAIKGK 135
Qy 211 IDVCIVLLQHGAEPTIRNTDGRFTALDLADPSAKAVLTGEYKDELLESARSGNEKMA 270
Db 136 VDVCVLLQHGANTIRNSQKTPLEADEATRPVLTGEYKDELLEAARSAGADRLLAL 195
Qy 271 LTPLNVNCHASDGRKSTPLHLAGYNRVKIVQLLLQHGADVHAKDGLVPLHNACSGH 330
Db 196 LTPLNVNCHASDGRSRSTPLHLAGYNRIGIVEILLANGADVHAKDGLVPLHNACSGH 255
Qy 331 YEVTLLVKGACVNMVMDLWQFTPLHFAASKRVEVCSLLSYGADPTLLNCHNKSIDL 390
Db 256 FDVTKLLIQAGANVNDLWAFTHLHFAASKRVEVCSLLSRGADPTLLNCHSKSAIDA 315
Qy 391 APTPOLKRLAYEPKGHSLHQAAREADVTRIKHLSLEMVNFKHPQTHETALHCAASPY 450
Db 316 APTRELRLERAFYKGHCLLDACKRCDVSRKULVCAEIVNFVHPYTGDTPLHLAVNSPD 375
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451 PRRKQICELLKRGANINEKTEFLTPHVAASEKAHNDVVEVVVKEAKVNALDNLGOTS 510
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 511 LHRAYCGLHQLCRLLLSVCGDPNIIISQFTALQMGNNVVOQLLOEIGISLGNSEADRLQ 570
 436 LHRCA--RDEQAVRLLSYAADTNIVSLSEGLTAQAQGLADSVLKLK-----NPPDSETHL 488
 571 LEAAKAGDVETVKCLCTVQ--SVNCRDIEGROSTPLHPAAGVYNNRVVVEYLLOHGDVHA 628
 489 LEAAKAGDLDVTRVIRVNLNPIVSNCRDLDRGSTPLHPAAGVYNNRVVVOFLHGAEVTA 548
 629 KDKGLVPLHNAACSYGHYEVAELLVKHGVANNVADLWKEFTPLHEAAKGYKIBCKLLQH 688
 549 ADKGLVPLHNAACSYGHYEVEVTELLVKHGANVNSDLWKEFTPLHEAAKGYKIBCKLLKH 608
 689 GADPTKQRDGNVPLDLVKDGTDTQDLRGGDAALLDAKKGCLARVKLSSPDVNCRD 748
 609 GADPMKQRDGNVPLDLVKESDHDVAELRGPALLDAKKGCLARVQLVTPFESINCRD 668
 749 TQGRHSTPLHNAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVDVAALLIKY 808
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 809 NACVNATDKWAPTPLHEAAKQRTQICALLAHGADPTLKNQEGQTPDLVSDADVALL 868
 729 KTVNATDKWAPTPLHEAAKQRTQICALLAHGADVNAQDKGGLIPLHNAASYGHLDIAALLIKH 788
 869 TAAMPSS-----ALPCKYKQVNLVGRSPGATADALSSGSPSS--LSAASLDNLSSGF 922
 789 QDAMATSLSQAL--SASTQSLTSSSPADPATAAAGTSSSSSSAILSPPTETVLLPTGA 847
 923 SELSSV-----VSSS-----GTEGASSLEKKEVPGVD--FSITQFVRLNGLEH 963
 848 SMILSVPLPLSSSTRISPAQGAANGAEGSSDDL--LPDADTITNVSGPLSQQLHH 905
 964 LMDIFERQITLDLVEMGHKELKIGINAYGHRHLKIGVERLISGQGLNPLYTLNLS 1023
 906 LIELEPERQITLDILAEMGHDDLKQGVSAVYGRFKILKIGIAQLS-----TT 953
 1024 GSG-----TILIDSPDKFQSVVEEMQSTVREHGGHAGGIFPNRYNLIKIKQVCK 1077
 954 GITGNVNLCTLLVDLLPDDKEVFAVEEEMQATIREHNDGQAGGYFTRYNIRVQVQNR 1013
 1078 KLWERYTHRRKEVSENNHANERMLFHGSPFNVAIHKGPDERHAYTGMFGAGIYFAE 1137
 1014 KLWERYAHRHQBIABENFLQSNRMLFHGSPFNVAIQRGDERHAYTGMFGAGIYFAE 1073
 1138 NSSKSNQVYVYGGGTGCPVHKDRSCYICHRQLLFCRVTLGKSPFQFSAMKMAHSPPGHH 1197
 1074 HSKSNQVYVYGGIGGICGPFHDKSCYVCPROLLLCRVALGKSFLOYSAMKMAHAPPGHH 1133
 1198 SVTGPSVNGLALAEVYVYRGQAYPEYLITYQIMRPGMVDG 1240
 1134 SVVGRPSAGGLHFAEYVYVYRGQAYPEYLITYQIVKPDSSSG 1176

RESULT 14
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 ID Q4S372.TETNG PRELIMINARY; PRT; 1047 AA.
 AC Q4S372.
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DE Chromosome 4 SCF14752, whole genome shotgun sequence. (Fragment).
 GN ORFNames=GSTENG0024768001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
 RA Maucell E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicolas S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segurens B.,
 RA Dasilva C., Salancoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Koutnik J., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter J., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC
 CC EMBL; CAAB01014752; CAG04910.1; -; Genomic DNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
 DR GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR012317; PARP_catalytic.
 DR Pfam; PF00023; ANK; 13.
 DR Pfam; PF00644; PARP; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 9.
 DR PROSITE; PS02097; ANK_REPEAT; 1.
 DR PROSITE; PS00088; ANK_REPEAT; 10.
 DR PROSITE; PS10509; PARP_CATALYTIC; 1.
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 FT NON TER 1047 1047
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 Best Local Similarity 60.5%; Pred. No. 9,1e-187;
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 DB 18 GEYKDELLESARSNGEEMKALLTPLNVNCHASDGRKSTPLHLAAGYNNRVKIVOLLQ 77
 QY 308 GADVHAKDKGLVPLHNAACSYGHYEVEVTELLVK----- 339
 DB 78 GADVHAKDKGLVPLHNAACSYGHYEVEVTELLVKVHTHTTHTRAQHTGCEWTLARPLTLEA 137
 QY 340 -----HGACVNMADLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLNCHNKAIDLAPT 393
 DB 138 ETVPQHGACVNMADLWQFTPLHEAASKNRVEVCSLLLSHGADPTLLNCHSKSSVDMAPT 197
 QY 394 POLKERLAYEPKSHLLOAAREADVTRIKHLSLEMVNFKHPQTHETALHCAASPYKCR 453
 DB 198 PELKERTYPEKSHLLOAAREADVAKAKSLVLEIINFKPHPHTHETAL----- 246
 QY 454 KQICELLIRKGANINEKTEKFTPLHVAASEK-----AHDVVVEVVVKEAKVNALDNLGOT 509
 DB 247 -----LHDSASRGCGGAHNDIMEVLQKHGAKVNALDNLGOT 282
 QY 510 SLHRAAYCGHLOTCLRLLSYCGDNNIIISQFTALQMGNNVVOQLLOEIGISLGNSEADRLQ 569
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QY 570 LLEAAKAGDVETVKLLCTVQSVNCRDIEGRQSTPLHFAAGVNRVSVVEYLLQHGADVHAK 629
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QY 630 DKGLVPLHNACSGHYEVAELLVKGAVNVADLWKFPLHFAAGKGYEICKLLQHG 689
DB 403 DKGLVPLHNACSGHYEVAELLVHVGASVNVADLWKFPLHFAAGKGYEICKLLKHG 462
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DB 463 ADPTKKNRDNTPDLVLKGDGTDIQLDLRGDAALLDAKKGCLARVKLSPDNVNCRD 522
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QY 810 ACVNATDKWFTPLHEAAQKGRITQCALLAHGADPTLKNQEGTPTLDLVLS----- 860
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QY 861 -----ADVSALLTAAMPSPALPSCYKQVNLVGRSPGATADALSGSPSPS 907
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QY 959 LGLEHLMDIFEREQITLDVLVEMGHKELKIGINAVGHRHKLKIGVERLISGQOGLNPLYL 1018
DB 743 -----EGGRRYRRAP-----AAGDHQPLP----- 762
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DB 1000 KMAHAPPGHHSVTRGSPVNGLAAYVYIRGEQAYPEYLITYQIVKPE 1047
RESULT 15
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ID Q8BXH7_MOUSE PRELIMINARY; PRT; 601 AA.
AC Q8BXH7;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 18.
DE 10 days neonate cerebellum cDNA, RIKEN full-length enriched library,
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RC MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Methods Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RC PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Davis M.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Bajic M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bono H., Chalk A.M.,
RA Banfalvi M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminicki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
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RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Sempole C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.H., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., Van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zdobych E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Pukada S., Kanamori-Katayama M., Suzuki M., Roki J., Atakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya S.,
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RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RC PubMed=16141073; DOI=10.1126/science.1112009;
RX RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
[4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01366;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaio I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldrilli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazar K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
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RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
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RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

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RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Kugawa I.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kugawa S.,
RA Miyazaki A., Sakai K., Sasai D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Szaubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
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RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kugawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koya S.,
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RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
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RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AK047094; BAC32960.2; -; mRNA.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank; 13.
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Best Local Similarity 97.2%; Pred. No. 6.3e-172;
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OM protein - protein search, using sw model

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Title: US-10-616-101-4

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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2	6464	100.0	1240	2	US-09-843-159B-4 Sequence 4, Appli
3	6108	94.5	1166	2	US-09-972-115A-6 Sequence 6, Appli
4	6053	93.6	1166	2	US-09-350-982C-5 Sequence 5, Appli
5	5877	90.9	1227	2	US-09-843-602-26 Sequence 26, Appli
6	5766	89.2	1100	2	US-09-696-668-3 Sequence 3, Appli
7	5766	89.2	1100	2	US-09-843-159B-3 Sequence 3, Appli
8	5760	89.1	1100	2	US-09-843-159B-9 Sequence 9, Appli
9	5731.5	88.7	1100	2	US-09-427-154-2 Sequence 2, Appli
10	5656	87.5	1083	2	US-09-843-159B-10 Sequence 10, Appli
11	5452	84.3	1267	2	US-09-972-115A-4 Sequence 4, Appli
12	5103.5	79.0	1327	2	US-09-196-387-2 Sequence 2, Appli
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17	3307	51.2	949	2	US-09-196-387-10 Sequence 10, Appli
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19	2913	45.1	583	2	US-09-843-159B-8 Sequence 8, Appli
20	2132.5	33.0	673	2	US-09-196-387-8 Sequence 8, Appli
21	2132.5	33.0	673	2	US-09-841-835-8 Sequence 8, Appli
22	892.5	13.8	4377	2	US-09-949-016-6978 Sequence 6978, Ap
23	878.5	13.6	1719	2	US-09-949-016-6966 Sequence 6966, Ap
24	878.5	13.6	1856	2	US-09-949-016-6964 Sequence 6964, Ap
25	878.5	13.6	1880	2	US-09-949-016-5876 Sequence 5876, Ap
26	878.5	13.6	1881	2	US-09-949-016-6965 Sequence 6965, Ap

ALIGNMENTS

RESULT 1

US-09-696-668-4
; Sequence 4, Application US/09696668
; Patent No. 6617102

GENERAL INFORMATION:

; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Ososovkaya, Valeria
; TITLE OF INVENTION: TANKRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS (US-09-696-668-4)
; FILE REFERENCE: A-68292-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/696,668
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-696-668-4

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RESULT 2
US-09-843-159B-4
; Sequence 4, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty

; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods c
; FILE REFERENCE: A-68292-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1240
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: US-09-843-159B-4

Query Match 100.0%; Score 6464; DB 2; Length 1240;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 VNLLRHGADPNARDNNWYTPLEHAAIKGKIDVICIVLLQHGAEPTIRNTDGTALDADP 240
Qy 241 SAKAVLTGEYKDBELLESARGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNVKI 300
Db 241 SAKAVLTGEYKDBELLESARGNEEKWALLTPLNVNCHASDGRKSTPLHLAGYNNVKI 300
Qy 301 VQLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAAS 360
Db 301 VQLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAAS 360
Qy 361 KNRVEVCSLLSYGADPTLLCHNKSAIDAPTPOLKERLAYEPKSHSLQAAREADVTR 420
Db 361 KNRVEVCSLLSYGADPTLLCHNKSAIDAPTPOLKERLAYEPKSHSLQAAREADVTR 420
Qy 421 IKKHLSEWYFHPQTHETALHCAASAPYKPKQICELLRKGANINEKTEFLTPH 480
Db 421 IKKHLSEWYFHPQTHETALHCAASAPYKPKQICELLRKGANINEKTEFLTPH 480
Qy 481 ASEKANDVVEVVKHAKVNDNLGQTSIHRAYCGHLQTCRLLSYGCDPNIISLQ 540
Db 481 ASEKANDVVEVVKHAKVNDNLGQTSIHRAYCGHLQTCRLLSYGCDPNIISLQ 540
Qy 541 FTALQMGNEVQQLQEGISLGNSEADRLLEAAKAGDVETVKLCVQSVNCRDIEGRQ 600
Db 541 FTALQMGNEVQQLQEGISLGNSEADRLLEAAKAGDVETVKLCVQSVNCRDIEGRQ 600
Qy 601 STPLHFAAGYNNRVSVVEYLLQHGADVHAKDGGGLVPLHNACSYGHEVTELLVKGAVVN 660
Db 601 STPLHFAAGYNNRVSVVEYLLQHGADVHAKDGGGLVPLHNACSYGHEVTELLVKGAVVN 660
Qy 661 VADLWKFTPLHEAAKKGKYEICKLLOHGADPTKKNRDGNTPLDLVKDGTDIQDLLRGD 720
Db 661 VADLWKFTPLHEAAKKGKYEICKLLOHGADPTKKNRDGNTPLDLVKDGTDIQDLLRGD 720
Qy 721 AALLDAKKGCLARVKLSPPDNVNCRDTCGRHSTPLHLAGYNNLEVAEYLLQHGADVN 780
Db 721 AALLDAKKGCLARVKLSPPDNVNCRDTCGRHSTPLHLAGYNNLEVAEYLLQHGADVN 780
Qy 781 AQDKGGIPLHNAASYGHVDVAALLIKYNACVNAATDKWAFPTPLHEAAKKGRTQLCALLA 840

Db 781 AODKGLIPLHNAAGYGHVDVAALLIKYNACVNATDKWAFPLHEAAQKGRTOCALILA 840
Qy 841 HGADPTLKNQSGOTPLDVSADDSALLTAAMPSPALSCYKQPVINGVRSPGATADALS 900
Db 841 HGADPTLKNQSGOTPLDVSADDSALLTAAMPSPALSCYKQPVINGVRSPGATADALS 900
Qy 901 SGSPSSLSAASLDNLSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSIITQFVRLG 960
Db 901 SGSPSSLSAASLDNLSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSIITQFVRLG 960
Qy 961 LEHLMDFPERQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTL 1020
Db 961 LEHLMDFPERQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTL 1020
Qy 1021 NTSGSGTILIDLSPDKFQSVSEEMQSTVREHRDGGHAGGIFNRYNLTKIKQVCNKKLW 1080
Db 1021 NTSGSGTILIDLSPDKFQSVSEEMQSTVREHRDGGHAGGIFNRYNLTKIKQVCNKKLW 1080
Qy 1081 ERYTHRRKEVSEENHNHANERMLFHGSPFVNAILHKGDFDERHAYTGGMFGAGIYFAENSS 1140
Db 1081 ERYTHRRKEVSEENHNHANERMLFHGSPFVNAILHKGDFDERHAYTGGMFGAGIYFAENSS 1140
Qy 1141 KSNQVYVIGGGTGCPCVHKDRSCYICHRQLLFCRVTLGKSLQFSAMQMAHSPPGHHSVT 1200
Db 1141 KSNQVYVIGGGTGCPCVHKDRSCYICHRQLLFCRVTLGKSLQFSAMQMAHSPPGHHSVT 1200
Qy 1201 GRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGWVG 1240
Db 1201 GRPSVNGLALAEYVIYRGEQAYPEYLITYQIMRPEGWVG 1240

RESULT 3

US-09-972-115A-6
; Sequence 6, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Platyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/128,577
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 60/129,123
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-115A-6

Query Match 94.5%; Score 6108; DB 2; Length 1166;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 75 MSGRCAGGACASAAAEEVPAARELPEACRNGDVERVKRLVTPEKVNSTRDTAGRKST 134
Db 1 MSGRCAGGACASAAAEEVPAARELPEACRNGDVERVKRLVTPEKVNSTRDTAGRKST 60
Qy 135 PLHFAAGFRKDVVEYLLQNGANVQARDGGILPLHNACSFGEAEVNNLLHGHADPNAR 194
Db 61 PLHFAAGFRKDVVEYLLQNGANVQARDGGILPLHNACSFGEAEVNNLLHGHADPNAR 120
Qy 195 DNNVNTPLHEAAIKGIDVICVILLQHGAEPTIRNTDGTALDLDPSAKAVLTGEYKDE 254
Db 121 DNNVNTPLHEAAIKGIDVICVILLQHGAEPTIRNTDGTALDLDPSAKAVLTGEYKDE 180

RESULT 4

US-09-350-982C-5
; Sequence 5, Application US/09350982C
; Patent No. 6455290

Qy 255 LLESARSNGEBKMWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAK 314
Db 181 LLESARSNGEBKMWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVOLLQHGADVHAK 240
Qy 315 DKGLVPLHNACSYGHYEVTELLVKGHCACVNAMDWQFTPLHFAASKNRVEVCSSLISYG 374
Db 241 DKGLVPLHNACSYGHYEVTELLVKGHCACVNAMDWQFTPLHFAASKNRVEVCSSLISYG 300
Qy 375 ADPTLLMCHNKSADLAPTQPKERLAYEFKGHSLLOAAAREADVTRIKKHLSELEWVNFKH 434
Db 301 ADPTLLMCHNKSADLAPTQPKERLAYEFKGHSLLOAAAREADVTRIKKHLSELEWVNFKH 360
Qy 435 PQTETHALCAAASPYPKRKQICELLRKAGANINEKTEKFTPLHFAASEKAHNDVVEVV 494
Db 361 PQTETHALCAAASPYPKRKQICELLRKAGANINEKTEKFTPLHFAASEKAHNDVVEVV 420
Qy 495 KHEAKVNALDNLGQTSLHRAAYCGHLOTCHLLISYGCDDPNIISLOGFTALQMGNEVQOL 554
Db 421 KHEAKVNALDNLGQTSLHRAAYCGHLOTCHLLISYGCDDPNIISLOGFTALQMGNEVQOL 480
Qy 555 LQEGISLGNSEADRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRV 614
Db 481 LQEGISLGNSEADRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRV 540
Qy 615 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGA VVNADLWKFTPLHEAA 674
Db 541 VVEYLLQHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGA VVNADLWKFTPLHEAA 600
Qy 675 AKGYEICKLLQHGADPTKKNRDGNTPLDVKDGDIDQLLRGDAALLDAKKGCLAR 734
Db 601 AKGYEICKLLQHGADPTKKNRDGNTPLDVKDGDIDQLLRGDAALLDAKKGCLAR 660
Qy 735 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNADKGGILPLHNA 794
Db 661 VKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNADKGGILPLHNA 720
Qy 795 SYGHVDVAALLIKYNACVNATDKWAFPLHEAAQKGRTOCALILA HADPTLKNQEGOT 854
Db 721 SYGHVDVAALLIKYNACVNATDKWAFPLHEAAQKGRTOCALILA HADPTLKNQEGOT 780
Qy 855 PLDVSADDSALLTAAMPSPALSCYKQPVINGVRSPGATADALS SGSPSSLSAASS 914
Db 781 PLDVSADDSALLTAAMPSPALSCYKQPVINGVRSPGATADALS SGSPSSLSAASS 840
Qy 915 LDNLSSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSIITQFVRLNGLHLMADI PEREQIT 974
Db 841 LDNLSSGSFSELSSVSSSGTEGASSLEKKEVPGVDFSIITQFVRLNGLHLMADI PEREQIT 900
Qy 975 LDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSGTILIDLSP 1034
Db 901 LDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPYLTLNTSGSGTILIDLSP 960
Qy 1035 DDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLTKIKQVCNKKLWERYTHRRKEVSEEN 1094
Db 961 DDKEFQSVSEEMQSTVREHRDGGHAGGIFNRYNLTKIKQVCNKKLWERYTHRRKEVSEEN 1020
Qy 1095 HNHANERMLFHGSPFVNAILHKGDFDERHAYTGGMFGAGIYFAENSSKSNQVYVIGGGTG 1154
Db 1021 HNHANERMLFHGSPFVNAILHKGDFDERHAYTGGMFGAGIYFAENSSKSNQVYVIGGGTG 1080
Qy 1155 CPVHKDRSCYICHRQLLFCRVTLGKSLQFSAMQMAHSPPGHHSVTGRPSVNGLALAEYV 1214
Db 1081 CPVHKDRSCYICHRQLLFCRVTLGKSLQFSAMQMAHSPPGHHSVTGRPSVNGLALAEYV 1140
Qy 1215 IYRGEQAYPEYLITYQIMRPEGWVG 1240
Db 1141 IYRGEQAYPEYLITYQIMRPEGWVG 1166

```

; GENERAL INFORMATION:
; APPLICANT: Bertheisen, Jens
; APPLICANT: Toma, Salvatore
; APPLICANT: Iacchi, Antonella
; TITLE OF INVENTION: Tankyrase Homolog Protein (THP), Nucleic Acids, and Methods Relat
; TITLE OF INVENTION: Same
; FILE REFERENCE: PHRM-0043
; CURRENT APPLICATION NUMBER: US/09/350,982C
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: (1102)..(1102)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc feature
; LOCATION: (2650)..(2650)
; OTHER INFORMATION: n is any nucleic acid
; US-09-350-982C-5

Query Match          93.6%; Score 6053; DB 2; Length 1166;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1157; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 75 MSGRCAGGGNACASAAAEEVPAARELFECACNGDVERVKRLVTPKVNSTRDTAGRKST 134
Db 1 MSGRCAGGGNACASAAAEEVPAARELFECACNGDVERVKRLVTPKVNSTRDTAGRKST 60

Qy 135 PLHPAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFGEAEVNVNLLRHGADPNAR 194
Db 61 PLHPAAGFGRKDVVEYLLQNGANVQARDGGLIPLHNACSFGEAEVNVNLLRHGADPNAR 120

Qy 195 DNWNYTPLHEAAIKGKIDVICVLVLOHGAEPTRINTDGRALTDLADPSAKAVLTGEYKDE 254
Db 121 DNWNYTPLHEAAIKGKIDVICVLVLOHGAEPTRINTDGRALTDLADPSAKAVLTGEYKDE 180

Qy 255 LLESARGNEEKMWALLTPLNVNCHASDGRKSTPLHLAAGYNRKIVQLLLOHGAADVAK 314
Db 181 LLESARGNEEKMWALLTPLNVNCHASDGRKSTPLHLAAGYNRKIVQLLLOHGAADVAK 240

Qy 315 DKGLDVLPHNACSYGHEVTELLVKHGACVNAMDWQFTPLHEAASKNRVEVCSLLLSYG 374
Db 241 DKGLDVLPHNACSYGHEVTELLVKHGACVNAMDWQFTPLHEAASKNRVEVCSLLLSYG 300

Qy 375 ADPTLLCHNKSAITDLAPTQPKERLAYEPKGHSLLOQAAREADVTRIKGHLGLEMVNFKH 434
Db 301 ADPTLLCHNKSAITDLAPTQPKERLAYEPKGHSLLOQAAREADVTRIKGHLGLEMVNFKH 360

Qy 435 POTHETALHCAASAPYKPKQICELLRLKGNINKEKTEPLPLHVASEKAHNDVVEVV 494
Db 361 POTHETALHCAASAPYKPKQICELLRLKGNINKEKTEPLPLHVASEKAHNDVVEVV 420

Qy 495 KHEAKVVALDNLGQTSLSHRAAYCGHLOTICRLLLSYGCDPNIIISLQGTALQMGNEVQOL 554
Db 421 KHEAKVVALDNLGQTSLSHRAAYCGHLOTICRLLLSYGCDPNIIISLQGTALQMGNEVQOL 480

Qy 555 LQEGISLGNSEADRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVS 614
Db 481 LQEGISLGNSEADRLLEAAKAGDVETVKKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVS 540

Qy 615 VVEYLLQHGADVAKDKGGLVPLHNACSYGHEVTELLVKHGAVNVNADLWKFTPLHEAA 674
Db 541 VVEYLLQHGADVAKDKGGLVPLHNACSYGHEVTELLVKHGAVNVNADLWKFTPLHEAA 600

Qy 675 AKGYEICKLLOHGAADPTKKNRDNPTPLDVKDGDITDIQDLRGDAALLDAAKKGCLAR 734
Db 601 AKGYEICKLLOHGAADPTKKNRDNPTPLDVKDGDITDIQDLRGDAALLDAAKKGCLAR 660
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Qy 735 VKKLSSPDNVNCRDQTGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGLIPIHNAA 794
Db 661 VKKLSSPDNVNCRDQTGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGLIPIHNAA 720

Qy 795 SYGHVDVAALLIKYNACVNATDKWAFPTPLHEAAQKGRTOQLCALLLAHGADPTLKNQEGQT 854
Db 721 SYGHVDVAALLIKYNACVNATDKWAFPTPLHEAAQKGRTOQLCALLLAHGADPTLKNQEGQT 780

Qy 855 PLDLVSADVDYVALLTAAMPSPALPSCYKQVNLGVRSPGATADALSSGSPSSSLSAASS 914
Db 781 PLDLVSADVDYVALLTAAMPSPALPSCYKQVNLGVRSPGATADALSSGSPSSSLSAASS 840

Qy 915 LDNLSSGFSLSVSSSGTEGASSLEKKEVPDPSITQFVRNLGLEHLMDFPEREQIT 974
Db 841 LDNLSSGFSLSVSSSGTEGASSLEKKEVPDPSITQFVRNLGLEHLMDFPEREQIT 900

Qy 975 LDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYTLTNTSGSTLIDLSP 1034
Db 901 LDVLVEMGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPYTLTNTSGSTLIDLSP 960

Qy 1035 DKKEFQSVBEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEEN 1094
Db 961 DKKEFQSVBEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEEN 1020

Qy 1095 HNHANERMLPHGSPFFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYVIGGGTG 1154
Db 1021 HNHANERMLPHGSPFFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYVIGGGTG 1080

Qy 1155 CPVHKDRSCVICHROQLLCFRTVLGKSPLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYV 1214
Db 1081 CPVHKDRSCVICHROQLLCFRTVLGKSPLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYV 1140

Qy 1215 IYRGEQAYPEYLITYQIMRPEGMVDG 1240
Db 1141 IYRGEQAYPEYLITYQIMRPEGMVDG 1166
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RESULT 5

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US-09-849-602-26
; Sequence 26, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseeng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105 (JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 1227
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-849-602-26
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Query Match          90.9%; Score 5877; DB 2; Length 1227;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1148; Conservative 8; Mismatches 47; Indels 50; Gaps 5;
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Qy 12 QGAQRGARVGAA-----HGTAPDPVFTAGSQAARALSASSPGGLALLAGPGLL 59
Db 1 QGAQRGARVGAAAGLRRSGDSREPSGPGPVRVSGGPRPPARGAGAPAPVAGAVAG---- 56

Qy 60 LRLALLLAVAAARIMSGRRACAG-----GACASAAAEVPAARELFEACRN 108
Db 57 -----CGGGQDHVGSFLRRRSGSLRDAAAEVPAARELFEACRN 96

Qy 109 GDVERVKRLVTPKVNSTRDTAGRKSTPLHPAAGFGRKDVVEYLLQNGANVQARDGGLIP 168
Db 109 GDVERVKRLVTPKVNSTRDTAGRKSTPLHPAAGFGRKDVVEYLLQNGANVQARDGGLIP 168
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Db 97 GDVERVKRLVTPKVNRSRTAGKSTKSTPLHFAAGFRGVVEYLLQNGANVQARDGGLIP 156
QY 169 LHNACSFHAEVNNLLRHGADPNARDNNYTPLEHAAIKGKIDVICIIVLQHGAPTIRN 228
Db 157 LHNACSFHAEVNNLLRHGADPNARDNNYTPLEHAAIKGKIDVICIIVLQHGAPTIRN 216
QY 229 TDGRTALDADPSAKAVLTGKIDELLESASRSGNEKMMALLTPLNVNCHASDGRKSTP 288
Db 217 TDGRTALDADPSAKAVLTGKIDELLESASRSGNEKMMALLTPLNVNCHASDGRKSTP 276
QY 289 LHLAAGYNNRVTIQLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNM 348
Db 277 LHLAAGYNNRVTIQLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNM 336
QY 349 LMQFTPLHAAAKNVEVCSLLSYGADPTLNCNKSAIDLAPTPOLKERLAYEFKGS 408
Db 337 LMQFTPLHAAAKNVEVCSLLSYGADPTLNCNKSAIDLAPTPOLKERLAYEFKGS 396
QY 409 LIQAAAREADVTRI KKHLSLEMVNFKHPQTHETALHCAAAPYPRKQICELLLRKGANIN 468
Db 397 LIQAAAREADVTRI KKHLSLEMVNFKHPQTHETALHCAAAPYPRKQICELLLRKGANIN 456
QY 469 ERTKEFLPLHVASAKHNDVVVVVHKAHVNALDNLGQTSLHRAAYCGHLQTCRLLLS 528
Db 457 ERTKEFLPLHVASAKHNDVVVVVHKAHVNALDNLGQTSLHRAAYCGHLQTCRLLLS 516
QY 529 YGCDPNIIISLOQFTALQMGNNVQOLLOEGISLGNSEADROLLEAKAGDVETVKLCVTV 588
Db 517 YGCDPNIIISLOQFTALQMGNNVQOLLOEGISLGNSEADROLLEAKAGDVETVKLCVTV 576
QY 589 QSVNCRDIEGRQSTPLHFAAGYNNRVSVEYLLQHGADVHAKDGLVPLHNACSYGHEV 648
Db 577 QSVNCRDIEGRQSTPLHFAAGYNNRVSVEYLLQHGADVHAKDGLVPLHNACSYGHEV 636
QY 649 ABLLVKGAVNVADLWKFTPLHAAAAGKYBI CKLLQHGADPTKQRDGNTPLDLVKD 708
Db 637 ABLLVKGAVNVADLWKFTPLHAAAAGKYBI CKLLQHGADPTKQRDGNTPLDLVKD 696
QY 709 GDTDTQDILLRGDAALLDAKGLCLARVKLSGPDVNCNCRDTCGRHSTPLHLAGYNNLEV 768
Db 697 GDTDTQDILLRGDAALLDAKGLCLARVKLSGPDVNCNCRDTCGRHSTPLHLAGYNNLEV 756
QY 769 ABYLLQHGADVNAQDKGLIPLHNAASYGHVDVVAALLIKYNACVNATDKWAPTPLHAAQ 828
Db 757 ABYLLQHGADVNAQDKGLIPLHNAASYGHVDVVAALLIKYNACVNATDKWAPTPLHAAQ 816
QY 829 KGRTOCALLLAHAGADPTLKNQEGQTPDLVSADVSALLTAAMPSPALPSYCKPQVLNG 888
Db 817 KGRTOCALLLAHAGADPTLKNQEGQTPDLVSADVSALLTAAMPSPALPSYCKPQVLNG 876
QY 889 VRSPGATADALSSGSPSSLSAASSLNLGSPFSELSSVSSSTEGASSLEKKEVPQV 948
Db 877 VRSPGATADALSSGSPSSLSAASSLNLGSPFSELSSVSSSTEGASSLEKKEVPQV 936
QY 949 DFSITQFVNGLGHLMDIIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLI 1008
Db 937 DFSITQFVNGLGHLMDIIFEREQITLDVLVEMGHKELKEIGINAYGHRHKLKIGVERLI 996
QY 1009 SQCGGLNPYLTINTSGSGTILDLSPDDKEFQSVVEEMQSTVREHRDGGHAGGIFNRYNI 1068
Db 997 SQCGGLNPYLTINTSGSGTILDLSPDDKEFQSVVEEMQSTVREHRDGGHAGGIFNRYNI 1056
QY 1069 LKIQVCNKKLWERYTHRRKEVSENNHANERMLFHGSPFFVNAIHHKGFDRHAYIGGM 1128
Db 1057 LKIQVCNKKLWERYTHRRKEVSENNHANERMLFHGSPFFVNAIHHKGFDRHAYIGGM 1116
QY 1129 FCAGIYFAENSSKSNQYVYIGGGTGCPVHK--DRSCYICHRQLLFCRVTLGFSFLQFSAM 1187
Db 1117 FCAGIYFAENSSKSNQYVYIGGGTGQVFTKTDLTFTATAALL--PGNLGKVFPAVQCN 1174
QY 1188 KMAHSPGHHSTGRPSVNGLALAEYVIYRGQAYPEYLITYQIMRPEGMVDG 1240
Db 1175 ENGTSPGHHSTGRPSVNGLALAEYVIYRGQAYPEYLITYQIMRPEGMVDG 1227

RESULT 6
US-09-696-668-3
; Sequence 3, Application US/09696668
; Patent No. 6617102
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Chan, Eva
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; APPLICANT: Osbovska, Valeria
; TITLE OF INVENTION: TANKRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND METHODS (C
; FILE REFERENCE: A-68292-1/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/696,668
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-696-668-3
Query Match 89.2%; Score 5766; DB 2; Length 1100;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1099; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 141 GFGKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNNY 200
Db 1 GFGKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNNLLRHGADPNARDNNY 60
QY 201 PLHAAIKGKIDVICIIVLQHGABPTIRNTDORTALDADPSAKAVLTGEYKDELLESAR 260
Db 61 PLHAAIKGKIDVICIIVLQHGABPTIRNTDORTALDADPSAKAVLTGEYKDELLESAR 120
QY 261 SGNEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVTIQLLQHGADVHAKDGLV 320
Db 121 SGNEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVTIQLLQHGADVHAKDGLV 180
QY 321 PLHNACSYGHEVTELLVKGACVNMADLQFTPLHAAASKNRVEVCSSLLSYGADPTLL 380
Db 181 PLHNACSYGHEVTELLVKGACVNMADLQFTPLHAAASKNRVEVCSSLLSYGADPTLL 240
QY 381 NCHNKSADLAPTQPKERLAYEFKGSLLQAAAREADVTRI KKHLSLEMVNFKHPQTHET 440
Db 241 NCHNKSADLAPTQPKERLAYEFKGSLLQAAAREADVTRI KKHLSLEMVNFKHPQTHET 300
QY 441 ALHCAAAASPYPRKQICELLLRKGANINKEKTEFLTPHVASAKHNDVVVVVHKAHV 500
Db 301 ALHCAAAASPYPRKQICELLLRKGANINKEKTEFLTPHVASAKHNDVVVVVHKAHV 360
QY 501 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLOQFTALQMGNNVQOLLOEGIS 560
Db 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDPNIIISLOQFTALQMGNNVQOLLOEGIS 420
QY 561 LGNSEADRLLEAAKAGDVETVKLCVTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVEYLL 620
Db 421 LGNSEADRLLEAAKAGDVETVKLCVTVQSVNCRDIEGRQSTPLHFAAGYNNRVSVEYLL 480
QY 621 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGAVNVADLWKFTPLHAAAKGYE 680
Db 481 QHGADVHAKDGLVPLHNACSYGHEVTELLVKGAVNVADLWKFTPLHAAAKGYE 540
QY 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGDITDIQDLRGDAALLDAAKKGCLARVKLSS 740
Db 541 ICKLLQHGADPTKKNRDGNTPLDLVKDGDITDIQDLRGDAALLDAAKKGCLARVKLSS 600
QY 741 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 800
Db 601 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660

QY 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOLCALLLAHAGADPTLKNQEGQTPDLVLS 860
DB 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOLCALLLAHAGADPTLKNQEGQTPDLVLS 720
QY 861 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLGS 920
DB 721 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLGS 780
QY 921 SFSELSVVSSSGTEGASLEKKEVGVDFSIQFVRNLGLEHLMDFIFEREQITLDVLVE 980
DB 781 SFSELSVVSSSGTEGASLEKKEVGVDFSIQFVRNLGLEHLMDFIFEREQITLDVLVE 840
QY 981 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILIDLSPDDKEFQ 1040
DB 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILIDLSPDDKEFQ 900
QY 1041 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 1100
DB 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
QY 1101 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTGCPCVHKD 1160
DB 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTGCPCVHKD 1020
QY 1161 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ 1220
DB 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ 1080
QY 1221 AYPEYLITYQIMRPEGWVDG 1240
DB 1081 AYPEYLITYQIMRPEGWVDG 1100

RESULT 7

US-09-843-159B-3
; Sequence 3, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-2/RMS/DHR
; CURRENT APPLICATION NUMBER: US/09/843,159B
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/596,668
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-159B-3

Query Match 89.2%; Score 5766; DB 2; Length 1100;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1099; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 141 GFGKDVVEYLLQNGANYQVARDGGGLPLHNACSFGEAEVNNLLLRHGDAPNARDNWNVT 200
DB 1 GFGKDVVEYLLQNGASVQVARDGGGLPLHNACSFGEAEVNNLLLRHGDAPNARDNWNVT 60
QY 201 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRALDLADPSAKAVLTGYKKDELLESAR 260
DB 61 PLHEAAIKGKIDVCIVLLQHGAEPTIRNTDGRALDLADPSAKAVLTGYKKDELLESAR 120
QY 261 SGNEEKMALLTPLNVNCHASGRKSTPLHLAAGYNVRKIVOLLQHGADVHAKDKGLV 320

DB 121 SGNEEKMALLTPLNVNCHASGRKSTPLHLAAGYNVRKIVOLLQHGADVHAKDKGLV 180
QY 321 PLHNACSYGHYVTELLVKHGACVNMADLWQPTPLHEAAKSRVEVCSLLLSYGADPTLL 380
DB 181 PLHNACSYGHYVTELLVKHGACVNMADLWQPTPLHEAAKSRVEVCSLLLSYGADPTLL 240
QY 381 NCHNKSADLAPTPOLKERLAYEFKGHSLQAREADVTRI KKHLSLEWNVFKHPQTHET 440
DB 241 NCHNKSADLAPTPOLKERLAYEFKGHSLQAREADVTRI KKHLSLEWNVFKHPQTHET 300
QY 441 ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVVVVGHAEKV 500
DB 301 ALHCAAAAPYPRKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVVVVGHAEKV 360
QY 501 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDBNIIISLOGFTALONGNENVOQLQEGIS 560
DB 361 NALDNLGQTSLHRAAYCGHLQTCRLLLSYGCDBNIIISLOGFTALONGNENVOQLQEGIS 420
QY 561 LGNSEADROLLEAAKAGADVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
DB 421 LGNSEADROLLEAAKAGADVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
QY 621 QHGADVHAKDKGGLVPLHNACSYGHYVAEELLVKHGAVNVNADLWKFTPLHEAAAKGYE 680
DB 481 QHGADVHAKDKGGLVPLHNACSYGHYVAEELLVKHGAVNVNADLWKFTPLHEAAAKGYE 540
QY 681 ICKLLLOHGADPTKNRDGNTPLDLVKDGTDIQDLIRGDAALLDAKKGCLARVKLSS 740
DB 541 ICKLLLOHGADPTKNRDGNTPLDLVKDGTDIQDLIRGDAALLDAKKGCLARVKLSS 600
QY 741 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 800
DB 601 PDNVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVD 660
QY 801 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOLCALLLAHAGADPTLKNQEGQTPDLVLS 860
DB 661 VAALLIKYNACVNATDKWAFTPLHEAAQKGRTOLCALLLAHAGADPTLKNQEGQTPDLVLS 720
QY 861 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLGS 920
DB 721 ADDVSALLTAAMPSPALPCYKQVNLGVRSPGATADALSSGSPSSLSAASSLDNLGS 780
QY 921 SFSELSVVSSSGTEGASLEKKEVGVDFSIQFVRNLGLEHLMDFIFEREQITLDVLVE 980
DB 781 SFSELSVVSSSGTEGASLEKKEVGVDFSIQFVRNLGLEHLMDFIFEREQITLDVLVE 840
QY 981 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILIDLSPDDKEFQ 1040
DB 841 MGHKELKEIGINAYGHRHKLKIGVERLISGQOGLNPLYTLNTSGSGTILIDLSPDDKEFQ 900
QY 1041 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 1100
DB 901 SVEEEMQSTVREHRDGGHAGGIFNRYNLIKQKVCNKKLWERYTHRRKEVSEENHNHANE 960
QY 1101 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTGCPCVHKD 1160
DB 961 RMLFHGSPFVNAILHKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGGTGCPCVHKD 1020
QY 1161 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ 1220
DB 1021 RSCYICHRQLLFCRVTLGKSFLOFSAMKMAHSPPGHHSVTGRPSVNGLALAEYVIYRGEQ 1080
QY 1221 AYPEYLITYQIMRPEGWVDG 1240
DB 1081 AYPEYLITYQIMRPEGWVDG 1100

RESULT 8

US-09-843-159B-9
; Sequence 9, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin

APPLICANT: Chan, Evan
APPLICANT: Xu, Xiang
APPLICANT: Huang, Betty
TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
FILE REFERENCE: A-68292-2/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/843,159B
CURRENT FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 09/696,668
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: US 09/427,154
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 1100
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic mutant
US-09-843-159B-9

Query Match 89.1%; Score 5760; DB 2; Length 1100;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1098; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 141 GFGKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 200
DB 1 GFGKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60
QY 201 PLHEAAIKGIDVCIIVLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 260
DB 61 PLHEAAIKGIDVCIIVLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 120
QY 261 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAKDKGLV 320
DB 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAKDKGLV 180
QY 321 PLHNACSYGHEVTELLVKHGACVNAVDLWQFTPLHEAASKNRVEVCILLSYGADPTLL 380
DB 181 PLHNACSYGHEVTELLVKHGACVNAVDLWQFTPLHEAASKNRVEVCILLSYGADPTLL 240
QY 381 NCHNKSALDLAPTQPKERLAYEFKSHLSLQAAAREADVTRIKKHLSEWVNFKHPQTHET 440
DB 241 NCHNKSALDLAPTQPKERLAYEFKSHLSLQAAAREADVTRIKKHLSEWVNFKHPQTHET 300
QY 441 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAKV 500
DB 301 ALHCAASPYPKRKQICELLRKGANINEKTEFLTPLHVASEKAHNDVVEVVKHEAKV 360
QY 501 NALDNLGOTSLHRAAYCGHLOTCRLLSYGCDPNIIISLQGTALQNGNENVOQLQEGIS 560
DB 361 NALDNLGOTSLHRAAYCGHLOTCRLLSYGCDPNIIISLQGTALQNGNENVOQLQEGIS 420
QY 561 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
DB 421 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
QY 621 QHGADVHAKDKGLVPLHNACSYGHEVTELLVKHGACVNVNADLWKFTPLHEAAAKGYE 680
DB 481 QHGADVHAKDKGLVPLHNACSYGHEVTELLVKHGACVNVNADLWKFTPLHEAAAKGYE 540
QY 681 ICKLLOHGADPTKKNRDGNTPLDIVKGDGTDI QDLRGDAALLDAKGCCLARVKKLSS 740
DB 541 ICKLLOHGADPTKKNRDGNTPLDIVKGDGTDI QDLRGDAALLDAKGCCLARVKKLSS 600
QY 741 PNVNCRDTQGRHSPTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
DB 601 PNVNCRDTQGRHSPTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
QY 801 VAALLIKYNACVNAQDKWAFPTPLHEAAQKGRTOCALLLAHGADPTLKNQEQGTPDLIVS 860
DB 661 VAALLIKYNACVNAQDKWAFPTPLHEAAQKGRTOCALLLAHGADPTLKNQEQGTPDLIVS 720

QY 861 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSPSSLSAASLDNLSG 920
DB 721 ADDVSALLTAAMPSPALPSCYKPOVLNGVRSPGATADALSSGSPSPSSLSAASLDNLSG 780
QY 921 SFSLSVSSVSSGTEGASSLEKKEVPVDFSIITQFVRNLGLEHLMDFPERQITLDVLVE 980
DB 781 SFSLSVSSVSSGTEGASSLEKKEVPVDFSIITQFVRNLGLEHLMDFPERQITLDVLVE 840
QY 981 MGHEKELKEIGINAYGHRHKLTKGVERLISGQGLNPVLTNTSGSTLIDLSPDDKEFQ 1040
DB 841 MGHEKELKEIGINAYGHRHKLTKGVERLISGQGLNPVLTNTSGSTLIDLSPDDKEFQ 900
QY 1041 SVEEMOSTVREHRDGGHAGGIFNRYNLIKTKQCNKKLWERYTHRRKEVSEENHNHANE 1100
DB 901 SVEEMOSTVREHRDGGHAGGIFNRYNLIKTKQCNKKLWERYTHRRKEVSEENHNHANE 960
QY 1101 RMLFHGSPFVNAILTKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGTCPCVHKD 1160
DB 961 RMLFHGSPFVNAILTKGFDERHAYIGMFGAGIYFAENSSKSNQVYVIGGTCPCVHKD 1020
QY 1161 RSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTCRPSVNGIALLAEYVIYRGEQ 1220
DB 1021 RSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTCRPSVNGIALLAEYVIYRGEQ 1080
QY 1221 AYPEYLITYQIMRPEGWVDG 1240
DB 1081 AYPEYLITYQIMRPEGWVDG 1100

RESULT 9

US-09-427-154-2

; Sequence 2, Application US/09427154

; Patent No. 6589725

; GENERAL INFORMATION:

; APPLICANT: Luo, Ying

; APPLICANT: Chan, Eva

; APPLICANT: Xu, Xiang

; APPLICANT: Huang, Betty

; TITLE OF INVENTION: TANKYRASE H, COMPOSITIONS INVOLVED IN THE CELL CYCLE AND

; TITLE OF INVENTION: METHODS OF USE

; FILE REFERENCE: A-68292-DJB/RMS/DAV

; CURRENT APPLICATION NUMBER: US/09/427,154

; CURRENT FILING DATE: 1999-10-25

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 1100

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-427-154-2

Query Match 88.7%; Score 5731.5; DB 2; Length 1100;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1095; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 141 GFGKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 200
DB 1 GFGKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVNLLRHGADPNARDNNYNT 60
QY 201 PLHEAAIKGIDVCIIVLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 260
DB 61 PLHEAAIKGIDVCIIVLQHGAEPTIRNTDGRALTDLADPSAKAVLTGEYKDELLESAR 120
QY 261 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAKDKGLV 320
DB 121 SGNEEKWALLTPLNVNCHASDGRKSTPLHLAAGNVRKIVOLLQHGADVHAKDKGLV 180
QY 321 PLHNACSYGHEVTELLVKHGACVNAVDLWQFTPLHEAASKNRVEVCILLSYGADPTLL 380
DB 181 PLHNACSYGHEVTELLVKHGACVNAVDLWQFTPLHEAASKNRVEVCILLSYGADPTLL 240
QY 381 NCHNKSALDLAPTQPKERLAYEFKSHLSLQAAAREADVTRIKKHLSEWVNFKHPQTHET 440

Db 241 NCHNKSALDAPTQPKERLAYEFKSHLLQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Qy 441 ALHCAAASPPKPKQICELLRLKGANINEKTEPLTLHVASEKAHNDVVEVVVYKHAHV 500
Db 301 ALHCAAASPPKPKQICELLRLKGANINEKTEPLTLHVASEKAHNDVVEVVVYKHAHV 360
Qy 501 NALDNLGOTSILHRAAYCGHLOTCRLLSYGCDPNIISLQGFALOMGNENVQQLQEGIS 560
Db 361 NALDNLGOTSILHRAAYCGHLOTCRLLSYGCDPNIISLQGFALOMGNENVQQLQEGIS 420
Qy 561 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
Db 421 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Qy 621 QHGADVHAKDGGVPLPLHNACSYGHEVAELLVKGAVVNVADLWKFTPLHFAAGYKGYE 680
Db 481 QHGADVHAKDGGVPLPLHNACSYGHEVAELLVKGAVVNVADLWKFTPLHFAAGYKGYE 540
Qy 681 ICKLLQHGADPTKKNRDGNTPLDVKGDTDIQDILLRGDAALLDAKKGCLARVKLSS 740
Db 541 ICKLLQHGADPTKKNRDGNTPLDVKGDTDIHYLLRGDAALLDAKKGCLARVKLSS 600
Qy 741 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 601 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Qy 801 VAALLIKYNACVNATDKWFTPLHFAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 860
Db 661 VAALLIKYNACVNATDKWFTPLHFAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 720
Qy 861 ADDVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSLSAASLDNLG 920
Db 721 ADDVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSLSAASLDNLG 780
Qy 921 SFSBLSVSSSGTEGASSLEKKEVPVDFSIITQFVRLNGLHLMDFEREQITDLVLE 980
Db 781 SFSBLSVSSSGTEGASSLEKKEVPVDFSIITQFVRLNGLHLMDFEREQITDLVLE 840
Qy 981 MGHEKELKEIGNAYGHRHKLKGVRLISGQGLNPYLTNTSGSGLTILDLSPDDKEFQ 1040
Db 841 MGHEKELKEIGNAYGHRHKLKGVRLISGQGLNPYLTNTSGSGLTILDLSPDDKEFQ 900
Qy 1041 SVEEMOSTVREHDDGGHAGGIFNRYNLTKQVCKNKKLMERYTHRRKEVSEENHNHANE 1100
Db 901 SVEEMOSTVREHDDGGHAGGIFNRYNLTKQVCKNKKLMERYTHRRKEVSEENHNHANE 960
Qy 1101 RMLFHGSPFNNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGPCVHKD 1160
Db 961 RMLFHGSPFNNAIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGPCVHKD 1020
Qy 1161 RSCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSVNGLALAEYVYIRGEQ 1220
Db 1021 -SCYICHRQLLFCRVTLGKSPLOFSAMKMAHSPGHHSVTGRPSVNGLALAEYVYIRGEQ 1079
Qy 1221 AYPEYLITYQIMRPEGWVDG 1240
Db 1080 AYPEYLITYQIMRPEGWVDG 1099

RESULT 10
US-09-843-159B-10
; Sequence 10, Application US/09843159B
; Patent No. 6887675
; GENERAL INFORMATION:
; APPLICANT: Luo, Yin
; APPLICANT: Chan, Evan
; APPLICANT: Xu, Xiang
; APPLICANT: Huang, Betty
; TITLE OF INVENTION: Tankyrase H, Compositions Involved in the Cell Cycle and Methods
; FILE REFERENCE: A-68292-2/RMS/DRH
; CURRENT APPLICATION NUMBER: US/09/843,159B
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/696,668

; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 09/427,154
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic mutant
US-09-843-159B-10

Query Match 87.5%; Score 5656; DB 2; Length 1083;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1079; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 141 GFRKDVVEYLLQNGANVQARDGGLIPLHNACSFHAEVNVNLLRHHGADPNARDNNY 200
Db 1 GFRKDVVEYLLQNGASVQARDGGLIPLHNACSFHAEVNVNLLRHHGADPNARDNNY 60
Qy 201 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGTALDLADPSAKAVLTGEYKKBELLESAR 260
Db 61 PLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGTALDLADPSAKAVLTGEYKKBELLESAR 120
Qy 261 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLQHGADVHAKDGLV 320
Db 121 SGNEEKMMALLTPLNVNCHASDGRKSTPLHLAGYNNRVKIVQLLQHGADVHAKDGLV 180
Qy 321 PLHNACSYGHEVTELLVKGACVNAAMDLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 380
Db 181 PLHNACSYGHEVTELLVKGACVNAAMDLMQFTPLHEAASKNRVEVCSLLLSYGADPTLL 240
Qy 381 NCHNKSALDAPTQPKERLAYEFKSHLLQAAREADVTRIKKHLSELMVNFKHPQTHET 440
Db 241 NCHNKSALDAPTQPKERLAYEFKSHLLQAAREADVTRIKKHLSELMVNFKHPQTHET 300
Qy 441 ALHCAAASPPKPKQICELLRLKGANINEKTEPLTLHVASEKAHNDVVEVVVYKHAHV 500
Db 301 ALHCAAASPPKPKQICELLRLKGANINEKTEPLTLHVASEKAHNDVVEVVVYKHAHV 360
Qy 501 NALDNLGOTSILHRAAYCGHLOTCRLLSYGCDPNIISLQGFALOMGNENVQQLQEGIS 560
Db 361 NALDNLGOTSILHRAAYCGHLOTCRLLSYGCDPNIISLQGFALOMGNENVQQLQEGIS 420
Qy 561 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 620
Db 421 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLL 480
Qy 621 QHGADVHAKDGGVPLPLHNACSYGHEVAELLVKGAVVNVADLWKFTPLHFAAGYKGYE 680
Db 481 QHGADVHAKDGGVPLPLHNACSYGHEVAELLVKGAVVNVADLWKFTPLHFAAGYKGYE 540
Qy 681 ICKLLQHGADPTKKNRDGNTPLDVKGDTDIQDILLRGDAALLDAKKGCLARVKLSS 740
Db 541 ICKLLQHGADPTKKNRDGNTPLDVKGDTDIQDILLRGDAALLDAKKGCLARVKLSS 600
Qy 741 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 601 PDNVNCRDTQGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 660
Qy 801 VAALLIKYNACVNATDKWFTPLHFAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 860
Db 661 VAALLIKYNACVNATDKWFTPLHFAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 720
Qy 861 ADDVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSLSAASLDNLG 920
Db 721 ADDVSALLTAAMPSPALPSCYKQVINGVRSPGATADALSSGSPSSLSAASLDNLG 780
Qy 921 SFSBLSVSSSGTEGASSLEKKEVPVDFSIITQFVRLNGLHLMDFEREQITDLVLE 980
Db 781 SFSBLSVSSSGTEGASSLEKKEVPVDFSIITQFVRLNGLHLMDFEREQITDLVLE 840


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; NAME/KEY: misc feature
; LOCATION: (787)..(787)
; OTHER INFORMATION: The 'Xaa' at location 787 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (788)..(788)
; OTHER INFORMATION: The 'Xaa' at location 788 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (789)..(789)
; OTHER INFORMATION: The 'Xaa' at location 789 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (790)..(790)
; OTHER INFORMATION: The 'Xaa' at location 790 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (791)..(791)
; OTHER INFORMATION: The 'Xaa' at location 791 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (792)..(792)
; OTHER INFORMATION: The 'Xaa' at location 792 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (793)..(793)
; OTHER INFORMATION: The 'Xaa' at location 793 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (794)..(794)
; OTHER INFORMATION: The 'Xaa' at location 794 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (795)..(795)
; OTHER INFORMATION: The 'Xaa' at location 795 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (796)..(796)
; OTHER INFORMATION: The 'Xaa' at location 796 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (797)..(797)
; OTHER INFORMATION: The 'Xaa' at location 797 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (798)..(798)
; OTHER INFORMATION: The 'Xaa' at location 798 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (799)..(799)
; OTHER INFORMATION: The 'Xaa' at location 799 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (800)..(800)
; OTHER INFORMATION: The 'Xaa' at location 800 stands for Lys, Asn, Arg, Ser, Thr, Ile
; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (801)..(801)
; OTHER INFORMATION: The 'Xaa' at location 801 stands for Lys, Asn, Arg, Ser, Thr, Ile

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; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
; NAME/KEY: misc feature
; LOCATION: (802)..(802)

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Query Match 84.3%; Score 5452; DB 2; Length 1267;

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Best Local Similarity 86.2%; Pred. No. 0;
Matches 1072; Conservative 6; Mismatches 161; Indels 4; Gaps 2;

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Qy 1 RCSARGAAGCGQAGRGARVGAAGHTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLL 60

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Db 26 RCLRRRGAGCGQAGRGARVGAAGHTAPDPVTAGSQAARALSASSPGGLALLLAGPGLLL 85

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Qy 61 RLIALALLAVAAARIMSGRRRCAGGGAACASAAAEEVPAARELFEACNGDVERKRLVTP 120

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Db 86 RLIALALLAVAAARIMSGRRRCAGGGAACASAAAEEVPAARELFEACNGDVERKRLVTP 145

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Qy 121 EKNVSRDTAGRKSTPLHFAAGFGKDVVEVLLQNGANVQARDGGGLIPLHNACSFGHAEV 180

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Db 146 EKNVSRDXAGRKSTPLHFAAGFGKDVVEVLLQNGANVQARDGGGLIPLHNACSFGHAEV 205

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```

Qy 181 VNLLRHGADPNARDNNWYTPPLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGTALDADP 240

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Db 206 IXLLLLHXAPNARDNNWYTPPLHEAAIKGKIDVICIVLLQHGAEPTIRNTDGTALDADP 265

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```

Qy 241 SAKAVLTGEYKQDELLESARGSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRKI 300

```

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Db 266 SAKAVLTGEYKQDELLESARGSGNEEKMMALLTPLNVNCHASDGRKSTPLHLAAGYNRKI 325

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Qy 301 VOULLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAAS 360

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Db 326 VOULLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGACVNMADLWQFTPLHEAAS 385

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Qy 361 KNRVEVCSLLSYGADPTLLNCHNKSALDAPTPQKRLAYEFKGHSLLOAAREADVTR 420

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Db 386 KNRVEVCSLLSYGADPTLLNCHNKSALDAPTPQKRLAYEFKGHSLLOAAREADVTR 445

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Qy 421 IKKHLSEMVNFQHPQTHALHCAAAAPYKPKQICELLRLKGANINEKTEFLTPLHV 480

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Db 446 IKKHLSEMVNFQHPQTHALHCAAAAPYKPKQICELLRLKGANINEKTEFLTPLHV 505

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Qy 481 ASEKANDVVEVVKHAKVNALDNLGOTSILHRAAYCGHLQTCRLLLSYGCDPNIISQ 540

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Db 506 ASEKANDVVEVVKHAKVNALDNLGOTSILHRAAYCGHLQTCRLLLSYGCDPNIISQ 565

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Qy 541 FTALQMGNNVQQLQEGISLGNSEADRLLEAAKAGDVETVKKLCVQSVNCRDIEGRQ 600

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Db 566 FTALQMGNNVQQLQEGISLGNSEADRLLEAAKAGDVETVKKLCVQSVNCRDIEGRQ 625

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Qy 601 STPLHFAAGYNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGAVVN 660

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Db 626 STPLHFAAGYNRVSVVEYLLQHGADVHAKDGLVPLHNACSYGHEVTELLVKGAVVN 685

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Qy 661 VADLWKFTPLHEAAAKGKYEICKLLQHGADPTKKNRDGNTPLDLVKDGDITDQLLRGD 720

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Db 686 VADLWKFTPLHEAAAKGKYEICKLLQHGADPTKKNRDGNTPLDLVKDGDITDQLLRGD 745

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Qy 721 AALIDAAKKGCLARVKKLSPPDNVNCRDTCGRHSTPLHLAAGYNNLEVAEYLLQHGADV 780

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Db 746 AVLLDAAKKGCLARVKKLSPPDNVNCRDTCGRHSTPLHL-AGXXXXXXXXXXXXXXXXX 804

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Qy 781 AQDKGGGLPLHNAASYGHVDVAALLIKYNCAVNTDKWAFPLHEAAKGRGTQLCALLA 840

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Db 805 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 864

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Qy 841 HGADPTLKNQEGOTPLDLVSADVDVALLTAAMPSPALPSCYKPOVLNGVRSPGATADALS 900

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Db 865 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 924

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Qy 901 SGSPSSPSLSAASLDNLSGSFSELSSVSSSGTEGASSLEKKEVPGVDFPSITQFVRNLG 960

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Db 925 SGSPSSPSLSAASLDNLSGSFSELSSVSSSGTEGASSLEKKEVPGVDFPSITQFVRNLG 984

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QY 961 LEHLMDFPERQITLDVLEMGHKKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTL 1020
 DB 985 LEHLMDFPERQITLDVLEMGHKKELKEIXINAYGHRHKLKISFERLISGQGLNPLYTL 1044
 QY 1021 NTSGSGTILDLSPDKKEFQSVVEEMQSTVREHRDGHAGGIFNRYNLIKIOKVCNK--- 1077
 DB 1045 NTSGSGTILDLSPDKKEFQSVVEEMQSTVREHRDGHAGGIFNRYNLIKIOKVCNRKI 1104
 QY 1078 KLWERYTHRRKEVSEENHNANERMLFHGSPFVNALIHKGDFERHAYIGMFGAGIYPAE 1137
 DB 1105 RHEERYTHRRKEVSEENHNANERMLFHGSPFVNALIHKGDFERHAYIGMFGAGIYPAE 1164
 QY 1138 NSSKNQYVYIGGGTGPVHKDRSCYIICHRQLLCRVTLGKSLFQFSAMKHAHSPPGHH 1197
 DB 1165 NSSKNQYVYIGGGTGPVHKDRSCYIICHRQLLCRVTLGKSLFQFSAMKHAHSPPGHH 1224
 QY 1198 SVTGRPSVNGLAELAEVYIRGQAYPEYLITTYQIMRPEGMVDG 1240
 DB 1225 SVTGRPSVNGLAELAEVYIRGQAYPEYLITTYQIMRPEGMVDG 1267

RESULT 12

US-09-196-387-2

; Sequence 2, Application US/09196387

; Patent No. 627613

; GENERAL INFORMATION:

; APPLICANT: de Lange, Titia

; APPLICANT: Smith, Susan

; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS

; TITLE OF INVENTION: OF USE THEREOF

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Klauber & Jackson

; STREET: 411 Hackensack Avenue, 4th Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/196,387

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/095,225

; FILING DATE: June 10, 1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-487-5900

; TELEFAX: 201-343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1327 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

US-09-196-387-2

Query Match

Best Local Similarity 79.0%; Score 5103.5; DB 2; Length 1327;

Matches 963; Conservative 110; Mismatches 128; Indels 15; Gaps 3;

QY

22 AAHGTPDPVVTAGSQAARALSASSPGGLALLAGPLLRLILLALLAVAAARIMSGRCA 81

DB 112 SAAGVAPNPAGSGNNSPSSSSPTSSSSSSPSG-----SSLAESPAAAGVSSTAPL 165
 QY 82 GGAACASAAAFAVPAARELFEACRNGDVERVKLVTPKEKYNRSDTAGRKSTPLHFAAG 141
 DB 166 GFGAAGPGTGPVPAVGALLRELLEACRNGDVSVRKLVDAANYNNAKMAGRKSPLHFAAG 225
 QY 142 FORKDVVEYLQNGANVOARDGGGLIPLHNACSFHAEVWNLRLRHGADPNARDNWNYP 201
 DB 226 FORKDVVEHLLQNGANVARDGGGLIPLHNACSFHAEVWNLRLRHGADPNARDNWNYP 285
 QY 202 LHEAAIKGKIDVICIVLQHGAEPTIRNTDGRDALDAPSAKAVLTGYEKDDELLESARS 261
 DB 286 LHEAAIKGKIDVICIVLQHGADPNIRNTDGRSALDAPSAKAVLTGYEKDDELLEARS 345
 QY 262 GNEEKWALLPLNVNCHASGRKSTPLHLAAGYNRVKTIVOLLQHGADVHAKDGLVP 321
 DB 346 GNEEKWALLPLNVNCHASGRKSTPLHLAAGYNRVKTIVOLLQHGADVHAKDGLVP 405
 QY 322 LHNACSYGHEVTELLVKHGACVNAWDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLN 381
 DB 406 LHNACSYGHEVTELLVKHGACVNAWDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLN 465
 QY 382 CHNKSALDAPTPOLKERLAYEFKGHSLLQAAREADVTRI KHL SLEWVNFKHPOTHETA 441
 DB 466 CHGSAVDMAPTPELRERLTVEFKGHSLLQAAREADLAKVKKTLALEIINFKQPQSHETA 525
 QY 442 LHCAASPYPKRKQICELLKRGANINEKTEFLPLHVAASEKANDVVEVVKHEAKVN 501
 DB 526 LHCAVASLHPKRVQVTELLRKGANVNEKNDFMTPLHVAERANDVNEVLHKGAKVN 585
 QY 502 ALDNLGQTSLHRAAYCGHLQTCRLLLSYCGDPNIIISLOGFTALOMGNENVOQLLEGISL 561
 DB 586 ALDTLQGTALHRAALAGHLQTCRLLLSYSGDPSIISLOGFTAAQMGNEAVQOILSESTPI 645
 QY 562 GNSEADRLLEAAKAGDVETVKKLTQVQSNVCRDIEGRQSTPLHFAAGYNRVSVVEYLQ 621
 DB 646 RTSDVDVRLLEASKAGDLETQKLCSSQNVNCRDIEGRHSTPLHFAAGYNRVSVVEYLH 705
 QY 622 HGADVHAKGGLVPLHNACSYGHEVAELLVKHGAVNVADLWKFETPLHEAAAKGYEI 681
 DB 706 HGADVHAKGGLVPLHNACSYGHEVAELLVKHGASVNVADLWKFETPLHEAAAKGYEI 765
 QY 682 CKLLLOHGADPTKKNRDCNTPLDLVKDGDITDQLLRGDAALLDAKKGCLARVKLSPP 741
 DB 766 CKLLLOHGADPTKKNRDCNTPLDLVKDGDITDQLLRGDAALLDAKKGCLARVKLCTP 825
 QY 742 DVNCRDITQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDV 801
 DB 826 ENINCRDITQGRNSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDI 885
 QY 802 AALLIKYNACVNAWDLWQFTPLHEAAAKQRTQCALLLAHGADPTLKQEGOTPLDLVSA 861
 DB 886 AALLIKYNTCVNAWDLWQFTPLHEAAAKQRTQCALLLAHGADPTLKQEGOTPLDLATA 945
 QY 862 DVVSALLTAAMPSPALPCYKPOVLNGVRSFGATADALSSGSPSSSLSAASLNLGSG 921
 DB 946 DDIRALLIDAMPPEALPTCFKQAT-----VVSASLISPASTFCSLSAASINDLTP 998
 QY 922 FSELSSVSVSSSGTEGASLEKK--EVPQGVDFSIOTQVRNLGLEHMDIFPERQITLDVLA 979
 DB 999 LAELAVGASNAGDAAGTERKSGEVAGLDWNISQFLKSLGLEHLRDI FETEQITLDVLA 1058
 QY 980 EMGHKELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLNTSGSGTILDLSPDKKEF 1039
 DB 1059 DMGHEELKEIGINAYGHRHKLKIGVERLISGQGLNPLYTLNTSGSGTILDLSPDKKEF 1118
 QY 1040 QSVREEMOSTVREHRDGHAGGIFNRYNLIKIOKVCNKLWERYTHRRKEVSEENHNAN 1099
 DB 1119 QSVREEMOSTVREHRDGHAGGIFNRYNLIKIOKVCNKLWERYTHRRKEVSEENHNAN 1178
 QY 1100 ERMFLFHGSPFVNALIHKGDFERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGPVHK 1159

Db 1179 ERMFLHSGSPFINAIHKGFDERHAYIGMGAGIYFAENSSKSNQYVYVIGGGTGPCTHK 1238
Qy 1160 DRSCYICHRQLLCRVTLGKSFLOFSAMQWHAHSPPGHHSTVGRPSVNGLAELAEVYIRGE 1219
Db 1239 DRSCYICHRQLLCRVTLGKSFLOFSAMQWHAHSPPGHHSTVGRPSVNGLAELAEVYIRGE 1298
Qy 1220 QAYPEYLITYQIMRPE 1235
Db 1299 QAYPEYLITYQIMKPE 1314

RESULT 13
US-09-841-835-2
; Sequence 2, Application US/09841835
; Patent No. 6506587
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/841.835
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1327 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-841-835-2

Query Match 79.0%; Score 5103.5; DB 2; Length 1327;
Best Local Similarity 79.2%; Pred. No. 0;
Matches 963; Conservative 110; Mismatches 128; Indels 15; Gaps 3;
Qy 22 AAHGTAPDPVTAGQAARLASASPGGLALLAGPGLLLRLALLLAAVAAARIMSGRCA 81
Db 112 SAAGVAPNPAGSGNNSPSSSSPTSSSSSPSPG-----SSLASPEAAGVSTAPL 165
Qy 82 GGGACASAAAEVPAARELPACRNGDVERVKRLVTPKVNSRDTAGRKSTPLHFAAG 141
Db 166 GPGAGGFGTGVPAVSGALRELLERACRNGDVSRLVDAAANAKDWAARKSSPLHFAAG 225
Qy 142 FGRKDVVEYLILQNGANYQARDGGLIPLHNACSFGEAEVNVNLLLRHGADPNARDNNYTP 201
Db 226 FGRKDVVEHLILQMGANVHARDGGLIPLHNACSFGEAEVNVNLLLRHGADPNARDNNYTP 285

Qy 202 LHEAAIKGIDVICVILLOHGAETPIRNTDGTALDPSAKAVLTGCEYKKDELLESARS 261
Db 286 LHEAAIKGIDVICVILLOHGAETPIRNTDGTALDPSAKAVLTGCEYKKDELLESARS 345
Qy 262 GNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLVP 321
Db 346 GNEEKWALLTPLNVNCHASDGRKSTPLHLAAGYNRVKIVQLLQHGADVHAKDKGLVP 405
Qy 322 LHNACSYGHVEVTELLVKGHCANVMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLN 381
Db 406 LHNACSYGHVEVTELLVKGHCANVMDLWQFTPLHEAASKNRVEVCSLLLSYGADPTLLN 465
Qy 382 CHNKSALDAPTQLKRLAYEPKSHSLQAAAREADVTRIKKLSLSEMVNPKPQTHETA 441
Db 466 CHGKSAVDMAPTPELRERLTIEFKGSHSLQAAAREADVTRIKKLSLSEMVNPKPQTHETA 525
Qy 442 LHCAASAPYKPKQICELLIRKGANINEKTKFELPLHVASEKAHNDVVEVVKHEAKVN 501
Db 526 LHCAVASLHPKPKQVTELLIRKGANINEKTKFELPLHVASEKAHNDVVEVVKHEAKVN 585
Qy 502 ALDNLGQTSIHLRAAYCGHLOTCRLLLSYCGDPNIIISLQGFALOMGNENVOQLLQEGISL 561
Db 586 ALDNLGQTSIHLRAAYCGHLOTCRLLLSYCGDPNIIISLQGFALOMGNENVOQLLQEGISL 645
Qy 562 GNSEADROLLEAAKAGDVETVKLCCTVQSVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQ 621
Db 646 RTSDDVYRLLEASKAGDLETVKLCSSQNVNCRDIEGRQSTPLHFAAGYNRVSVVEYLLH 705
Qy 622 HGADVHAKDKGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAAAKGYEI 681
Db 706 HGADVHAKDKGLVPLHNACSYGHEVAELLVKGAVNVNADLWKFTPLHEAAAKGYEI 765
Qy 682 CKLLLOHGADPTKKNRDGNTPLDLVKDGDPTDIQDLIRGDAALDLDAKKGCLARVKLSPP 741
Db 766 CKLLLOHGADPTKKNRDGNTPLDLVKDGDPTDIQDLIRGDAALDLDAKKGCLARVKLSPP 825
Qy 742 DVNCRDTQGRHSTPLHLAAGYNVLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDV 801
Db 826 ENTNCRDTQGRNTPHLAAGYNVLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDI 885
Qy 802 AALLIKYNACVNATDKWAFPLHEAAKQKGTQCALLLAHGADPTLKNQSGQTPLDLVSA 861
Db 886 AALLIKYNACVNATDKWAFPLHEAAKQKGTQCALLLAHGADPTLKNQSGQTPLDLVSA 945
Qy 862 DVYSALLTAAMPSPALPSCYKPOVLNGVRSFGATADALSSGSPSPSSLSAASSLDNLSSGS 921
Db 946 DDIRALLIDAMPPEALPTCFKPQAT-----VVSASLISPASTPSCLSAASSLDNLTP 998
Qy 922 FSELSSVSSSGTEGASSLEKK--EYVGDVFSITQFVRLNGLGLEHMDIIFEREQITLDVLV 979
Db 999 LABLVAGSAGNAGDGAAGTERKEGEVAGLDNMIISQFLKSLGLEHLRDIIFETEITLDVLA 1058
Qy 980 EMGHKELKEIGINAYGHRHKLIKGVERLISQQQLNPYLTLNTSGSGTITLIDLSPDDKEF 1039
Db 1059 DMGHEELKEIGINAYGHRHKLIKGVERLISQQQLNPYLTLNTSGSGTITLIDLAPDEKEY 1118
Qy 1040 QSVVEEMQSTVREHRDGGHAGGIFNRYNLIKIKVCKNKKLWERYTHRRKEVESENNHNAN 1099
Db 1119 QSVVEEMQSTVREHRDGGHAGGIFNRYNLIKIKVCKNKKLWERYTHRRKEVESENNHNAN 1178
Qy 1100 ERMFLHSGSPFINAIHKGFDERHAYIGMGAGIYFAENSSKSNQYVYVIGGGTGPCTHK 1159
Db 1179 ERMFLHSGSPFINAIHKGFDERHAYIGMGAGIYFAENSSKSNQYVYVIGGGTGPCTHK 1238
Qy 1160 DRSCYICHRQLLCRVTLGKSFLOFSAMQWHAHSPPGHHSTVGRPSVNGLAELAEVYIRGE 1219
Db 1239 DRSCYICHRQLLCRVTLGKSFLOFSAMQWHAHSPPGHHSTVGRPSVNGLAELAEVYIRGE 1298
Qy 1220 QAYPEYLITYQIMRPE 1235
Db 1299 QAYPEYLITYQIMKPE 1314

RESULT 14	
US-09-972-115A-8	
; Sequence 8, Application US/09972115A	
; Patent No. 6599728	
; GENERAL INFORMATION:	
; APPLICANT: Geron Corporation	
; APPLICANT: Gregg, Morin B.	
; APPLICANT: Walter, Funk D.	
; APPLICANT: Mieczyslaw, Piatyszek A.	
; TITLE OF INVENTION: A Second Mammalian Telomerase	
; FILE REFERENCE: 080/003C	
; CURRENT APPLICATION NUMBER: US/09/972,115A	
; CURRENT FILING DATE: 2001-10-05	
; PRIOR APPLICATION NUMBER: US 60/128,577	
; PRIOR FILING DATE: 2000-04-10	
; PRIOR APPLICATION NUMBER: US 60/129,123	
; PRIOR FILING DATE: 1999-04-13	
; NUMBER OF SEQ ID NOS: 64	
; SOFTWARE: PatentIn version 3.1	
; SEQ ID NO 8	
; LENGTH: 1327	
; TYPE: PRT	
; ORGANISM: Homo sapiens	
US-09-972-115A-8	
Query Match 79.0%; Score 5103.5; DB 2; Length 1327;	
Best Local Similarity 79.2%; Pred. No. 0;	
Matches 963; Conservative 110; Mismatches 128; Indels. 15; Gaps 3;	
QY	22 AAHTGAPDPVTTAGSQAARALSASSPGGLALLAGFLLRLRLALLLAVAAARIMSGRCA 81
DB	112 SAAGVAPNPAGSGSNSSPSSSTSSSSSSPSSFG-----SSLAESPAAAGVSTAPL 165
QY	82 GCGAACAASAAAVAPAAELFEACRNGDVVERKLVTPTEKVNDRDTAGRKSTPLHFAAG 141
DB	166 GFGAAGPGTGVPAVSGALRELEACRNGDVSVKRLVDAANVAKMDAGRKSSPLHFAAG 225
QY	142 FORKDVVEYLLQNGANVOARDGGILPLHNACSFHAEVNVNLLRHGADPNARDNWNVTP 201
DB	226 FORKDVVEYLLQNGANVHARDGGILPLHNACSFHAEVNVNLLRHGADPNARDNWNVTP 285
QY	202 LHEAAIKGKIDVICVILLQHGABPTIRNTDRTALDLPDSAKAVLTGEYKDDLEESARS 261
DB	286 LHEAAIKGKIDVICVILLQHGADPNIRNTDGSALDLPDSAKAVLTGEYKDDLEESARS 345
QY	262 GNEEKMALLTPLNVNCHASDRKSTPLHLAGYNRVKIVQLLQHGADVHAKDGLVP 321
DB	346 GNEEKMALLTPLNVNCHASDRKSTPLHLAGYNRVIRIVQLLQHGADVHAKDGLVP 405
QY	322 LHNACSYGHYETELLVKGACVNAWDLWOFTPLHEAASKNREVEVCSLLLSHGADPTLVN 381
DB	406 LHNACSYGHYETELLVKGACVNAWDLWOFTPLHEAASKNREVEVCSLLLSHGADPTLVN 465
QY	382 CHNKSAIDLAPTQPKERLAYBFKSHLSLQAAREADVTRIKKHSLEWMVNFKHPOTHETA 441
DB	466 CHKSAVDNAPTPELRELTLYEFKSHLSLQAAREADLAKVKTALALEINFQPOSHETA 525
QY	442 LHCAASAPYKPKQICELLRRKGANINEKTEFLPLHVASKANDNVVVVVKHKAQN 501
DB	526 LHCAVASLHPKPKQVTELLLRKANVNEKNKDFMTPLHVAERAHNDVMEVLHKGAKVN 585
QY	502 ALDNLGQTSLHRAACVGHLOCTRLLSYGCDDNIIISLOGFTALONGNENVOQLLOEGLSL 561
DB	586 ALDNLGQTSLHRAALAGHLQTCRLLSYGSDDPSIIISLOGFTAAQNGNEAVQOILSESTPI 645
QY	562 GNSEADROLLEAAKAGDVETKVLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVEYLLQ 621
DB	646 RTSVDVYRLLEASAKGDLFTVQKLCSSQNVNCRDIEGRHSTPLHFAAGYNRVSVVEYLLH 705
QY	622 HGADVHAKDGGVLPLHNAACSYGHYEVAELLVKGAVNVADLWKFTPLHEAAAKGKVEI 681
DB	706 HGADVHAKDGGVLPLHNAACSYGHYEVAELLVRHGASVNVADLWKFTPLHEAAAKGKVEI 765

QY	682 CKLLIQLHGADPTKKNRDGNTPLDLVKDGDITDQILLRGDAALLDAKKGCLARVKLSSP 741
DB	766 CKLLIQLHGADPTKKNRDGNTPLDLVKEGDITDQILLKGDAALLDAKKGCLARVKLCTP 825
QY	742 DNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASGHVDV 801
DB	826 ENINCRDTQGRNSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASGHVDI 885
QY	802 AALLIKYNACVNAATDKWAFPTLHEAAQKGRQTCALLAHAGADPTLKNQEGOTPLDLVSA 861
DB	886 AALLIKYNACVNAATDKWAFPTLHEAAQKGRQTCALLAHAGADPTKKNQEGOTPLDLATA 945
QY	862 DDVSALLTAAMPSPSALPSCYKQVNLGVRSFGATADALSSGSPSSSLSAASSLNLSSG 921
DB	946 DDIRALLIDAMPPEALPTCFKQAT-----VVSASLISPASTFSCLSAASSIDNLJGP 998
QY	922 FSELSSVSVSSGTEGASSLEKK--BVPQVDPSITQFVNLGLEHLMDFEREQITLDVLV 979
DB	999 LAELAVGASNAGDGAAGTERKEGEVAGLDWNISQFLKSLGLEHLRDIPTETQITLDVLA 1058
QY	980 EMGHKELKEIGINAYGHRHKLKGVRLISGOGLNPVLTNTSGGTILIDLSPDDKEF 1039
DB	1059 DMGHEELKEIGINAYGHRHKLKGVRLISGOGLNPVLTTHCVNQGTILLDLAPEDKEY 1118
QY	1040 OSVEEEMOSTVREHRDGGHAGGIFNRYNLIKQVCNKKLMERYTHRRKEVSEENHNHAN 1099
DB	1119 OSVEEEMOSTVREHRDGGHAGGIFNRYNIRIKQVNNKLRERFCHRQKEVSEENHNHN 1178
QY	1100 ERMPLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGCPTHK 1159
DB	1179 ERMPLFHGSPFNVAIIHKGFDERHAYIGMFGAGIYFAENSSKSNQYVYIGGGTGCPTHK 1238
QY	1160 DRSCYICHRQLLCFRTVLGKSFLOFSAMKMAHSPGHHSVTPGRPSVNGLALEYVYRGE 1219
DB	1239 DRSCYICHRQLLCFRTVLGKSFLOFSAMKMAHSPGHHSVTPGRPSVNGLALEYVYRGE 1298
QY	1220 QAYPEYLITYQIMRPE 1235
DB	1299 QAYPEYLITYQIMRPE 1314

RESULT 15

US-09-972-115A-2

; Sequence 2, Application US/09972115A

; Patent No. 6599728

; GENERAL INFORMATION:

; APPLICANT: Geron Corporation

; APPLICANT: Gregg, Morin B.

; APPLICANT: Walter, Funk D.

; APPLICANT: Mieczyslaw, Piatyszek A.

; TITLE OF INVENTION: A Second Mammalian Telomerase

; FILE REFERENCE: 080/003C

; CURRENT APPLICATION NUMBER: US/09/972,115A

; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: US 60/128,577

; PRIOR FILING DATE: 2000-04-10

; PRIOR APPLICATION NUMBER: US 60/129,123

; PRIOR FILING DATE: 1999-04-13

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 1333

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(1)

; OTHER INFORMATION: The 'Xaa' at location 1 stands for Lys, Asn, Arg, Ser, Thr, Ile,

; OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, T

; NAME/KEY: misc feature

; LOCATION: (2)..(2)

4

OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
NAME/KEY: Tyr, Trp, Cys, or Phe.
LOCATION: (32)..(32)
OTHER INFORMATION: The 'Xaa' at location 32 stands for Lys, Asn, Arg, Ser, Thr, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
NAME/KEY: misc feature
LOCATION: (33)..(33)
OTHER INFORMATION: The 'Xaa' at location 33 stands for Lys, Asn, Arg, Ser, Thr, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
NAME/KEY: misc feature
LOCATION: (34)..(34)
OTHER INFORMATION: The 'Xaa' at location 34 stands for Lys, Asn, Arg, Ser, Thr, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
NAME/KEY: misc feature
LOCATION: (35)..(35)
OTHER INFORMATION: The 'Xaa' at location 35 stands for Lys, Asn, Arg, Ser, Thr, Ile,
OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
OTHER INFORMATION: Tyr, Trp, Cys, or Phe.
NAME/KEY: misc feature
LOCATION: (36)..(36)
OTHER INFORMATION: The 'Xaa' at location 36 stands for Lys, Asn, Arg, Ser, Thr, Ile,
Query Match 77.8%; Score 5031.5; DB 2; Length 1333;
Best Local Similarity 86.7%; Pred. No. 0; Mismatches 135; Indels 9; Gaps 2;
Matches 983; Conservative 7;
116 RLVTPEKVNSTRAGKSTPLHFAAGFGKQVVEYLLQNGANVQARDGGLIPLHNACSF 175
200 RLVTPEKVNXXTXGRKSTPLHFPAGFGKXKXLYLLQNGANXKLYNGGLIPLHXACSF 259
176 GHAEVNVLLRHGADPNARDNNYTPLEHAAIKGKIDVCIVLLQHGAEPTIRNTDGTAL 235
260 GHAKINLLRHGADPNARDNNYTPLEHAAIKGKIDVCIVLLQHGAEPTIRNTDGTAL 319
236 DLADPSAKAVLTGEYKDBELLESARSNGEKNMALLTPLNVNCHASDGRKSTPLHLAAGY 295
320 DLADPSAKAVLTGEYKDBELLESARSNGEKNMALLTPLNVNCHASDGRKSTPLHLAAGY 379
296 NRKIVQLLQHGADVHAKDKGLVPLHNACSYGHVEVTELLVHKGACVNMAMDLAQFTPL 355
380 NRKIVQLLQHGADVHAKDKGLVPLHNACSYGHVEVTELLVHKGACVNMAMDLAQFTPL 439
356 HEAASKNRVVCSSLISYGADPTLNCNKNKSAIDLAPTQPKERLAYEFKGHSLLQAARE 415
440 HEAASKNRVVCSSLISYGADPTLNCNKNKSAIDLAPTQPKERLAYEFKGHSLLQAARE 499
416 ADVTRIKKHLISLEWVNFKHPOTHALCAAAAPYKPKQICELLLRKGANINEKTEPL 475
500 ADVTRIKKHLISLEWVNFKHPOTHALCAAAAPYKPKQICELLLRKGANINEKTEPL 559
476 TPLHVASEKAHNDVVEVVVVKHAKVNALDNLQTSILHRAAYCGHLQTCRLLLSYGCDPNI 535
560 TPLHVASEKAHNDVVEVVVVKHAKVNALDNLQTSILHRAAYCGHLQTCRLLLSYGCDPNI 619
536 ISLQGFALQMGNNVQQLQEGISLGNSEADQLLEAAKAGDVETVKKLCITVQSVNCRD 595
620 ISLQGFALQMGNNVQQLQEGISLGNSEADQLLEAAKAGDVETVKKLCITVQSVNCRD 679
596 IEGRQSTPLHFAAGNVRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGHVEVAELLVKH 655
680 IEGRQSTPLHFAAGNVRVSVVEYLLQHGADVHAKDKGLVPLHNACSYGHVEVAELLVKH 739
656 GAVNVADLWKEFTPLHEAAAKGKYEICKLLQHGADPTKKNRDGNTPLDLVKDGTDIQD 715
740 GAVNVADLWKEFTPLHEAAAKGKYEICKLLQHGADPTKKNRDGNTPLDLVKDGTDIQD 799
716 LIRGDAALLDRAKGLARVKKLSPPDNVNCRDQTQGRHSTPLHLA--AGYNNLEVAEYLL 773
800 XLRGDAVLLDRAKGLARVKKLSPPDNVNCRDQTQGRHSTPLHLAAGXXXXXXXXXXXX 859

QY 774 QHGADVNAODKGGGLIPLHNAASYGHVDVAALLIKYNACVNATDKWATPLHEAAQKGRTO 833
Db 860 XX 919
QY 834 LCALLLAHAGADPTLKNQEGOTPLDLIVSADDSALLTAAMPSPALPSCYKQVNLNGVRSPG 893
Db 920 XX 979
QY 894 ATADALSSGSPSPSSLSAASSLDNLGSGFSSELSSVSSSGTEGASSLEKKEVPGVDFSI 953
Db 980 ATADALSSGSPSPSSLSAASSLDNLGSGFSSELSSVSSSGTEGASSLEKKEVPGVDFSI 1039
QY 954 QFVRNLGLEHLMDFPERQITLIDLVEHMGHKLKEIGINAYGHRHKLKIGVERLLISGOOG 1013
Db 1040 QFVRNLGLEHLMDFXREQITLIDLVEHMGHKLKEIXINAYGHRHKLKIGVERLLISGOOG 1099
QY 1014 INPYLTNTSGGTILIDLSPDDKEFQSVBEEMOSTVREHRDGGHAGGIFNRYNLIKIQK 1073
Db 1100 INPYLTNTSGGTILIDLSPDDKEFQSVBEEMOSTVREHRDGGHAGGIFNRYNLIKIQK 1159
QY 1074 VCNK-----KLWERYTHRRKEVSEENHNANERMLFHGSPFVNAILHKGDERHAYIG 1126
Db 1160 VCNXXXXXAKIRHEERYTHRRKEVSEENHNANERMLFHGSPFVNAILHKGDERHAYIG 1219
QY 1127 GMFGAGIYFAENSCKSNQYVYGIGGTGCPVHKORSYICHRQLLFCRVTLGKSLQFSA 1186
Db 1220 GMFGAGIYFAENSCKSNQYVYGIGGTGCPVHKORSYICHRQLLFCRVTLGKSLQFSA 1279
QY 1187 MKMAHSPGHSVTCRPSVNGLALAEYVYIRGEQAYPEYLITYQIMRPEGMVDG 1240
Db 1280 MKMAHSPGHSVTCRPSVNGLALAEYVYIRGEQAYPEYLITYQIMRPEGMVDG 1333

Search completed: December 18, 2006, 17:37:14
Job time : 46.423 secs.

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OM protein - protein search, using sw model

Run on: December 18, 2006, 17:55:21 ; Search time 40.3471 Seconds
(without alignments)
2975.278 Million cell updates/sec

Title: US-10-616-101-4

Perfect score: 6464

Sequence: 1 RCSARRGAAGGGAQRGARV.....AYPEYLITYQIMRPEGMDG 1240

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 381649 seqs, 96809478 residues

Total number of hits satisfying chosen parameters: 381649

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PTCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	878.5	13.6	1880	7 US-11-050-875-628	Sequence 628, App
2	878.5	13.6	1881	7 US-11-050-875-629	Sequence 629, App
3	877	13.6	1330	7 US-11-293-697-3237	Sequence 3237, Ap
4	714.5	11.1	919	7 US-11-293-697-4122	Sequence 4122, Ap
5	527	8.2	743	7 US-11-371-354-56501	Sequence 56501, A
6	505.5	7.8	685	6 US-10-533-519-1308	Sequence 1308, Ap
7	478	7.4	765	7 US-11-375-615-56	Sequence 56, Appl
8	465	7.2	765	7 US-11-317-329-3	Sequence 3, Appl
9	465	7.2	765	7 US-11-317-329-34	Sequence 34, Appl
10	465	7.2	765	7 US-11-317-329-35	Sequence 35, Appl
11	465	7.2	765	7 US-11-317-329-36	Sequence 36, Appl
12	465	7.2	765	7 US-11-317-329-37	Sequence 37, Appl
13	465	7.2	765	7 US-11-317-329-38	Sequence 38, Appl
14	465	7.2	765	7 US-11-317-329-39	Sequence 39, Appl
15	465	7.2	765	7 US-11-317-329-40	Sequence 40, Appl
16	465	7.2	765	7 US-11-317-329-41	Sequence 41, Appl
17	465	7.2	765	7 US-11-317-329-42	Sequence 42, Appl
18	465	7.2	765	7 US-11-317-329-43	Sequence 43, Appl
19	465	7.2	765	7 US-11-317-329-44	Sequence 44, Appl
20	462	7.1	1061	7 US-11-397-222-4	Sequence 4, Appl
21	432	6.7	616	7 US-11-371-354-59433	Sequence 59433, A
22	411.5	6.4	1050	7 US-11-371-354-65355	Sequence 65355, A
23	408.5	6.3	435	7 US-11-371-354-13702	Sequence 13702, A
24	408.5	6.3	435	7 US-11-371-354-78380	Sequence 78380, A
25	398.5	6.2	1719	7 US-11-344-932-378	Sequence 378, App

ALIGNMENTS

RESULT 1

US-11-050-875-628

; Sequence 628, Application US/11050875

; Publication No. US20060263786A1

; GENERAL INFORMATION:

; APPLICANT: CompuGen Ltd

; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF COLON CANCER

; FILE REFERENCE: 1847 1001

; CURRENT APPLICATION NUMBER: US/11/050.875

; CURRENT FILING DATE: 2005-01-27

; NUMBER OF SEQ ID NOS: 1583

; SEQ ID NO 628

; LENGTH: 1880

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-050-875-628

Query Match 13.6%; Score 878.5; DB 7; Length 1880;

Best Local Similarity 25.8%; Pred. No. 1.4e-47;

Matches 292; Conservative 157; Mismatches 375; Indels 307; Gaps 28;

Qy	105	ACRNDGVERKRLVTPKVNRSRD	TAGRKSTPLHFAAGFGRKDVVEYLLQNGANVQARDG	164
Db	51	ASKEGHVKNVVELLHKE-IILETTTKGNTALHIAAGQDEVVRELVNYGANVNAQSK	109	
Qy	165	GLIPLHNACSPGHAEVNVNLLRHGADPNARDNNWYTPPLHAAIKKIDVICVILLOHGAEP	224	
Db	110	GFTFLYMAAQENHLEHVVKFLLENGANQVATEDGFTPLAVALQQGHENVAHLINYGTKG	169	
Qy	225	TI-----RNTDGRITADLP	SAKAVLTGEYKKDELLESARSGNEEKWALLTPLN	275
Db	170	KVRLPALHIAARNDDTRTA-----AVLLQNDPNPDLV--SKTG-----FTPLH	210	
Qy	276	VNCHASDGRKS-----TPHLAAGYNRVKIVOLLQHQADVHAKDKG	317	
Db	211	IAAHVENLVAQLLNRGASVNFPTQNGITPLHIAARRGNVIMVRLLDLRGAQIETTKD	270	
Qy	318	DLVPLHNACSGHYEVTELLVKGACVNMDLWFTPLHAAAKNRVVCSSILLSYGADP	377	
Db	271	ELTPLHCAARNGHVRISILLDHGAPIQAKTKNGLSPIHMAAQGDHLDVCLLLQYDAE-	329	
Qy	378	TLLCHNKSATDLAPTQPKERLAEYFKGSLQAAREADVTRIKCHLSLEWVNFKEPQT	437	
Db	330	-----ID-----DIT-----LD	336	
Qy	438	HETALHCAASFPYPRKQICELLRKGANINERTKEFTPLHVAASEKAHNDVVEVVKHE	497	

Db 337 HLTPHVA---HCGHHRVAKVLLDKGAKPNSRALNGFTPLHIAACKKNHVVMELLILKTG 393
Qy 498 AKVNALNGLGOTS LHRAAAYCGHLOTCRLLSYGCDPNIISLGFTALQMG-----NENVQ 552
Db 394 ASIDAVTESGLTPLHVASFMGHLPTVKNLLQRGASPNVSNVKVETPLHMAARAGHTEVAK 453
Qy 553 QLLQE-----GISLGNSEADROLLE-----AAKAG 577
Db 454 YLLQNKAKVNAKADDTQPLHCAARIGHNTNMVKKLLENNANPNLATTAGHTPLHIAAREG 513
Qy 578 DVEVTKLCTVQ-SVNCRDIEGRQSTPLHFAAGYNNRVSVVYLLQHGADVHAKDKGLVP 636
Db 514 HVEITVLALEKEAQACMTKKG--FTPLHVAAGYNNRVVAELLLERDAHPNAAKNGLTP 571
Qy 637 LHNACSYGHYEVABELLVKHGAVNVADLWK-FTPLHEAAAKGYEICKLLQHGADPTKK 695
Db 572 LHVAVHNNLDIVKLLPRGSGSPH-SPAWNGYTPPLHIAAKQNVQEVARSLLQYGSANAE 630
Qy 696 NRDGNTPDL-LVKDGTDIQDLIRGDAALLDAKKGCLARVKKLSPPDNVNCRTQGRHS 754
Db 631 SVQGVTPHLAAQEGHAEWVALL-----LSQANGNLKSG--L 668
Qy 755 TPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNACVNA 814
Db 669 TPLHVAQEGHVPVADVLIKHGVMVDATTRNGYTPLVASHYGNIKLVKFLQHQADVNA 728
Qy 815 TDKWAFTPLHAAQKGRTOCALLAHAGADPTLKNQEGQTPDL-----VS 860
Db 729 KTKLGYSPHQAQOQGTDIVTLKNGASPNVSSDGTTPLAIAKRLGYISVTDVLKVV 788
Qy 861 ADDVSALLTAAMPSPALPSC-----YKQ 884
Db 789 TDTSFVLVSDKHMSFPETVDEILDVSEDEGBELISFKAERRDRDVBKEILLDFVPK 848
Qy 885 VLNGVRSPGATADALSFGSPSSLS-----AASSLNLSSFSFELSSVSSSGTEGASS 939
Db 849 LDQVVEPAI-----PRIPCAMPETVIRSEEQASKEYDEDSLISSPATETSDN 900
Qy 940 LEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDVLVEMGHKELKEIGAINAYGHRHK 999
Db 901 ISPVASPVHTGFLVFSM-----VDARGSGMRGSRHN 931
Qy 1000 LIKGE-----RLISGQGLNPLYLTNTSGSGTILIDLSP-----1034
Db 932 GLRWIPPTCAAPTRITCLVKPKLSTPPPLAEEGLASRIIALGTGAQFLSPVIVE 991
Qy 1035 -----DDKEFQSVEEEMQSVREHROGCHAGGIFNRYNLIKQVCN 1076
Db 992 IPFHASHGRGDRELVLRSNGSVKKEH-----SRYGESYLDQILN 1033

RESULT 2
US-11-050-875-629
; Sequence 629, Application US/11050875
; Publication No. US20060263786A1
; GENERAL INFORMATION:
; APPLICANT: Compugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; TITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 1847.1001
; CURRENT APPLICATION NUMBER: US/11/050.875
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 1583
; SEQ ID NO 629
; LENGTH: 1881
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-875-629

Query Match 13.6%; Score 878.5; DB 7; Length 1881;
Best Local Similarity 25.8%; Pred. No. 1.4e-47;
Matches 292; Conservative 157; Mismatches 375; Indels 307; Gaps 28;

Qy 105 ACRNGDVERVKRLVTPKVNSTRDTAGKSTKSTPLHFAAGFGRKOVVEYLLQNGANYQARDG 164
Db 52 ASKEGHYKVMVVELLHKE-IILEFTTKGNTALHIAALAGQDEVVRELVNNGANYNAOSQK 110
Qy 165 GLTPLHNACSFHAEVNVNLLRLHGCADPNARDNNWYTPLEHAAIKGKIDVCIVLLQHGAE 224
Db 111 GFTPLYNAAQENHLEVVVKFLENGANQVATEDGFTPLAVALQGHENNVVAHLINYGTKG 170
Qy 225 TI-----RNTDGRATLDADPSAKAVLTGKYKDELLESARSNGEEOOMALLTPLN 275
Db 171 KVRPLPALHIAARNDTRTA-----AVLLQNDPNPDL--SKTG-----FTPLH 211
Qy 276 VNCHASGRKS-----TPLHLAGYNNRVKIIVOLLQHGADVHAKDKG 317
Db 212 IAAHYENLANVAQLLNNGASVNFPPQNGITPLHIASRRGNVIMVRLLLDRQALETCTKD 271
Qy 318 DLVPLHNACSYGHYEVTELLVKGACVNAWDLMOFTPLHEAASKNRVEVCSLLSYGADP 377
Db 272 ELTPLHCAARNGHVRISEILLDHGAPIQAKTKNGLSPIHMAAQGDHLDVRLLLQYDAE- 330
Qy 378 TLLNCHNKSAIDLAFTPOLKERLAYEPKSHSLLOAAREADVTRIKKHLSELMVNFKHPQT 437
Db 331 -----ID-----DIT-----LD 337
Qy 438 HETALHCAAAAPYKPKQICELLIRKCANINEKTEFLTPLHVASEKAHNDVVEVVKHE 497
Db 338 HLTPHVA---HCGHHRVAKVLLDKGAKPNSRALNGFTPLHIAACKKNHVVMELLILKTG 394
Qy 498 AKVNALNGLGOTS LHRAAAYCGHLOTCRLLSYGCDPNIISLGFTALQMG-----NENVQ 552
Db 395 ASIDAVTESGLTPLHVASFMGHLPTVKNLLQRGASPNVSNVKVETPLHMAARAGHTEVAK 454
Qy 553 QLLQE-----GISLGNSEADROLLE-----AAKAG 577
Db 455 YLLQNKAKVNAKADDTQPLHCAARIGHNTNMVKKLLENNANPNLATTAGHTPLHIAAREG 514
Qy 578 DVEVTKLCTVQ-SVNCRDIEGRQSTPLHFAAGYNNRVSVVYLLQHGADVHAKDKGLVP 636
Db 515 HVEITVLALEKEAQACMTKKG--FTPLHVAAGYNNRVVAELLLERDAHPNAAKNGLTP 572
Qy 637 LHNACSYGHYEVABELLVKHGAVNVADLWK-FTPLHEAAAKGYEICKLLQHGADPTKK 695
Db 573 LHVAVHNNLDIVKLLPRGSGSPH-SPAWNGYTPPLHIAAKQNVQEVARSLLQYGSANAE 631
Qy 696 NRDGNTPDL-LVKDGTDIQDLIRGDAALLDAKKGCLARVKKLSPPDNVNCRTQGRHS 754
Db 632 SVQGVTPHLAAQEGHAEWVALL-----LSQANGNLKSG--L 669
Qy 755 TPLHLAGYNNLEVAEYLLQHGADVNAQDKGLIPLHNAASYGHVDVAALLIKYNACVNA 814
Db 670 TPLHVAQEGHVPVADVLIKHGVMVDATTRNGYTPLVASHYGNIKLVKFLQHQADVNA 729
Qy 815 TDKWAFTPLHAAQKGRTOCALLAHAGADPTLKNQEGQTPDL-----VS 860
Db 730 KTKLGYSPHQAQOQGTDIVTLKNGASPNVSSDGTTPLAIAKRLGYISVTDVLKVV 789
Qy 861 ADDVSALLTAAMPSPALPSC-----YKQ 884
Db 790 TDTSFVLVSDKHMSFPETVDEILDVSEDEGBELISFKAERRDRDVBKEILLDFVPK 849
Qy 885 VLNGVRSPGATADALSFGSPSSLS-----AASSLNLSSFSFELSSVSSSGTEGASS 939
Db 850 LDQVVEPAI-----PRIPCAMPETVIRSEEQASKEYDEDSLISSPATETSDN 901
Qy 940 LEKKEVPGVDFSIQFVRNLGLEHLMDFEREQITLDVLVEMGHKELKEIGAINAYGHRHK 999
Db 902 ISPVASPVHTGFLVFSM-----VDARGSGMRGSRHN 932
Qy 1000 LIKGE-----RLISGQGLNPLYLTNTSGSGTILIDLSP-----1034
Db 933 GLRWIPPTCAAPTRITCLVKPKLSTPPPLAEEGLASRIIALGTGAQFLSPVIVE 992
Qy 1035 -----DDKEFQSVEEEMQSVREHROGCHAGGIFNRYNLIKQVCN 1076

Db 285 LHMTAVHGRFTRSTLNGEIDCVKDGNTPLHVAARYGHELLINTLTSGADTAKG 344
Qy 538 LQGTALOMGNENVOQLLOBEGISGNSEADQOLLEAAKAGDVETVKLCTVQSVNCRDIE 597
Db 345 IHSMPFLHAAALN-----AHSDDCKRL--SSGFEIDTPDKF----- 379
Qy 598 GRSQTPHFAAGYNRVSVVEYLLQHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGA 657
Db 380 GR--TCLHAAAAGGNVBCIKLLQSSGADFHKKCKGRTPHLYAAAANCHFHCIETLVTTGA 437
Qy 658 VNVADLWKFPTLHEAAA-----KGYEIC-KLLLQHG 689
Db 438 NVNETDWRGTALHYAAAADMORNTKILGNHNDSEBELERARELKEKATLCLFELOND 497
Qy 690 ADPTKNRDG-----NTPLDLVK-DG----- 709
Db 498 ANPSIRDKEGYNSHYAAAAYHRCQLELLERTNSGFESDSGATKSPHLAAYNHGHQA 557
Qy 710 -----DTDIQDLRGDAALDAAKKGCLARVKLSSP-----DNVNCRDTOGRH 753
Db 558 LEVLQSLVDLDIRD-EGRTALDLAAAFKGTCEVAALINPGASIFVKDNVTKR----- 610
Qy 754 STPLHLAGYNNLEVAEYLLQHGAD---VNAODKGLIPLHNAASYGHVDVAALLIKYN 809
Db 611 -TPLH-ASVINGHTLCURLLELIDNPENAVDVDAKAGTQPLMLAVAGHIDAVSLLEKE 668
Qy 810 ACVNATDKWFTPLHEAAQKRTQCALLLAHAGADPTLKQSGGTPLDLVSADD-----VS 865
Db 669 ANVDVILGCTALHRGIMTGHBCVQMLLEQEVSLCKDSRGRTPLHYAAAARGHATWLS 728
Qy 866 ALLTAAMPSPALPSYK 882
Db 729 ELLQWAL--SEEDCCFK 743

RESULT 5

US-11-371-354-56501
; Sequence 56501, Application US/11371354
; Publication No. US2006027594A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; PRIOR FILING DATE: 2006-03-07
; PRIOR FILING DATE: 2006-03-07
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 56501
; LENGTH: 743
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-56501

Query Match 8.2%; Score 527; DB 7; Length 743;
Best Local Similarity 24.0%; Pred. No. 1.3e-25;
Matches 201; Conservative 98; Mismatches 238; Indels 302; Gaps 19;

Qy 143 GRXDVVEYLLQNGANVOARDGGLIPLHNA-----CSFGHAEVNVNLLLRHGADPNARDNW 197
Db 2 GHREIVEHLHDHGAENHEDVDGRTALSVAAALCVPAKSHASVSVSLIDRGAETHDCDKD 61
Qy 198 NYTPHLEAAIKGIDKIDVICVILLOHGAEBPTIRNTDGTALDILADPSAKAVLTGEYKKBELLE 257
Db 62 GMTPLLVAAVEGHVDVVDLLEGGAD--VDHTD----- 92
Qy 258 SARSGNEBKWMALLTPLNVNCHASDGRKSTPLHLAGYNRVKIVOLLQHGADVHAKDKG 317
Db 93 -----NNGR--TPLLAASMGHASVNVNTLLFWGAAVDSIDSE 127
Qy 318 DLVPLHNACSYGHEVTELLVKGACVNAVDLQFTPLHEAASKNRVEVCSLLLSYGADP 377
Db 128 GRTVLSIASAGNVVVVTTLLDRGLDENHRDDAGWTPLHMAA----- 169
Qy 378 TLLNCHNKAIDLAPTQLKERLAYEFKSHLSLLQAAREADVTRIKKHLSLMVNFKHPQT 437
Db 170 -----PEGHRL----- 175
Qy 438 HETALHCAAAAPYKPKQICELLRLKGANINEKTEFLTPLHVASEKAHNDVVEVVVKHE 497
Db 176 -----ICEALIEOGARTNEIDNDGRIPFILASQSGHYDCVQILLLENK 217
Qy 498 AKYNALDNLGOTSILHRAAYCGHLQTCCELLLSYCDPNIIISLOGFTALQMGNENVQQLLOE 557
Db 218 SNIDQRYDGRNALRVAALLEGHRDIELLFSHGAD----- 252
Qy 558 GISLGNSEADQOLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNRVSVVE 617
Db 253 -----VNCKDADGRPT--LYILALENQLTMAE 277
Qy 618 YLLQHGADVHAKKGGLVPLHNACSYGHEVAELLVKHGAVNVVADLWKFPTLHEAAKG 677
Db 278 YFLENGANVEASDAEGRTALHVSQWGHMEMVQVLIAYHADVNAADNEKRSALQSAWQ 337
Qy 678 KYEICKLLLOHGADPTKKNRDNTPDLVDKGDGTDIDLLRGDAALLDAAKKGCLARVK 737
Db 338 HVKVQQLLIEHG-----AVVD----- 353
Qy 738 LSSPDNVNCRDIOGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYG 797
Db 354 -----HTCNOGATACIAAQEGHIDVQVLEHGADPNHADQFGRITAMVAAKNG 403
Qy 798 HVDVAALLIKYNACVNATDKWFTPLHEAAQKRTQCALLLAHAGADPTLK-NOEGQTPL 856
Db 404 HSQIIKLEKYGA--SSLNGCSPSPVHTMEQKPLQSLSSKV-----QSLTIKSNSSGST-- 455
Qy 857 DLVSADVDVALLTAAMPSPALPSYKQPVLENGVRSFGATADALSSGSPSSSL--SAASS 914
Db 456 ---GGGD-----MQPS-----LRGL--PNGTHAFSPSPSPSTVDROKSS 492
Qy 915 LDNLGSGFSBLSVSVSSGTGEGASSLEKEVPVGVDFISITQFVRNLGLEHLMIDIFEREQI 973
Db 493 LSNNSLKSSKNLSRLTSSSTATQ-----VPIDSFNLSFTTEQIQHSLPRSRRSQSI 546

RESULT 6

US-10-533-519-1308
; Sequence 1308, Application US/10533519
; Publication No. US20060263774A1
; GENERAL INFORMATION:
; APPLICANT: CLARK, HILARY
; APPLICANT: SCHOENFELD, JILL
; APPLICANT: VANLOOKEREN, MENNO
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
; TITLE OF INVENTION: RELATED DISEASES
; FILE REFERENCE: P1984R1 US
; CURRENT APPLICATION NUMBER: US/10/533,519

	CURRENT FILING DATE: 2005-04-28	
	PRIOR APPLICATION NUMBER: PCT/US03/34312	
	PRIOR FILING DATE: 2003-10-30	
	PRIOR APPLICATION NUMBER: US 60/423,394	
	PRIOR FILING DATE: 2002-11-01	
	NUMBER OF SEQ ID NOS: 2517	
	SEQ ID NO 1308	
	LENGTH: 685	
	TYPE: PRT	
	ORGANISM: Homo sapien	
	US-10-533-519-1308	
	Query Match 7.8%; Score 505.5; DB 6; Length 685;	
	Best Local Similarity 24.08; Pred. No. 2.8e-24;	
	Matches 195; Conservative 92; Mismatches 264; Indels 263; Gaps 19;	
QY	104 EACRNGDVERVKRLVTPKEKVNSTRDATGRKSTPLHFAAGFGKOVVEYLLQNGANVAQRDD	163
DB	2 EASQEGHLELVKYLLA-SGANVHATTATGDTALTAYACENGHTDVADVLLQAQADLDKQED	60
QY	164 -----CGLTPLHNACSFHAENVNLLRHGADPN-ARDNNWNYPLH	203
DB	61 MKTILEIDPAKHQEHSEGGRTPLMKAARAGHLCTVQFLISKGANVRNATANNHDVTWS	120
QY	204 EAAIKGKIDVICIVLLOHGAEPTTRNTDGRTAL-----DLADPSA	242
DB	121 LACAGGHLAVVELLAHGAUPTHRLDKGSTWLIEAAKGHTNVVSYYLLDPNNVLSVPTT	180
QY	243 KAVLTGEYKKDELLESARSNE-----EKOMALLTPLNVN-----CHASDGRKST	287
DB	181 DVSQLPPSQDSQPDRTSQENSPALLGVQKAVSTRVPTGSNSSQTTECLTPESCQT	240
QY	288 PLHLAAG-----YNRVKI VOLLHQHADVHAKGDVLPHLNACSGYHYETELLVKHGA	342
DB	241 TSNVASQSMPVTPSDVD-----DAFTESNHD-TALTLCAGGHEELVSVLIARDA	290
QY	343 CVNAMDLWQFTHPEAASKNRVECSLLLISYGADPTLLCNCHKNSAIDLAPTQPKERLAY	402
DB	291 KIEHRDKKGFTPLILAATAGHVGVVEILLDKGSD-----	324
QY	403 EPKGHSLLQAAREADVTRI KKHLSLEMVNFKHPOTHETALHCAASPYPKRKQICEILLR	462
DB	325 -----IEAQSE-----RTKDTPLSLACSG---GRQEVVDLLLL	354
QY	463 KGANINEKTKEFLTPLHVASSEKANDVVVVVXHEAKVNAL--DNLGOTSILHRAAYCGLH	520
DB	355 RGANKHEHRNVSDYTPLSLAASGGVYNIKILLNAGAENSRTGSKLGISPLMLAAMNHV	414
QY	521 QTCRLLSYSCDPIIISLOGFTTALQMGNENVQQLLEGISLGNSEADRQLLEAAKAGDVE	580
DB	415 PAVKLLLDMGSDIN-----	428
QY	581 TVVKLCTVQVNCRDIEGROSTPLHFAAGYNRVSVVEYLLQHGDADVHAKDGKGLVPLHNA	640
DB	429 -----AQIETNRNLTALTACFOGRAEVSLLLDKANVBRHAKTGTLPLMEA	475
QY	641 CSYCHYEVAELLVKHGA VNVNADI--WKFTPLHEAAAAGKYEICKLLOHGCADPTTKNRD	698
DB	476 ASGGYAEVGRVLLDKGADVNAVPPVSSSRD TALTTAADKGHYKFCELLIHGAHIDVFNKK	535
QY	699 GNTPLDLVKGDGTDITQDLLRGDAALLDAAKGGLARVKKLSSPNNVNCROTQGRHSTPLH	758
DB	536 GNTPLMLASNG-----	546
QY	759 LAAGYNNLEYAEYLLQHGADVNAODKGGLIPLHNAASYGHVDVAALLIK-----	807
DB	547 -----GHFDVVQLLVQAGADVDAADNRKI TPLMSAFKRGHKVQVYLKVENEQFPSPDIEC	601
QY	808 --YNACVNAATDKWAFTPLHEAAQ---KGRGTQLCA	836
DB	602 MRVIATI--TDKELLKKKCOCVFETIVAKADQOAA	633

Db 708 LKVLVEAGALDQVDSCTPLQLALRSRKGIMSFL--EGKEPSVATLGGSKP 759

RESULT 8

US-11-317-329-3

Sequence 3, Application US/11317329

Publication No. US20060105413A1

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Naohiro

TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

FILE REFERENCE: UM-06967

CURRENT APPLICATION NUMBER: US/11/317,329

CURRENT FILING DATE: 2005-12-22

PRIOR FILING DATE: US/10/128,174

PRIOR FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 765

TYPE: PRT

ORGANISM: Homo sapiens

US-11-317-329-3

Query Match 7.2%, Score 465; DB 7; Length 765;

Best Local Similarity 30.1%; Pred. No. 1.3e-21;

Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP---TPOLKERLAYEFKSHLSLQAAREADVTRIKKHLSEWMNFKHPQTHET 440

Db 338 KRALQLSDRKNLVRDELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386

Qy 441 ALHCAASPYPKRKQICELLRRKGANINEKTEPLTLHVASEKAKHNDVVEVVVKHEAKV 500

Db 387 DVDCQTASGY-----TPLLIAAQDQDPLCALLAHGADA 421

Qy 501 NALDNLGQTSLHRAAYCGHLQTCRLLSYCGDPNIISLOGFTALQMGNEVQQLQEGIS 560

Db 422 NRVEDGWAFLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471

Qy 561 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGVNRVSVVEYLL 620

Db 472 --NFENVARLLVSRAQ-----DPNLEAREGK--TPLHVAAYFGHVSLLVKLLT 514

Qy 621 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVNVVADLWKFTPLHEAAAKGYE 680

Db 515 SQGAELDAQQRNLRTPHLHVAERGVKRAIQHLKSGAVPDALDQSGYGPLHTAAARGKYL 574

Qy 681 ICKLLLOHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 740

Db 575 ICKMLRYGASLELPTHQGWTPHL-----AAYKGHL-EIIHLLA 613

Qy 741 PDVNCRDTCGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800

Db 614 ESHANMGALGAVNWTPLHLAARHGEAEVVSALLQCGADPNAAEQSGWTPHLAVQRSTFL 673

Qy 801 VAALLIKYNACVNATDKWFTPLHEAAKQKRTOLCALLAHGADPTLKNQEGQTPDL 858

Db 674 SVINLLEHNAVHARNKVGWTPAHLAALKGNATLKVLEAGALDQVDSCTPLQL 731

RESULT 9

US-11-317-329-34

Sequence 34, Application US/11317329

Publication No. US20060105413A1

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Naohiro

TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

FILE REFERENCE: UM-06967

CURRENT APPLICATION NUMBER: US/11/317,329

CURRENT FILING DATE: 2005-12-22

PRIOR FILING DATE: US/10/128,174

; PRIOR FILING DATE: 2002-04-23

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 34

; LENGTH: 765

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-317-329-34

Query Match 7.2%, Score 465; DB 7; Length 765;

Best Local Similarity 30.1%; Pred. No. 1.3e-21;

Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP---TPOLKERLAYEFKSHLSLQAAREADVTRIKKHLSEWMNFKHPQTHET 440

Db 338 KRALQLSDRKNLVRDELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386

Qy 441 ALHCAASPYPKRKQICELLRRKGANINEKTEPLTLHVASEKAKHNDVVEVVVKHEAKV 500

Db 387 DVDCQTASGY-----TPLLIAAQDQDPLCALLAHGADA 421

Qy 501 NALDNLGQTSLHRAAYCGHLQTCRLLSYCGDPNIISLOGFTALQMGNEVQQLQEGIS 560

Db 422 NRVEDGWAFLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471

Qy 561 LGNSEADROLLEAAKAGDVETVKLCTVQSVNCRDIEGRQSTPLHFAAGVNRVSVVEYLL 620

Db 472 --NFENVARLLVSRAQ-----DPNLEAREGK--TPLHVAAYFGHVSLLVKLLT 514

Qy 621 QHGADVHAKDKGGLVPLHNACSYGHYEVAELLVKHGAVNVVADLWKFTPLHEAAAKGYE 680

Db 515 SQGAELDAQQRNLRTPHLHVAERGVKRAIQHLKSGAVPDALDQSGYGPLHTAAARGKYL 574

Qy 681 ICKLLLOHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKKGCLARVKKLSS 740

Db 575 ICKMLRYGASLELPTHQGWTPHL-----AAYKGHL-EIIHLLA 613

Qy 741 PDVNCRDTCGRHSTPLHLAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800

Db 614 ESHANMGALGAVNWTPLHLAARHGEAEVVSALLQCGADPNAAEQSGWTPHLAVQRSTFL 673

Qy 801 VAALLIKYNACVNATDKWFTPLHEAAKQKRTOLCALLAHGADPTLKNQEGQTPDL 858

Db 674 SVINLLEHNAVHARNKVGWTPAHLAALKGNATLKVLEAGALDQVDSCTPLQL 731

RESULT 10

US-11-317-329-35

Sequence 35, Application US/11317329

Publication No. US20060105413A1

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Naohiro

TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

FILE REFERENCE: UM-06967

CURRENT APPLICATION NUMBER: US/11/317,329

CURRENT FILING DATE: 2005-12-22

PRIOR FILING DATE: US/10/128,174

PRIOR FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 35

LENGTH: 765

TYPE: PRT

ORGANISM: Homo sapiens

US-11-317-329-35

Query Match 7.2%, Score 465; DB 7; Length 765;

Best Local Similarity 30.1%; Pred. No. 1.3e-21;

Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP---TPOLKERLAYEFKSHLSLQAAREADVTRIKKHLSEWMNFKHPQTHET 440

Db 338 KRALQSDRKNLVPRDEELCIYENKVTPLQFLVAQSGVEQVRLLLA-----HEV 386
Qy 441 ALHCAAAASPYPKRKQICELLRLKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 500
Db 387 DVDCQTASGY-----TPLLIAAQDQDPDLCAALLAHGADA 421
Qy 501 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDDPNIISLQGFALQMGNNVQQLLEQGIS 560
Db 422 NRVDGEGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 561 LGNSEADQLLEAAKAGDVETVKKLTCTVQSVNCRDIEGROSTPLHFAAGYNNRVSVVEYLL 620
Db 472 --NFENVARLLVSQA-----DNLREAEKG--TPLHVAAYFGHVSIVKLTT 514
Qy 621 QHGADVHAKDKGGLVPLHNACSYPHYEVAELLVKHGAVNVADLWKFTPLHVAAGKGYE 680
Db 515 SQGAELDAQORNLRTPLHLAVERGKVRRAIQHLLKSGAVPDALDQSGYGLPHTAAARGKYL 574
Qy 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAKKGCLARVKKLSS 740
Db 575 ICKMLLYRGASLELPTHQGTPLHL-----AYKGHL-EIHLILA 613
Qy 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGAALGAVNWTPLHLAARHGEEAVVSALLQCGADPNAEQSGWTPHLAVQSTFL 673
Qy 801 VAALLIKYNACVNATDKWAFPTPLHAAKQKGTQOLCALLLAHAGADPTLKNQSGQTPDL 858
Db 674 SVINLLEHNAVHARNKVGWTPAHLAALKGNTAILKVLVEAGAQLDVQDQVSGCTPLQL 731
RESULT 11
US-11-317-329-36
; Sequence 36, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 36
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-36
Query Match 7.2%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;
Qy 385 KSAIDLAP-----TPOLKERLAYEPKGHSLLOQAAREADVTRIKKHLSELMVNFKHPQTHET 440
Db 338 KRALQSDRKNLVPRDEELCIYENKVTPLQFLVAQSGVEQVRLLLA-----HEV 386
Qy 441 ALHCAAAASPYPKRKQICELLRLKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 500
Db 387 DVDCQTASGY-----TPLLIAAQDQDPDLCAALLAHGADA 421
Qy 501 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDDPNIISLQGFALQMGNNVQQLLEQGIS 560
Db 422 NRVDGEGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 561 LGNSEADQLLEAAKAGDVETVKKLTCTVQSVNCRDIEGROSTPLHFAAGYNNRVSVVEYLL 620
Db 472 --NFENVARLLVSQA-----DNLREAEKG--TPLHVAAYFGHVSIVKLTT 514
Qy 621 QHGADVHAKDKGGLVPLHNACSYPHYEVAELLVKHGAVNVADLWKFTPLHVAAGKGYE 680
Db 515 SQGAELDAQORNLRTPLHLAVERGKVRRAIQHLLKSGAVPDALDQSGYGLPHTAAARGKYL 574
Qy 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAKKGCLARVKKLSS 740
Db 575 ICKMLLYRGASLELPTHQGTPLHL-----AYKGHL-EIHLILA 613
Qy 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGAALGAVNWTPLHLAARHGEEAVVSALLQCGADPNAEQSGWTPHLAVQSTFL 673
Qy 801 VAALLIKYNACVNATDKWAFPTPLHAAKQKGTQOLCALLLAHAGADPTLKNQSGQTPDL 858
Db 674 SVINLLEHNAVHARNKVGWTPAHLAALKGNTAILKVLVEAGAQLDVQDQVSGCTPLQL 731

Db 515 SQGAELDAQORNLRTPLHLAVERGKVRRAIQHLLKSGAVPDALDQSGYGLPHTAAARGKYL 574
Qy 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAKKGCLARVKKLSS 740
Db 575 ICKMLLYRGASLELPTHQGTPLHL-----AYKGHL-EIHLILA 613
Qy 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGAALGAVNWTPLHLAARHGEEAVVSALLQCGADPNAEQSGWTPHLAVQSTFL 673
Qy 801 VAALLIKYNACVNATDKWAFPTPLHAAKQKGTQOLCALLLAHAGADPTLKNQSGQTPDL 858
Db 674 SVINLLEHNAVHARNKVGWTPAHLAALKGNTAILKVLVEAGAQLDVQDQVSGCTPLQL 731
RESULT 12
US-11-317-329-37
; Sequence 37, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 37
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-37
Query Match 7.2%; Score 465; DB 7; Length 765;
Best Local Similarity 30.1%; Pred. No. 1.3e-21;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;
Qy 385 KSAIDLAP-----TPOLKERLAYEPKGHSLLOQAAREADVTRIKKHLSELMVNFKHPQTHET 440
Db 338 KRALQSDRKNLVPRDEELCIYENKVTPLQFLVAQSGVEQVRLLLA-----HEV 386
Qy 441 ALHCAAAASPYPKRKQICELLRLKGANINEKTEFTPLHVAASEKAHNDVVEVVKHEAKV 500
Db 387 DVDCQTASGY-----TPLLIAAQDQDPDLCAALLAHGADA 421
Qy 501 NALDNLGQTSLHRAAYCGHLOTCTRLLSYGCDDPNIISLQGFALQMGNNVQQLLEQGIS 560
Db 422 NRVDGEGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 561 LGNSEADQLLEAAKAGDVETVKKLTCTVQSVNCRDIEGROSTPLHFAAGYNNRVSVVEYLL 620
Db 472 --NFENVARLLVSQA-----DNLREAEKG--TPLHVAAYFGHVSIVKLTT 514
Qy 621 QHGADVHAKDKGGLVPLHNACSYPHYEVAELLVKHGAVNVADLWKFTPLHVAAGKGYE 680
Db 515 SQGAELDAQORNLRTPLHLAVERGKVRRAIQHLLKSGAVPDALDQSGYGLPHTAAARGKYL 574
Qy 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAKKGCLARVKKLSS 740
Db 575 ICKMLLYRGASLELPTHQGTPLHL-----AYKGHL-EIHLILA 613
Qy 741 PDVNCRTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGAALGAVNWTPLHLAARHGEEAVVSALLQCGADPNAEQSGWTPHLAVQSTFL 673
Qy 801 VAALLIKYNACVNATDKWAFPTPLHAAKQKGTQOLCALLLAHAGADPTLKNQSGQTPDL 858
Db 674 SVINLLEHNAVHARNKVGWTPAHLAALKGNTAILKVLVEAGAQLDVQDQVSGCTPLQL 731


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RESULT 13
US-11-317-329-38
; Sequence 38, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-38

Query Match
Best Local Similarity 30.1%; Score 465; DB 7; Length 765;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP----TPOLKERLAYEFKSHLSLQAAREADVTRIKKHLSELMVNFKHPQTHET 440
Db 338 KRALQLSDRKNLVRDEELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386
Qy 441 ALHCAASPYPRKQICELLRKGANINEKTEFLTPLVASEKAKHNDVVEVVVKEAKV 500
Db 387 DVDCQTASGY-----TPLLIAAQDQDPDLCALLAHGADA 421
Qy 501 NALDNLGQTSIHRAYCGHLQTCRLLLSYGCDPNIISLGFTALQMGNNVQQLQEGIS 560
Db 422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 561 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNNRVSVWEYLL 620
Db 472 --NFENVARLLVSRQA-----DPNLEAEGK--TPLHVAAYFGHVSILVKLLT 514
Qy 621 QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVADLWKFTPLHEAAAKGYE 680
Db 515 SQGAELDAQQRNLRTPLHLAVERGKVRAIQHLKSGAVPDALDQSGYGPLHTAAARGKYL 574
Qy 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKGCCLARVKKLSS 740
Db 575 ICKMLLYGASLELPTHQGWTPHLH-----AAYKGHL-EIIHLLA 613
Qy 741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGALGAVNWTPLHLAARHGEAEVVSALLQCGADPNAEQSGWTPHLAVQSTFL 673
Qy 801 VAALLIKYNACVNATDKWAFTPLEHAAKQRTQICALLAHGADPTLKNQEGQTPDL 858
Db 674 SVINLLEHNVHARNKVGWTPAHLAALKGNNTAILKVLVEAGAQLDVQDGVSCCTPLQL 731

RESULT 14
US-11-317-329-39
; Sequence 39, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-39

Query Match
Best Local Similarity 30.1%; Score 465; DB 7; Length 765;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP----TPOLKERLAYEFKSHLSLQAAREADVTRIKKHLSELMVNFKHPQTHET 440
Db 338 KRALQLSDRKNLVRDEELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386
Qy 441 ALHCAASPYPRKQICELLRKGANINEKTEFLTPLVASEKAKHNDVVEVVVKEAKV 500
Db 387 DVDCQTASGY-----TPLLIAAQDQDPDLCALLAHGADA 421
Qy 501 NALDNLGQTSIHRAYCGHLQTCRLLLSYGCDPNIISLGFTALQMGNNVQQLQEGIS 560
Db 422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 561 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNNRVSVWEYLL 620
Db 472 --NFENVARLLVSRQA-----DPNLEAEGK--TPLHVAAYFGHVSILVKLLT 514
Qy 621 QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVADLWKFTPLHEAAAKGYE 680
Db 515 SQGAELDAQQRNLRTPLHLAVERGKVRAIQHLKSGAVPDALDQSGYGPLHTAAARGKYL 574
Qy 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKGCCLARVKKLSS 740
Db 575 ICKMLLYGASLELPTHQGWTPHLH-----AAYKGHL-EIIHLLA 613
Qy 741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGALGAVNWTPLHLAARHGEAEVVSALLQCGADPNAEQSGWTPHLAVQSTFL 673
Qy 801 VAALLIKYNACVNATDKWAFTPLEHAAKQRTQICALLAHGADPTLKNQEGQTPDL 858
Db 674 SVINLLEHNVHARNKVGWTPAHLAALKGNNTAILKVLVEAGAQLDVQDGVSCCTPLQL 731
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-39

Query Match
Best Local Similarity 30.1%; Score 465; DB 7; Length 765;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP----TPOLKERLAYEFKSHLSLQAAREADVTRIKKHLSELMVNFKHPQTHET 440
Db 338 KRALQLSDRKNLVRDEELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386
Qy 441 ALHCAASPYPRKQICELLRKGANINEKTEFLTPLVASEKAKHNDVVEVVVKEAKV 500
Db 387 DVDCQTASGY-----TPLLIAAQDQDPDLCALLAHGADA 421
Qy 501 NALDNLGQTSIHRAYCGHLQTCRLLLSYGCDPNIISLGFTALQMGNNVQQLQEGIS 560
Db 422 NRVEDGWAPLHFAAQNGDDRTARLLLDHGACVDAQEREGWTPHLAAQN----- 471
Qy 561 LGNSEADRLLEAAKAGDVETVKLCTVQSVNCRDIEGROSTPLHFAAGYNNRVSVWEYLL 620
Db 472 --NFENVARLLVSRQA-----DPNLEAEGK--TPLHVAAYFGHVSILVKLLT 514
Qy 621 QHGADVHAKDKGGLVPLHNACSYGHEVAELLVKHGAVNVADLWKFTPLHEAAAKGYE 680
Db 515 SQGAELDAQQRNLRTPLHLAVERGKVRAIQHLKSGAVPDALDQSGYGPLHTAAARGKYL 574
Qy 681 ICKLLQHGADPTKKNRDGNTPLDLVKDGDTDIQDLLRGDAALLDAAKGCCLARVKKLSS 740
Db 575 ICKMLLYGASLELPTHQGWTPHLH-----AAYKGHL-EIIHLLA 613
Qy 741 PDNVNCRDTQGRHSTPLHLAAGYNNLEVAEYLLQHGADVNAQDKGGLIPLHNAASYGHVD 800
Db 614 ESHANMGALGAVNWTPLHLAARHGEAEVVSALLQCGADPNAEQSGWTPHLAVQSTFL 673
Qy 801 VAALLIKYNACVNATDKWAFTPLEHAAKQRTQICALLAHGADPTLKNQEGQTPDL 858
Db 674 SVINLLEHNVHARNKVGWTPAHLAALKGNNTAILKVLVEAGAQLDVQDGVSCCTPLQL 731

RESULT 15
US-11-317-329-40
; Sequence 40, Application US/11317329
; Publication No. US20060105413A1
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
; FILE REFERENCE: UM-06967
; CURRENT APPLICATION NUMBER: US/11/317,329
; CURRENT FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/128,174
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-317-329-40

Query Match
Best Local Similarity 30.1%; Score 465; DB 7; Length 765;
Matches 144; Conservative 65; Mismatches 181; Indels 88; Gaps 8;

Qy 385 KSAIDLAP----TPOLKERLAYEFKSHLSLQAAREADVTRIKKHLSELMVNFKHPQTHET 440
Db 338 KRALQLSDRKNLVRDEELCIYENKVTPLQFLVAQGSVEQVRLLLA-----HEV 386
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